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Networks of task co-activations

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ABSTRACT

Recent progress in neuroimaging informatics and meta-analytic techniques has enabled a novel domain of human brain connectomics research that focuses on task-dependent co-activation patterns across behavioral tasks and cognitive domains. Here, we review studies utilizing the BrainMap database to investigate data trends in the activation literature using methods such as meta-analytic connectivity modeling (MACM), connectivity-based parcellation (CPB), and independent component analysis (ICA). We give examples of how these methods are being applied to learn more about the functional connectivity of areas such as the amygdala, the default mode network, and visual area V5. Methods for analyzing the behavioral metadata corresponding to regions of interest and to their intrinsically connected networks are described as a tool for local functional decoding. We finally discuss the relation of observed co-activation connectivity results to resting state connectivity patterns, and provide implications for future work in this domain.

Introduction

The study of connectomics predominantly involves investigation of the functional and structural connectivity of the human brain through the use of functional magnetic resonance imaging (FMRI), diffusion tensor imaging (DTI), and structural MRI. To this end, a massive amount of data is being acquired, analyzed, and published to provide a more complete understanding of the organization and interactions between cortical and subcortical brain regions that enable human cognition. Prominent and valued databasing projects include BrainMap (http://brainmap.org; Fox and Lancaster, 2002; Laird et al., 2005a), Neurosynth (http://neurosynth.org; Yarkoni et al., 2011), OpenfMRI.org, 1000 Functional Connectomes/INDI (Mennes et al., in press), the Human Connectome Project (Van Essen et al., 2013), BIRN (Fennema-Notestine, 2009; Keator et al., 2008), OASIS (Marcus et al., 2007a), and XNAT Central (Marcus et al., 2007b). Two decades of progress in neuroinformatics research is now coming to fruition, as these databases are being used to aggregate, synthesize, and mine the collective work of the neuroimaging community. Many of these projects archive resting state FMRI (rs-FMRI), DTI, or structural MRI data, but others focus on neuroimaging results acquired during activation studies. While these data are less recognized in connectomics discussions, the repositories of the task-based FMRI and PET literature offer significant opportunity to expand our knowledge of task-dependent functional connectivity.

Here, we review studies describing task co-activation networks, which identify and examine networks of brain regions that are consistently observed to activate in coordination with each other across a range of experimental neuroimaging tasks and paradigms. These networks are derived from meta-analytic methods, in which sets of activation patterns are extracted across multiple published studies in the form of three-dimensional stereotactic coordinates and assessed for convergent spatial locations. We review a range of meta-analytic techniques for investigation of task co-activation networks, from meta-analytic connectivity modeling (MACM) that examines seed-based co-activations for a user-defined region of interest, to connectivity-based parcellation (CBP) that computes these MACM patterns at the level of voxels and investigates their similarity using clustering techniques, to independent component analysis (ICA) of large scale brain networks archived in a task activation database. We also address how activation databases may allow functional interpretation of regions or networks of interest via forward or reverse inference methods. While the methodology differs, each of these methods has been developed to provide a more

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complete understanding of functional connectivity, but in the context of while active during a range of goal-directed tasks.

Many of these approaches have been implemented in conjunction with the BrainMap database, which has been a key resource for developing and applying meta-analytic methods in both healthy and clinical populations across a range of behavioral conditions examining action, cognition, emotion, perception, and interoception (Laird et al., 2009a). The BrainMap database was created in 1988 and has been in steady development since. In addition to published three-dimensional stereotactic coordinates in Talairach (Talairach and Tournoux, 1988) or MNI (Collins et al., 1994; Evans et al., 1993) space that both standardize and summarize the spatial locations of brain activations, BrainMap also archives extensive metadata that furnish formalized descriptions of a study's experimental design, including subject population and behavioral task conditions, as well as relevant details of imaging and analysis parameters (Fox et al., 2005). Given the prior success of BrainMap to provide a schema of annotations for functional neuroimaging studies, this metadata taxonomy was eventually extended into a cognitive paradigm ontology (CogPO; Turner and Laird, 2012) for use by other databasing projects.

The introduction of a coordinate-based meta-analysis method by Turkeltaub et al. (2002) led to dramatic increases in the utility and application of BrainMap. This algorithm allowed neuroimagers interested in pooling brain activation patterns to assess groups of studies for consistency and spatial convergence. Since then, the activation likelihood estimation (ALE) method has gone through several iterations of improvements and extensions (Eickhoff et al., 2009, 2011, 2012; Laird et al., 2005b; Turkeltaub et al., 2012), and has been applied in currently over 200 published meta-analyses across a wide range of cognitive neuroscience topics. ALE meta-analyses can be performed using the BrainMap *GingerALE* application (http://brainmap.org/ale).

Meta-analytic connectivity modeling

The majority of published ALE meta-analyses are carried out by domain experts who limit their literature searches to an often-narrow set of inclusion criteria, which are focused on specific paradigms of interest. Instead of limiting such synthesis of studies to a particular domain, other meta-analytic approaches have sought to examine functional co-activations of a given region of interest across a domain-arching pool of studies examining different mental tasks and functions (Koski and Paus, 2000; Postuma and Dagher, 2006). This general concept was extended across the whole brain and applied to a larger corpus of the literature when Toro et al. (2008) mined 3402 experiments (published in a total of 825 scientific papers) in the BrainMap database and seeded regions to identify the corresponding whole-brain co-activation profile of these seeds. Thus for every voxel in stereotactic space, they produced a meta-analytic co-activation image that contained a complete three-dimensional volume of that voxel's individual co-activations with the whole brain, yielding nearly 45,000 individual brain volumes (one for every 4 mm^3 voxel in the brain). The result was a query tool that allowed a user to graphically specify a region of interest and be shown an image of which regions co-activate with that seed location. Toro et al. noted that the individual meta-co-activation maps were strongly similar to seed-based correlation maps derived from rs-FMRI data, and many of the volumes presented complex patterns of cortical and subcortical regions of co-activation. Given that a group of regions consistently reported to concurrently change activity across various experiments associated with coordinated execution of mental goals, the authors followed that they therefore were functionally connected. Using this method, Toro et al. were able to recover canonical functional brain networks of many cognitive domains, such as the cortico-diencephalo-cerebellar motor network, the default mode network, and the fronto-parietal attention network. Notably, these co-activation maps demonstrated some of the brain's fundamental connectivity principles, such as a higher degree of connectivity in the near-neighborhood of the seed region, as well as symmetric interhemispheric connections (Fig. 1). This study was the first to propose that meta-analytic co-activations provide a novel measure of functional connectivity, which reflects task-based activations, and is therefore complementary to resting state correlations. Source code for a co-activation map graphic user interface has been made available for this work, available at http://coactivationmap.sourceforge.net.

Once it was established that meta-analytic task co-occurrences provide an alternate means to examining functional connectivity, a new method was introduced for interrogation of whole brain co-activation patterns of user-defined seed regions, which was termed meta-analytic connectivity modeling (MACM). The first step of performing MACM on a region of interest is to filter a task activation database, such as BrainMap or NeuroSynth, for those experiments that feature at least one focus of activation within the seed region. Only studies reporting group analyses of functional mapping experiments of healthy subjects should be considered in the search, while those dealing with disease or drug effects or any other between-subject comparison should be excluded. For the analysis of significant co-activations and task-dependent functional connectivity, a meta-analysis, such as activation likelihood estimation, is performed over all foci of the retrieved experiments to quantify their convergence. As all of the experiments are identified in the database by virtue of featuring at least one activation within the seed region, the highest degree of convergence will inevitably be found in that region. Significant convergence outside the seed indicates the above-chance recruitment of additional areas whenever the seed was active, i.e., significant co-activation. MACM was first applied to provide new insight into the task-based functional connectivity of regions of the default mode network (Laird et al., 2009b), the amygdala (Robinson et al., 2010) and the parietal operculum (Eickhoff et al., 2010). This approach is part of the growing field of investigations into the functional connectivity of specific pre-defined seed regions. Such studies usually start with an anatomically (by external knowledge of histological or macroscopical brain architecture) or functionally (by activation information from prior neuroimaging experiments or meta-analyses) defined region of interest, often derived from a previous study (Jakobs et al., 2012). The aim of seed-based connectivity mapping is to identify brain regions that are significantly related to and presumably interact with the seed.

In Laird et al. (2009b), regions of the default mode network (DMN) were isolated from in the BrainMap database by performing an ALE meta-analysis of all coordinates reported as task-related *decreases* during cognitive subtraction experiments using rest or fixation as a control condition. Once identified, these regions of convergence deactivation were then individually seeded and analyzed using MACM to identify their whole-brain co-activation patterns in the context of task-related *increases*, which included both within-DMN and non-DMN connections. Fig. 2 illustrates how the network of task-related decreases showed substantial overlap with a seed region's co-activation network for some regions (e.g., posterior cingulate cortex and right middle temporal gyrus), while other seeds demonstrated minimal overlap (e.g., right inferior parietal cortex and ventral anterior cingulate cortex). This suggested increased or reduced coherence, respectively, between a region's role in DMN functioning and their role in task-based activity across a range of behavioral conditions (Laird et al., 2009b).

The MACM approach can also be applied as a means to investigate the functional interactions of histologically defined areas to provide a link between (micro-) structure, function, and connectivity (Bzdok et al., in press; Eickhoff et al., 2010). Alternatively, a key application is the characterization of morphometric findings, i.e., brain regions showing atrophy in a particular group of patients or a significant association with a particular behavioral trait (Reetz et al., 2012). Such findings are as commonplace in the literature as they are difficult to interpret. The main challenge lies in the fact that the investigation used to

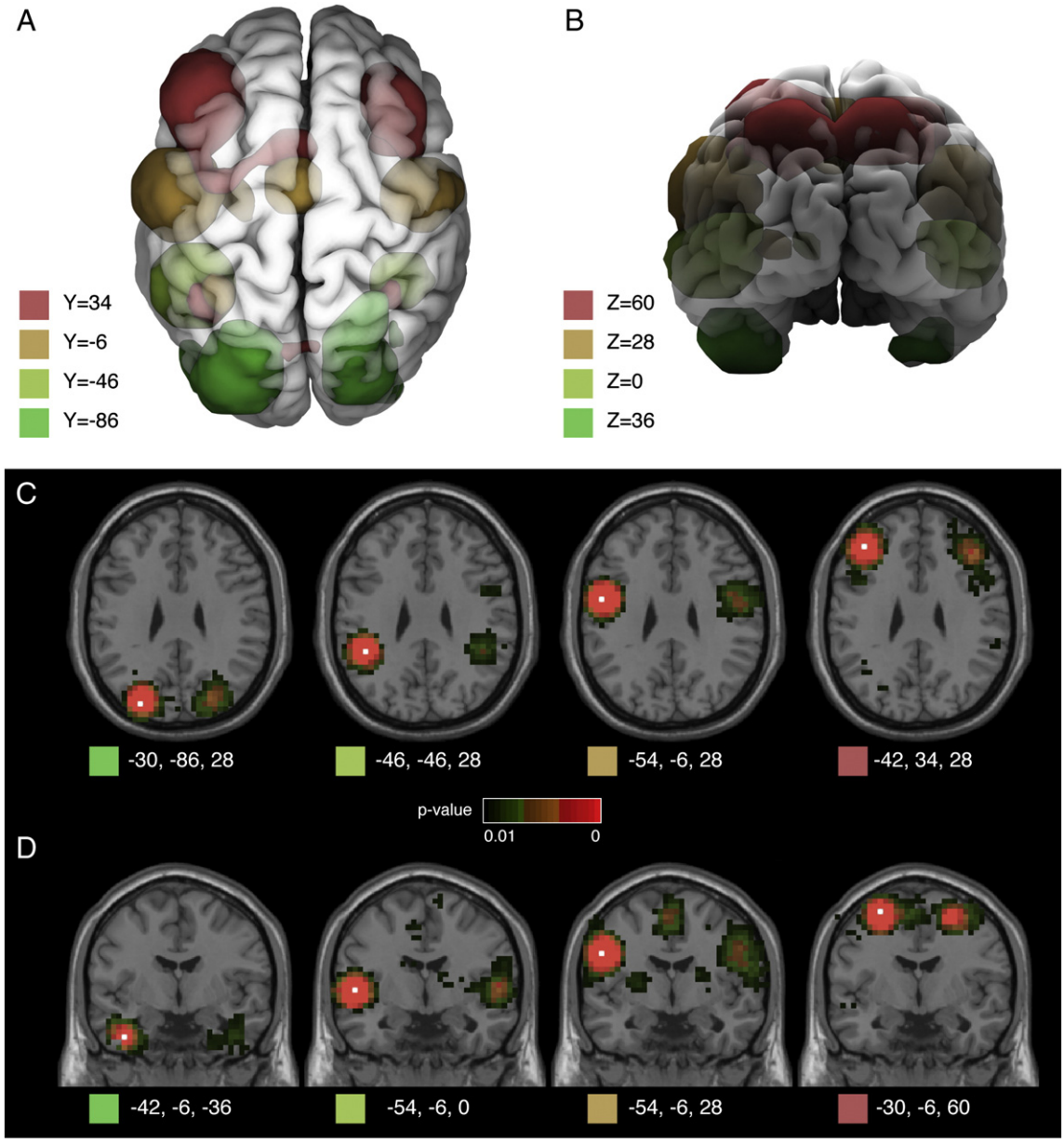

Fig. 1. Meta-analytic maps demonstrating symmetric interhemispheric co-activations. In one of the first applications that examined task-based functional connectivity patterns using a database approach, a graphical user interface was created that allowed users to specify a seed location, which produced corresponding whole-brain meta-analytic co-activation profiles. Co-activation networks corresponding to seed location voxels are shown. Seed regions in a given hemisphere generally showed strong co-activation with symmetric regions in the opposite hemisphere, as shown for volume reconstructions (A, B) as well as specific slices in the axial (C) and coronal planes (D). Seed locations are indicated by the white squares seen in the slice images. For more details, see http://coactivationmap.sourceforge.net and Toro et al. (2008).

provide the respective effect (usually some form of voxel-based morphometry or cortical thickness mapping) does inherently not contain any information about the function or connectivity associated with the respective findings, opening the door for subjective and hence potentially biased reverse inference (Poldrack, 2006). MACM analyses can be performed using the BrainMap *Sleuth* (http://brainmap.org/sleuth) and *GingerALE* applications (http://brainmap.org/ale); alternatively, co-activation maps can be generated within the web interface of the NeuroSynth Project (http://neurosynth.org).

Connectivity-based parcellation

A new and still developing extension of MACM analyses is its application to connectivity-based parcellation (CBP) as an approach to identify functionally homogenous sub-clusters of voxels within a seed region. The key idea behind CBP is to perform whole-brain connectivity analysis individually for each and every voxel within the seed region of interest. The connection strength of all other voxels in the brain are then recorded and aggregated into an $N_s \times N_t$ connectivity matrix, with N_s being the number of voxels in the seed region and N_t the number of voxels in the rest of the brain serving as the target. The difference in these whole-brain connectivity profiles is then computed between any pair of voxels with the seed region, yielding a distance matrix reflecting the dissimilarity between all different seed voxels (cf. Johansen-Berg et al., 2004 for an early implementation of this idea). The next step in a CBP analysis is to cluster the seed voxels into distinct groups in such a manner that the voxels within a cluster feature a similar whole brain connectivity pattern, whereas the patterns of the different clusters are maximally different. The actual clustering method has, however, varied greatly over studies. Early

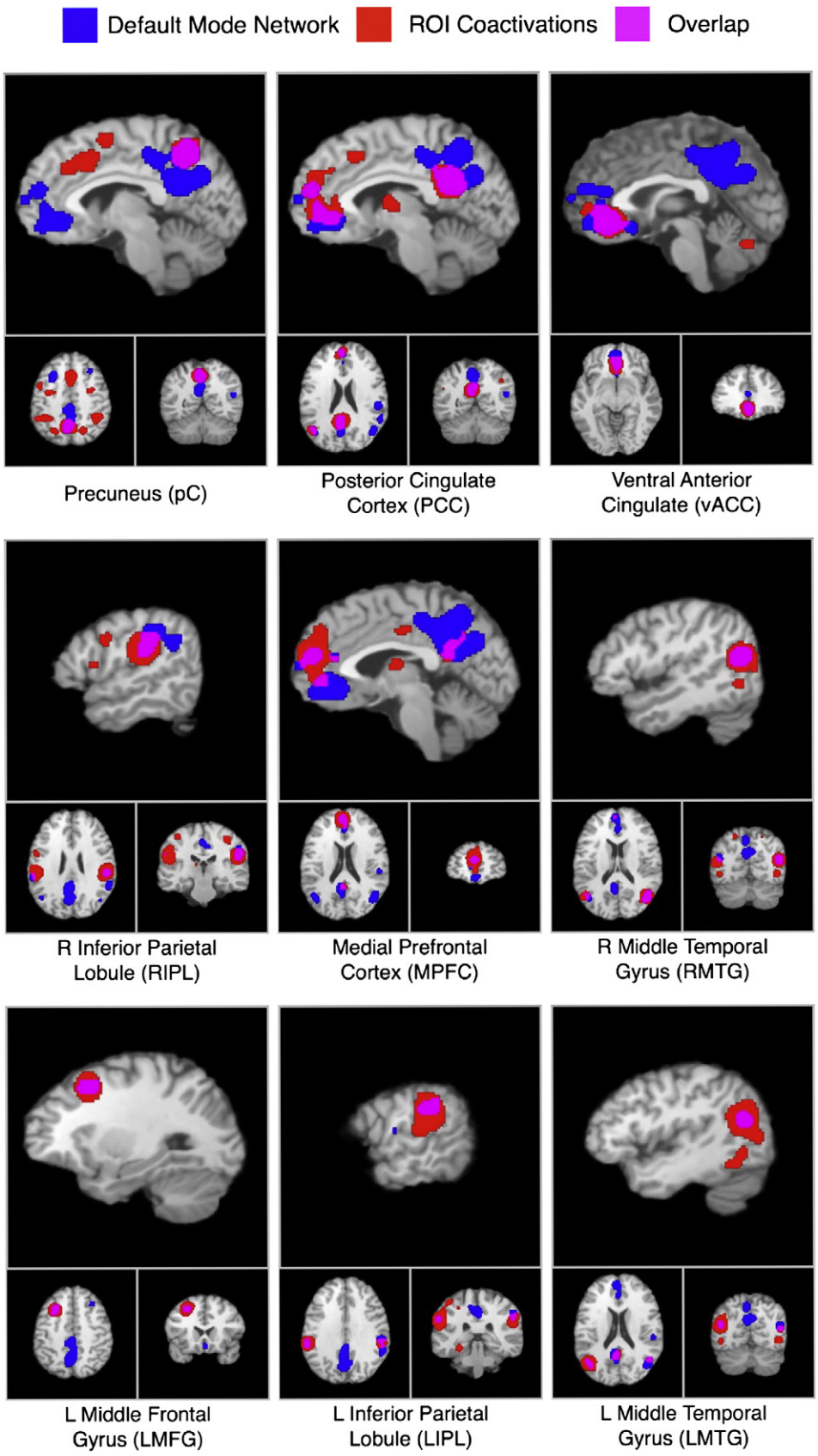

Fig. 2. Meta-analytic connectivity modeling. Composite images are shown of the meta-analytic default mode network of task-related *decreases* (blue) and MACM maps of task-related *increases* for each seed region of the DMN (red). Substantial overlap was observed for some regions (e.g., PCC and RMTG), while other regions showed minimal overlap (e.g., RIPL and vACC). For more details, see Laird et al. (2009b).

applications have used a semi-automated approach based on spectral reordering of the distance matrix (Johansen-Berg et al., 2004; Kelly et al., 2010), while later applications have used *k*-means (Cauda et al., 2011; Kahnt et al., 2012; Kim et al., 2010; Nanetti et al., 2009) or hierarchical clustering analysis (Bellec et al., 2006; Bzdok et al., in press; Cordes et al., 2002).

It is important to note that the CBP approach described above is completely independent of the modality on which the whole-brain connectivity profiles are based. While originally described for anatomical connectivity measures based on diffusion-weighted images (Johansen-Berg et al., 2004) and resting state functional connectivity (Cordes et al., 2002; Kelly et al., 2010; Kim et al., 2010; van den Heuvel et al., 2008), the very same concept may also be applied to task-based functional connectivity measures, i.e., MACM. Similar to procedures employed in the other modalities mentioned above, the whole-brain co-activation pattern is first computed for each voxel within the seed region. Subsequently, a distance matrix is computed, indicating the degree of dissimilarity between the co-activation profiles of each voxel. Finally, the voxels are clustered into distinct sub-regions of the original seed based on this information. In order to characterize the differences in whole-brain co-activation patterns between the ensuing clusters and hence the variations in connectivity that drove the parcellation of the seed region, follow-up MACM analyses are usually performed using the derived clusters as seeds. MACM-CBP is a relatively new technique for identifying connectivity-based sub-regions of a seed volume, but has already provided new insight into the functional segregation of the pre-SMA and SMA (Eickhoff et al., 2011), dorsolateral prefrontal cortex (Cieslik et al., 2013), and the amygdala (Bzdok et al., in press). Using this technique, Fig. 3 illustrates the remarkable correspondence observed between cytoarchitectonic- (left) and connectivity- (right) based parcellations of the amygdala into the laterobasal, centromedial, and superficial nuclei groups. The study by Bzdok et al. (in press) is an excellent example of how newly developed neuroimaging analysis methods are providing the means to investigate concurrence across structural, connectional, and functional sub-specialization, which is critical for progress in connectomics research.

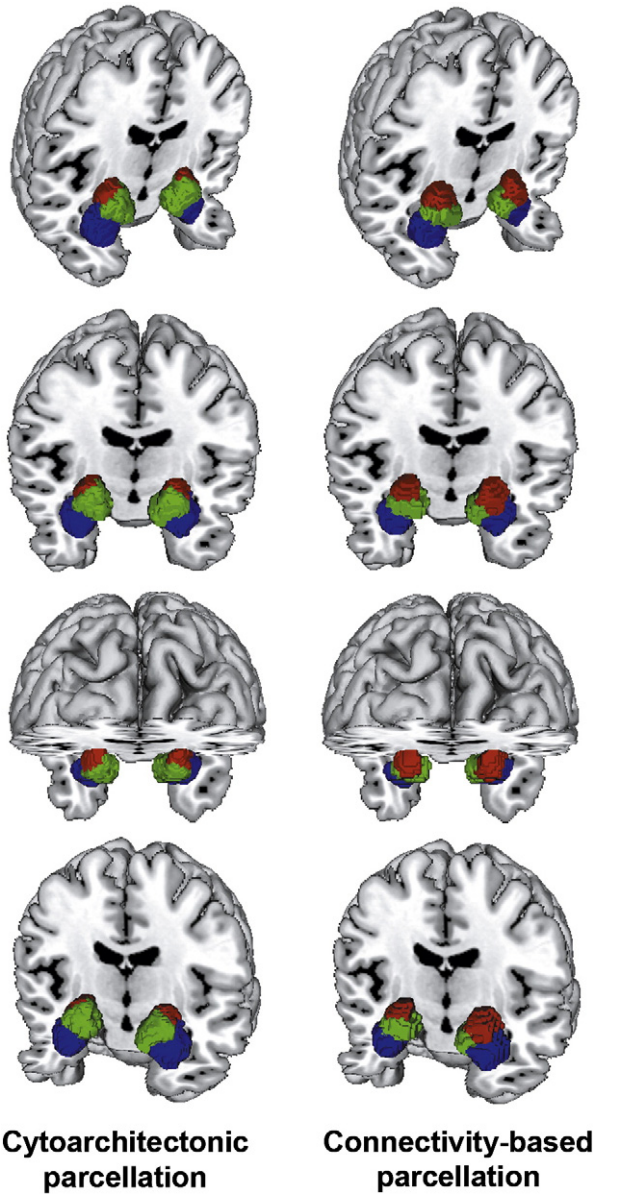

Fig. 3. Connectivity-based parcellation. Both cytoarchitectonic (left) and connectivity-based (right) parcellation analyses were performed, yielding a strong agreement in spatial continuity and localization for sub-regions corresponding to the laterobasal (blue), centromedial (red), and superficial (green) nuclei groups. For more details, see Bzdok et al. (in press).

Discovery of ICA-derived co-activation networks

The early correlational work of Biswal et al. (1995) provided a tantalizing hint that functionally connected networks could be studied in resting state FMRI data. During the mid to late 2000's an increasingly large group of neuroimagers became intrigued by the investigation of resting state networks (RSNs) derived from independent component analysis (ICA) of rs-FMRI data. With the advent of ICA to the neuroimaging community, the trend of studying individual seed-based networks was broadened to utilize resting state data to simultaneously investigate many of the brain's functionally connected RSNs at once (Beckmann et al., 2005; Damoiseaux et al., 2006). Using ICA, FMRI data are decomposed into sets of d networks, which typically range from a low model order (e.g., $d = 20$) to a high model order (e.g., $d = 100$). Generally speaking, low model ICA decompositions provide a broad assessment of large-scale resting state networks, while high model decompositions offer more finely-grained examination of these networks, yet also provide a more complete understanding of the complexities associated with how the low model order networks fractionate into higher model order sub-networks as d is increased (Abou-Elseoud et al., 2010).

Given evidence that the brain's functional networks could be extracted from correlations of co-activation data (Toro et al., 2008), and the first set of results provided by MACM (Eickhoff et al., 2010; Laird et al., 2009b; Robinson et al., 2010), it was hypothesized that meaningful inferences could be made across a broad range of functional brain networks by direct comparison of co-activation networks with resting state networks. Thus, in a seminal publication, Smith et al. (2009) independently applied ICA to two types of data: first, from data acquired during rs-FMRI in 36 individual subjects, and second, to group results of task activation patterns from 7342 neuroimaging experiments (1687 publications) archived in the BrainMap database. For the BrainMap data, co-occurrence of different activation locations was investigated across the range of tasks in the database by using ICA to estimate the low model order (i.e., $d = 20$) set of spatial maps and associated time series of the major networks of covariance in the brain. When ICA is applied to BrainMap data, which are 3D sets of Gaussian modeled activation images, the fourth dimension of the data matrix analyzed refers “experiment ID” (rather than “time” in rs-FMRI data), such that each time point in one component's “time course” describes how strongly the observed spatial map relates to that particular experiment's activation image in BrainMap. When the results of these independent analyses were compared using spatial Pearson cross correlation, Smith et al. demonstrated that over two-

thirds of the non-artifactual networks at $d = 20$ matched across resting state and task-based conditions (e.g., 10 of 20 components), and that functional characterization of these networks was possible using BrainMap metadata. These networks have also been extracted from the NeuroSynth database (Yarkoni et al., 2011) using a topic mapping approach (Poldrack et al., 2012), adding to the evidence that these networks represent fundamental components of the brain's functional architecture. Moreover, when the BrainMap task networks were closely examined by Laird et al. (2011) in comparison to the ICA-derived resting state networks observed by Biswal et al. (2010), it was shown that the degree of correspondence across the sets of resting state and task co-activation networks increased from the initial estimate provided by Smith et al. (2009). Indeed, 12 of the non-artifactual components were an excellent match to those published by Biswal et al., whereas four components were a close partial match. This improved rate of agreement was attributed to the greater sample size studied, which was increased from 36 subjects in Smith et al. (2009) to 306 subjects in Biswal et al. (2010). Ongoing work is being carried out to assess the degree of agreement for higher model orders (e.g., $d = 70, 100$). Regardless, the Smith et al. (2009) study demonstrated that the major task-based functional networks in the active brain show similar organization to those of the majority of the networks of spontaneous covariation in the resting brain. The important implication here is that the resting state can be shown to be inclusive of the brain's functional dynamics from a range of mental tasks. Moreover, there is an intrinsic organization to the brain's functional networks, whose topography is invariable during rest and task.

Functional interpretation of co-activation networks

Across different imaging modalities, mapping the whole-brain connectivity of large-scale brain networks or specific regions of interest generates quantitative and statistically testable information concerning connectivity and interactions across neural regions. In rs-FMRI, relating functional brain networks to specific mental functions is difficult, since by definition the resting state lacks behavioral specificity. Although recent work demonstrates that intrinsic connectivity networks can be related to specific behavioral measures (Meier et al., 2012; Mennes et al., 2011), more progress is needed to address this gap in our knowledge. The combination of meta-analytic investigations and databases such as BrainMap offer an opportunity for this in that they also allow inference on the characteristics and properties of experiments that underlie the co-activations. A wealth of information concerning the experimental design and methodological details of each archived experiment is coded in BrainMap according to a well-defined taxonomy, which has been refined by experts in the field for nearly two decades. Neuroinformatics tools have subsequently been developed to exploit this valuable source of information to provide associations with psychological constructs and thus potential functional interpretations for a specific region or regions of interest.

As a follow-up to the Smith et al. (2009) publication, Laird et al. (2011) sought to provide a more complete functional characterization of the 20 low model order networks. In this study, a slightly larger volume of the literature was available in BrainMap, and hence included 8637 experiments from 1840 publications. The BrainMap metadata taxonomy includes the fields of “Behavioral Domain” and “Paradigm Class” that characterize experiments resulting in activation of the specified region of interest. The behavioral domain (BD) of a particular experiment identifies the mental process isolated by the statistical contrast of images, and includes the main categories of cognition, action, perception, emotion, and interoception, as well as their related sub-categories (Fox et al., 2005). Paradigm class (PC) categorizes the specific task employed in the published study (Turner and Laird, 2012). A metadata matrix that quantified the relationships between the ICA component images and BrainMap experimental metadata for BDs and PCs was generated and analyzed with hierarchical clustering to determine groupings of similar metadata classes as well as similar sets of networks. Fig. 4 provides a summary of the spatial topography of the 20 low order BrainMap co-activation networks shown by Laird et al. (2011), which match those originally presented by Smith et al. (2009) and demonstrate strong correspondence to resting state networks. Clustering results revealed that the BrainMap co-activation networks could be classified into 4 groups relevant to their associated mental processes: [1] emotional and interoceptive processes that included networks for limbic and medial temporal areas, subgenual ACC and OFC, bilateral basal ganglia and thalamus, bilateral anterior insula and anterior cingulate cortex; [2] motor and visuospatial integration, coordination, and execution that included premotor and supplementary motor cortices, DLPFC and posterior parietal cortices, hand areas of the primary sensorimotor cortices, and superior parietal lobule; [3] visual perception, including visual association cortices, as well as lateral and medial posterior occipital cortices; and [4] higher cognitive processes that included the default mode network, cerebellar network, right-lateralized fronto-parietal cortices, auditory cortices, mouth areas of the primary sensorimotor cortices, and left-lateralized fronto-parietal cortices. Complete functional explication of the BrainMap behavioral metadata associated with these networks was provided by Laird et al. (2011), and the results of these analyses have been shared with the community with the aim that they will be useful for functional interpretations of observed resting state networks in both healthy and clinical investigations (www.brainmap.org/icns).

While this prior work focuses on developing methods to examine the functional or behavioral interpretation of large-scale brain networks using BrainMap metadata, similar methods may be applied to individual regions of interest. Subsequent to applying MACM, functional decoding may be performed on a given region of interest, again using the BD and PC metadata fields. The behavioral functions consistently associated with the particular part of the brain identified as a region of interest are quantitatively inferred by testing which of the different BDs and PCs are significantly over-represented among the experiments that featured activation in the seed. In other words, a BrainMap metadata analysis identifies which types of experiments are more likely than one would expect by chance to result in activation of the seed region. Similarly, functional interpretation techniques are also provided by the NeuroSynth Project (Yarkoni et al., 2011; http://neurosynth.org). In contrast to BrainMap, which relies on manual annotation of neuroimaging experiments by its user community, NeuroSynth has implemented automated harvesting of three-dimensional stereotactic and annotations that are tagged for each publication representing terms that occur at high frequency (i.e., 20 or more studies). A list of several thousand text-mined terms has been generated that allows quantitative associations to be made between a specific term and a given region of interest. NeuroSynth's web interface provides access to tools capable of quickly generating dynamic meta-analysis maps representing term-based maps or co-activation maps.

Using their different frameworks for manual and automated annotations, BrainMap and NeuroSynth provide tools for examining both forward inference (i.e., how likely is the region activated given a particular taxonomic label?) and reverse inference (i.e., how likely is a particular taxonomic label given activation in this region?) (Yarkoni et al., 2011). In other words, forward inference on the functional characterization tests the probability of observing activity in a brain region given knowledge of the psychological process, whereas reverse inference tests the probability of a psychological process being present given knowledge of activation of a particular brain region. While both are usually considered in the functional interpretation of an effect, reverse inference is somewhat closer to the colloquial meaning of the question “what is this region doing?”. However, the results of this reverse inference analyses are also more dependent on the *a priori* structure of the database queried or the kind of experiments that are routinely carried in functional neuroimaging studies. That is, if a

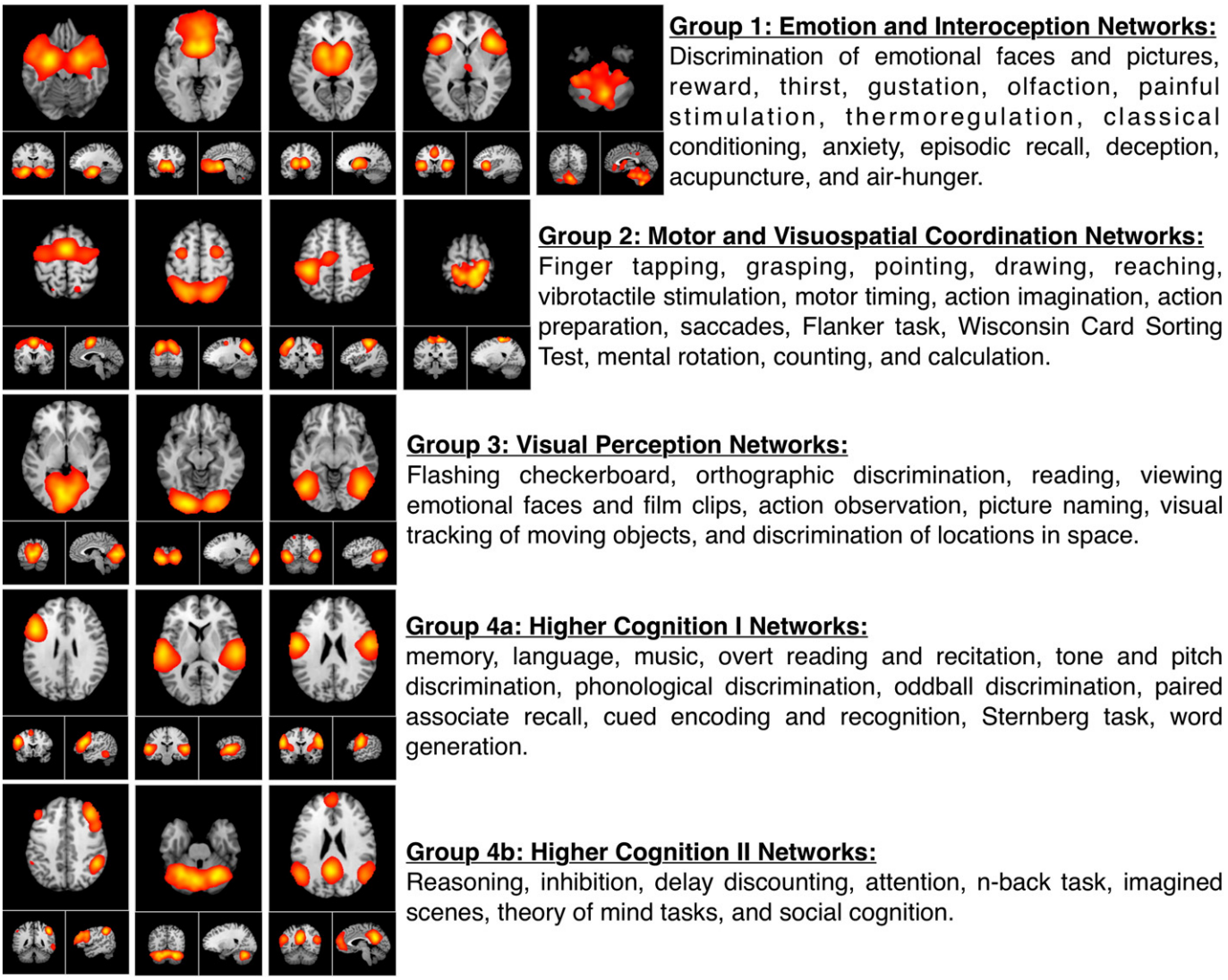

Fig. 4. ICA-derived co-activation networks. ICA was used to decompose BrainMap experiment images into 20 spatially co-occurring maps of task co-activation networks. The spatial topography of these maps is seen after the ICA maps were converted to *z* statistic images and thresholded at $z > 4$. Hierarchical clustering was performed on the corresponding BrainMap metadata for each network, yielding groups of similar network functions. Group 1 was associated with emotional and interoceptive processes, Group 2 with motor and visuospatial integration and execution, Group 3 with visual perception, and Group 4 with higher cognition. Two of the observed components were artifactual (not shown). For more details, see Laird et al. (2011).

database contained a dramatically larger percentage of studies focusing on emotion as compared to cognition or action, then there may be an increased probability of observing emotion in association with a given region of interest, simply due to the over-representation of studies.

The BrainMap behavioral metadata procedure was initially presented by Laird et al. (2009b) in a functional characterization of regions of the default mode network. Other studies have utilized this functional characterization method for regions of interest, such as the amygdala (Bzdok et al., in press), caudate (Robinson et al., 2012), and the orbitofrontal cortex (Zald et al., in press). A new method of providing automated functional labels to a region or regions of interest has been released as part of the Mango software package (http://ric.uthscsa.edu/mango; Lancaster et al., 2012).

Comparisons to resting state connectivity

What has been learned thus far is that task-based co-activation networks demonstrate remarkable correspondence to other measures of functional connectivity, such as resting state connectivity. However, this is not to say that these sets of networks from dramatically disparate data sources are identical. While MACM may reveal brain regions showing significant task-based functional connectivity with a seed region, this describes only one particular aspect of brain connectivity among many others (cf. Eickhoff and Grefkes, 2011). Consequently, the obtained results may potentially reflect biases in experimental design, analysis, or reporting of neuroimaging results that have not yet been characterized. Regardless, they do reflect a very specific and important aspect of functional brain networks. As a result, the multi-modal assessment of functional connectivity using multiple independent measures aimed at delineating different characteristics of brain networks has become an important line of research. Generally, the most commonly employed method for studying multi-modal functional connectivity is to compare task-based connectivity to correlations in low-frequency BOLD activation in the absence of a particular task, i.e., resting state analyses.

To exemplify this type of comparison, we focus on a region in the vicinity of right visual area V5 (Malikovic et al., 2007) that was previously found to show convergent evidence for structural aberrations in an ALE meta-analysis of voxel-based morphometry studies in patients diagnosed with autism-spectrum disorder (ASD; Nickl-Jockschat et al., 2012). This ROI (Fig. 5, inset) was seeded in the BrainMap

database, yielding 198 experiments (performed on 2811 subjects and reporting a total of 3320 foci). As seen in Fig. 5A, MACM results across these 198 experiments indicated significant co-activation between the V5 region affected in ASD and the bilateral lateral occipital cortex, inferior parietal cortex, inferior frontal cortex including the ventral premotor cortex and BA 44 (Broca's area), and anterior insula and frontal operculum ($P < 0.05$, cluster-level corrected for multiple comparisons). A separate analysis was then performed in which the same right visual area V5 region was seeded in resting state FMRI data from a group of 132 healthy subjects derived from the NKI/Rockland sample (Nooner et al., 2012), using standard preprocessing and analysis methods. Fig. 5B reveals that the resting state approach yielded much more extensive functional connectivity in comparison to the MACM approach with almost all posterior parts of the brain, including the ventral and dorsal occipital cortex, as well as the inferior and superior parietal lobe. Significant resting state connectivity with the premotor cortex was also found, but with a stronger emphasis on its dorsal aspect than observed in the task-dependent data. When computing the conjunction between both approaches, the occipital and parietal regions that featured significant MACM and resting state connectivity with the V5 seed closely resembled those found in the MACM analysis (Fig. 5C). In turn, significant frontal connectivity that was robust over both analyses was only observed in a small cluster of the left precentral gyrus and a larger one in the right inferior frontal gyrus located within BA 44 and the adjacent ventral premotor cortex.

In light of the as-yet limited number of studies combining MACM and resting state functional connectivity analyses (Cieslik et al., 2013; Eickhoff et al., 2011; Jakobs et al., 2012; Reetz et al., 2012; Rottschy et al., in press), the above results obtained for the V5 region that was shown to be structurally affected in ASD features several typical aspects. First, all of these previous studies demonstrated the presence of robust networks of functional interaction with a seed region that are likewise present in both approaches for mapping whole-brain functional interactions. Given the independent nature of the data as well as the conceptual and methodological differences between MACM and resting state analyses, this convergence holds important implications. In particular, the ensuing regions may be considered a "core" network that is robustly interacting with the seed independent of whether the subjects are in a self-referentially, endogenously controlled mind-wandering state (cf. Schilbach et al., 2012 for a psychological interpretation of this mental state) or in an exogenously driven state imposed by a structured experimental paradigm. That is, these regions showing significant association across methods and mental states may be deemed the most robust and consistent interactions of the seed. Another rather frequent observation is the fact that in addition to this core network there are usually also appreciable differences in the revealed interactions. These differences demonstrate that in spite of the same underlying concept of "functional connectivity", MACM and resting state analyses actually do reflect different information about brain connectivity. In this respect, resting state correlations often tend to show a more extensive network when thresholded at the same level of significance. In contrast, regions exhibiting significant MACM co-activation but not resting state functional connectivity are much more sparse. Nevertheless, as shown by the example focusing on right visual area V5, those regions nevertheless commonly exist (e.g., the anterior insula/frontal operculum). There are multiple different factors that may contribute to this kind of pattern. The potentially most interesting one pertains to the difference in mental states, i.e., endogenously vs. exogenously orientation of attention. Following this line of reasoning, the differences observed between MACM and resting state analyses could reflect differences in functional interaction that are conditioned upon the current mental state of the subjects. However, technical and conceptual differences between both approaches, as alluded to above, may not be discounted either. Consequently, it must remain open at present, whether the observed differences reflect primarily differential biases (or even artifacts) of the two methods or true differences in interaction patterns of the seed region dependent on the mental state of the subjects.

Limitations or considerations for the co-activation approach

The meta-analytic approach for identifying functionally co-activated brain networks is an appealing area of connectomics research since it allows for insight into the brain's connectivity during the engagement of goal-directed behavior. However, this behavior is not limited to a single, specific task, but encompasses a diverse range of tasks. This is both an advantage and a disadvantage, depending on one's research perspective. Although we place much emphasis on the results of Smith et al. (2009), which revealed strong *similarity* between resting state and co-activation networks, it is important to consider that these networks are not explicitly *identical*. Recent work by Mennes et al. (2013) has shown that the relationship between intrinsic and extrinsic connectivity is quite complex, and that evoked interaction patterns show weaker correspondence to intrinsic connectivity networks, particularly for subcortical and limbic regions, as well as primary sensorimotor areas. There is no substitute for the precision, temporal resolution, and power of a carefully controlled task-based neuroimaging experiment, and we do not advocate abandonment of this domain of research. Rather, we promote simultaneous and symbiotic exploration of what knowledge may be gleaned from a meta-analytic co-activation perspective.

Forward progress in developing meta-analytic methods can be challenging as this data is sometimes construed as being too highly variable and noisy. Clusters of functional brain activations have highly complex and rich shape in three-dimensional space. Extracting the centers of masses of these clusters and analysis of the reported foci of these locations represents a dramatic loss in spatial sensitivity and specificity. Moreover, pooling foci across studies results in a loss of precision with respect to various experimental parameters, such as scanner strength, imaging acquisition and analysis, subject sample size and individual variability, and variations in behavioral conditions. However, it can be reasoned that observation of consistent results across studies despite this variability represents an undeniably powerful response of the brain to task and should therefore be examined to the fullest. Furthermore, the fact that the brain's co-activation patterns can be disentangled to extract functional brain networks not only validates that meta-analysis is indeed an experimentally valid source of data, but it is also telling us something extraordinary about brain organization and how we conceptualize the associations between behavioral tasks and the mental operations they elicit.

Conclusion

While one of the more novel aspects of human connectomics research, task co-activation networks are providing biologically meaningful insight into functional brain dynamics and interactions. Meta-analytic connectivity modeling, connectivity-based parcellation, and behavioral metadata analyses have been successfully applied to regions of the default mode network, visual area V5, and the amygdala, among others. Resting state analyses are undeniably powerful, yet co-activation connectivity via the task activation literature offers a quantitative means to address the behavioral and experimental specificity of a region of interest. Moreover, although there is much work yet to be done, preliminary studies have shown that the level of convergence and divergence in co-activation connectivity and resting state connectivity is quite complex, and may offer increased insight into the relationship between external and internal orienting of attention. Future examination of task co-occurrence networks will focus on elucidating these patterns, and on applying the methods described here to AN even larger array OF cortical and subcortical brain regions.

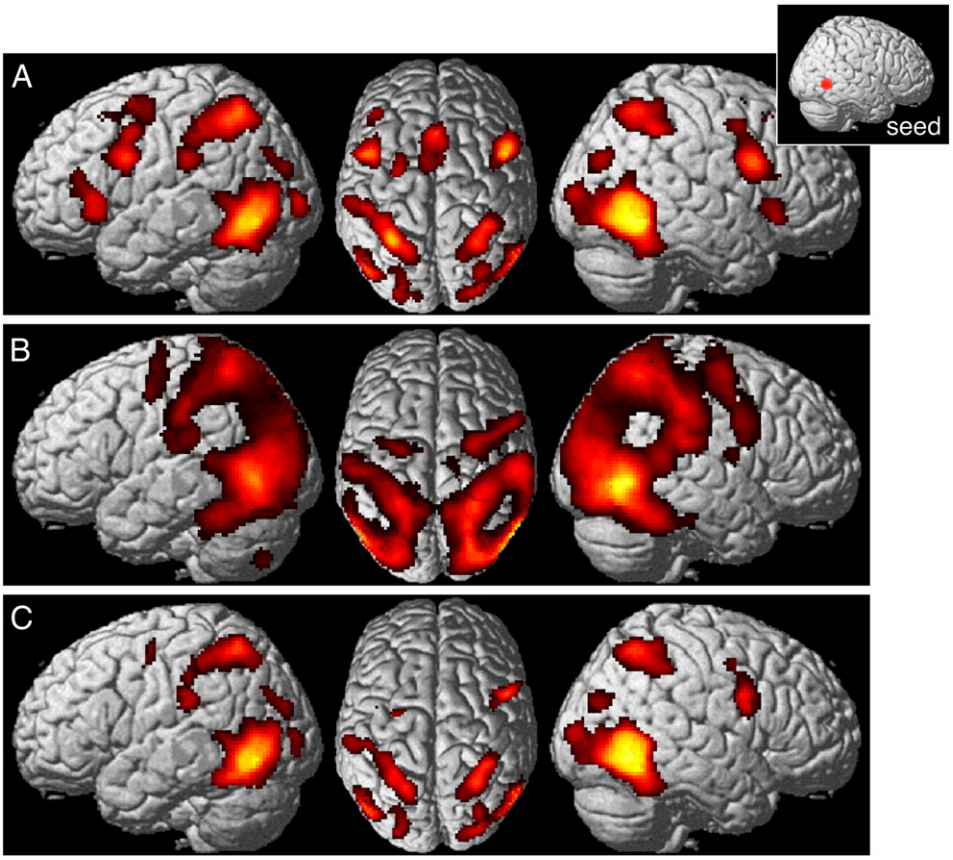

Fig. 5. MACM and resting state functional connectivity of right visual area V5. Previous ALE meta-analysis of VBM studies identified convergent structural aberrations in a region of visual area V5 in ASD patients (Nickl-Jockschat et al., 2012; shown in inset). Results of independent MACM-based functional connectivity (A) and resting state functional connectivity (B) analyses are shown for this V5 seed region. Both sets of connectivity results are visualized at $P < 0.05$, cluster-level corrected for multiple comparisons. Conjunction analysis (C) revealed significant overlap between occipital and parietal regions.

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References

Abou-Elseoud, A., Starck, T., Remes, J., Nikkienen, J., Tervonene, O., Kiviniemi, V., 2010. The effect of model order selection in group PICA. Hum. Brain Mapp. 31, 1207–1216.

Beckmann, C.F., De Luca, M., Devlin, J.T., Smith, S.M., 2005. Investigations into resting-state connectivity using independent component analysis. Philos. Trans. R. Soc. Lond. 36, 1001–1013.

Bellec, P., Perlbarg, V., Jbabdi, S., Pelegrini-Issac, M., Anton, J.L., Doyon, J., Benali, H., 2006. Identification of large-scale networks in the brain using fMRI. Neuroimage 29, 1231–1243.

Biswal, B., Zerrin Yetkin, F., Haughton, V., Hyde, J., 1995. Functional connectivity in the motor cortex of resting human brain using echo-planar MRI. Magn. Reson. Med. 34, 537–541.

Biswal, B.B., Mennes, M., Zuo, X.N., Gohel, S., Kelly, C., Smith, S.M., Beckmann, C.F., Adelstein, J.S., Buckner, R.L., Colcombe, S., Dogonowski, A.M., Ernst, M., Fair, D., Hampson, M., Hoptman, M.J., Hyde, J.S., Kiviniemi, V.J., Kötter, R., Li, S.J., Lin, C.P., Lowe, M.J., Mackay, C., Madden, D.J., Madsen, K.H., Margulies, D.S., Mayberg, H.S., McMahon, K., Monk, C.S., Mostofsky, S.H., Nagel, B.J., Pekar, J.J., Peltier, S.J., Petersen, S.E., Riedl, V., Rombouts, S.A., Rypma, B., Schlaggar, B.L., Schmidt, S., Seidler, R.D., Siegle, G.J., Sorg, C., Teng, G.J., Veijola, J., Villringer, A., Walter, M., Wang, L., Weng, X.C., Whitfield-Gabrieli, S., Williamson, P., Windischberger, C., Zang, Y.F., Zhang, H.Y., Castellanos, F.X., Milham, M.P., 2010. Toward discovery science of human brain function. Proc. Natl. Acad. Sci. 107, 4734–4739.

Bzdok, D., Laird, A.R., Zilles, K., Fox, P.T., Eickhoff, S.B., 2013. An investigation of the structural, connectional, and functional subspecialization in the human amygdala. Hum. Brain Mapp. (in press).

Cauda, F., D'Agata, F., Sacco, K., Duca, S., Geminiani, G., Vercelli, A., 2011. Functional connectivity of the insula in the resting brain. Neuroimage 55, 8–23.

Cieslik, E.C., Zilles, K., Caspers, S., Roski, C., Kellermann, T.S., Jakobs, O., Langner, R., Laird, A.R., Fox, P.T., Eickhoff, S.B., 2013. Is there "One" DLPFC in cognitive action control? Evidence for heterogeneity from co-activation-based parcellation. Cereb. Cortex 23, 223–229.

Collins, D.L., Neelin, P., Peters, T.M., Evans, A.C., 1994. Automatic 3D intersubject registration of MR columetric data in standardized Talairach space. J. Comput. Assist. Tomogr. 18, 192–205.

Cordes, D., Haughton, V., Carew, J.D., Arkanakis, K., Maravilla, K., 2002. Hierarchical clustering to measure connectivity in fMRI resting-state data. Magn. Reson. Imaging 20, 305–317.

Damoiseaux, J.S., et al., 2006. Consistent resting-state networks across healthy subjects. Proc. Natl. Acad. Sci. U. S. A. 103, 13848–13853.

Eickhoff, S.B., Grefkes, C., 2011. Approaches for the integrated analysis of structure, function and connectivity of the human brain. Clin. EEG Neurosci. 42, 107–121.

Eickhoff, S.B., Laird, A.R., Grefkes, C., Wang, L.E., Zilles, K., Fox, P.T., 2009. Coordinate-based activation likelihood estimation meta-analysis of neuroimaging data: a random-effects approach based on empirical estimates of spatial uncertainty. Hum. Brain Mapp. 30, 2907–2926.

Eickhoff, S., Jbabdi, S., Caspers, S., Laird, A.R., Fox, P.T., Zilles, K., Behrens, T., 2010. Anatomical and functional connectivity of cytoarchitectonic areas within the human parietal operculum. J. Neurosci. 30, 6409–6421.

Eickhoff, S.B., Bzdok, D., Laird, A.R., Roski, C., Caspers, S., Zilles, K., Fox, P.T., 2011. Co-activation patterns distinguish cortical modules, their connectivity and functional differentiation. Neuroimage 57, 938–949.

Eickhoff, S.B., Bzdok, D., Laird, A.R., Kurth, F., Fox, P.T., 2012. Activation likelihood estimation revisited. Neuroimage 59, 2349–2361.

Evans, A.C., Collins, D.L., Mills, S.R., Brown, E.D., Kelly, R.L., Peters, T.M., 1993. 3D statistical neuroanatomical models from 305 MRI volumes. Proceedings of IEEE-Nuclear Science Symposium and Medical Imaging Conference 1813–1817.

Fennema-Notestine, C., 2009. Enabling public data sharing: encouraging scientific discovery and education. Methods Mol. Biol. 569, 25–32.

Fox, P.T., Lancaster, J.L., 2002. Mapping context and content: the BrainMap model. Nat. Rev. Neurosci. 3, 319–321.

Fox, P.T., Laird, A.R., Fox, S.P., Fox, M., Uecker, A.M., Crank, M., Koenig, S.F., Lancaster, J.L., 2005. BrainMap taxonomy of experimental design: description and evaluation. Hum. Brain Mapp. 25, 185–198.

Jakobs, O., Langner, R., Caspers, S., Roski, C., Cieslik, E.C., Zilles, K., Laird, A.R., Fox, P.T., Eickhoff, S.B., 2012. Across-study and within-subject functional connectivity of a right temporo-parietal junction subregion involved in stimulus-context integration. Neuroimage 60, 2389–2398.

Johansen-Berg, H., Behrens, T.E., Robson, M.D., Drobnjak, I., Rushworth, M.F., Brady, J.M., Smith, S.M., Higham, D.J., Matthews, P.M., 2004. Changes in connectivity

profiles define functionally distinct regions in human medial frontal cortex. Proc. Natl. Acad. Sci. U. S. A. 101, 13335–13340.
Kahnt, T., Chang, L.J., Park, S.Q., Heinzle, J., Haynes, J.D., 2012. Connectivity-based parcellation of the human orbitofrontal cortex. J. Neurosci. 32, 6240–6250.
Keator, D.B., Grethe, J.S., Marcus, D., Ozyurt, B., Gadde, S., Murphy, S., et al., 2008. A national human neuroimaging collaboratory enabled by the Biomedical Informatics Research Network (BIRN). IEEE Trans. Inf. Technol. Biomed. 12, 162–172.
Kelly, C., Uddin, L.Q., Shehzad, Z., Margulies, D.S., Castellanos, F.X., Milham, M.P., Petrides, M., 2010. Broca's region: linking human brain functional connectivity data and non-human primate tracing anatomy studies. Eur. J. Neurosci. 32, 383–398.
Kim, J.H., Lee, J.M., Jo, H.J., Kim, S.H., Lee, J.H., Kim, S.T., Seo, S.W., Cox, R.W., Na, D.L., Kim, S.I., Saad, Z.S., 2010. Defining functional SMA and pre-SMA subregions in human MFC using resting state fMRI: functional connectivity-based parcellation method. Neuroimage 49, 2375–2386.
Koski, L., Paus, T., 2000. Functional connectivity of the anterior cingulate cortex within the human frontal lobe: a brain-mapping meta-analysis. Exp. Brain Res. 133, 55–65.
Laird, A.R., Lancaster, J.L., Fox, P.T., 2005a. BrainMap: the social evolution of a functional neuroimaging database. Neuroinformatics 3, 65–78.
Laird, A.R., Fox, M., Price, C.J., Glahn, D.C., Uecker, A.M., Lancaster, J.L., Turkeltaub, P.E., Kochunov, P., Fox, P.T., 2005b. ALE meta-analysis: controlling the false discovery rate and performing statistical contrasts. Hum. Brain Mapp. 25, 155–164.
Laird, A.R., Eickhoff, S.B., Kurth, F., Fox, P.M., Uecker, A.M., Turner, J.A., Robinson, J.L., Lancaster, J.L., Fox, P.T., 2009a. ALE meta-analysis workflows via the BrainMap database: progress towards a probabilistic functional brain atlas. Front. Neuroinformatics 3, 23.
Laird, A.R., Eickhoff, S.B., Li, K., Robin, D.A., Glahn, D.C., Fox, P.T., 2009b. Investigating the functional heterogeneity of the default mode network using coordinate-based meta-analytic modeling. J. Neurosci. 29, 14496–14505.
Laird, A.R., Fox, P.M., Eickhoff, S.B., Turner, J.A., Ray, K.L., McKay, D.R., Glahn, D.C., Beckmann, C.F., Smith, S.M., Fox, P.T., 2011. Behavioral interpretations of intrinsic connectivity networks. J. Cogn. Neurosci. 23, 4022–4037.
Lancaster, J.L., Laird, A.R., Eickhoff, S.B., Martinez, M.J., Fox, P.M., Fox, P.T., 2012. Automated regional behavioral analysis for human brain images. Front. Neuroinformatics 6, 23.
Malikovic, A., Amunts, K., Schleicher, A., Mohlberg, H., Eickhoff, S.B., Wilms, M., Palomero-Gallagher, N., Armstrong, E., Zilles, K., 2007. Cytoarchitectonic analysis of the human extrastriate cortex in the region of V5/MT+: a probabilistic, stereotaxic map of area hOc5. Cereb. Cortex 17, 562–574.
Marcus, D.S., Wang, T.H., Parker, J., Csernansky, J.G., Morris, J.C., Buckner, R.L., 2007a. Open Access Series of Imaging Studies (OASIS): cross-sectional MRI data in young, middle aged, nondemented, and demented older adults. J. Cogn. Neurosci. 19, 1498–1507.
Marcus, D.S., Olsen, T.R., Ramaratnam, M., Buckner, R.L., 2007b. The Extensible Neuroimaging Archive Toolkit: an informatics platform for managing, exploring, and sharing neuroimaging data. Neuroinformatics 5, 11–34.
Meier, T.B., Wildenberg, J.C., Liu, J., Chen, J., Calhoun, V.D., Biswal, B.B., Meyerand, M.E., Birn, R.M., Prabhakaran, V., 2012. Parallel ICA identifies sub-components of resting state networks that covary with behavioral indices. Front. Hum. Neurosci. 6, 281.
Mennes, M., Zuo, X.N., Kelly, C., Di Martino, A., Zang, Y.F., Biswal, B., Castellanos, F.X., Milham, M.P., 2011. Linking inter-individual differences in neural activation and behavior to intrinsic brain dynamics. Neuroimage 54, 2950–2959.
Mennes, M., Kelly, C., Colcombe, S., Castellanos, F.X., Milham, M.P., 2013. The extrinsic and intrinsic functional architectures of the human brain are not equivalent. Cereb. Cortex 23, 223–229.
Mennes, M., Biswal, B.B., Castellanos, F.X., Milham, M.P., 2013. Making data sharing work: the FCP/INDI experience. Neuroimage. http://dx.doi.org/10.1016/j.neuroimage.2012.10.064 (in press).
Nanetti, L., Cerliani, L., Gazzola, V., Renken, R., Keysers, C., 2009. Group analyses of connectivity-based cortical parcellation using repeated k-means clustering. Neuroimage 47, 1666–1677.
Nickl-Jockschat, T., Habel, U., Michel, T.M., Manning, J., Laird, A.R., Fox, P.T., Schneider, F., Eickhoff, S.B., 2012. Brain structure anomalies in autism spectrum disorder—A meta-analysis of VBM studies using anatomic likelihood estimation. Hum. Brain Mapp. 33, 1470–1489.
Nooner, K.B., Colcombe, S.J., Tobe, R.H., Mennes, M., Benedict, M.M., Moreno, A.L., Panek, L.J., Brown, S., Zavitz, S.T., Li, Q., Sikka, S., Gutman, D., Bangaru, S., Schlachter, R.T., Kamiel, S.M., Anwar, A.R., Hinz, C.M., Kaplan, M.S., Rachlin, A.B., Adelsberg, S., Cheung, B., Khanuja, R., Yan, C., Craddock, C.C., Calhoun, V., Courtney, W., King, M., Wood, D., Cox, C.L., Kelly, A.M., Di Martino, A., Petkova, E., Reiss, P.T., Duan, N., Thomsen, D., Biswal, B., Coffey, B., Hoptman, M.J., Javitt, D.C., Pomara, N., Sidtis, J.J., Koplewicz, H.S., Castellanos, F.X., Leventhal, B.L., Milham, M.P., 2012. The NKI-Rockland sample: a model for accelerating the pace of discovery science in psychiatry. Front. Neurosci. 6, 152.
Poldrack, R.A., 2006. Can cognitive processes be inferred from neuroimaging data? Trends Cogn. Sci. 10, 59–63.
Poldrack, R.A., Mumford, J.A., Schonberg, T., Kalar, D., Barman, B., Yarkoni, T., 2012. Discovering relations between mind, brain, and mental disorders using topic mapping. PLoS Comp. Biol. 8, e1002707.
Postuma, R.B., Dagher, A., 2006. Basal ganglia functional connectivity based on a meta-analysis of 126 positron emission tomography and functional magnetic resonance imaging publications. Cereb. Cortex 16, 1508–1521.
Reetz, K., Dogan, I., Rolfs, A., Binkofski, F., Schulz, J.B., Laird, A.R., Fox, P.T., Eickhoff, S.B., 2012. Investigating function and connectivity of morphometric findings — Exemplified on cerebellar atrophy in spinocerebellar ataxia 17 (SCA17). Neuroimage 62, 1354–1366.
Robinson, J.L., Laird, A.R., Glahn, D.C., Lovallo, W.R., Fox, P.T., 2010. Meta-analytic connectivity modelling: delineating the functional connectivity of the human amygdala. Hum. Brain Mapp. 31, 173–184.
Robinson, J.L., Laird, A.R., Glahn, D.C., Blangero, J., Sanghera, M.K., Pessoa, L., Fox, P.M., Uecker, A., Friehs, G., Young, K.A., Griffin, J.L., Lovallo, W.R., Fox, P.T., 2012. The functional connectivity of the human caudate: an application of meta-analytic connectivity modeling with behavioral filtering. Neuroimage 60, 117–129.
Rottschy, C., Caspers, S., Roski, C., Reetz, K., Dogan, I., Schulz, J.B., Zilles, K., Laird, A.R., Fox, P.T., Eickhoff, S.B., 2013. Differentiated parietal connectivity of frontal regions for “what” and “where” memory. Brain Struct. Funct. (in press).
Schilbach, L., Bzdok, D., Timmermans, B., Fox, P.T., Laird, A.R., Vogeley, K., Eickhoff, S.B., 2012. Introspective minds: using ALE meta-analyses to study commonalities in the neural correlates of emotional processing, social & unconstrained cognition. PLoS One 7, e30920.
Smith, S.M., Fox, P.T., Miller, K.L., Glahn, D.C., Fox, P.M., Mackay, C.E., Filippini, N., Watkins, K.E., Toro, R., Laird, A.R., Beckmann, C.F., 2009. Correspondence of the brain's functional architecture during activation and rest. Proc. Natl. Acad. Sci. U. S. A. 106, 13040–13045.
Talairach, J., Tournoux, P., 1988. Co-planar Stereotaxic Atlas of the Human Brain. Thieme, New York.
Toro, R., Fox, P.T., Paus, T., 2008. Functional coactivation map of the human brain. Cereb. Cortex 18, 2553–2559.
Turkeltaub, P.E., Eden, G.F., Jones, K.M., Zeffiro, T.A., 2002. Meta-analysis of the functional neuroanatomy of single-word reading: method and validation. Neuroimage 16, 765–780.
Turkeltaub, P.E., Eickhoff, S.B., Laird, A.R., Fox, M., Wiener, M., Fox, P., 2012. Minimizing within-experiment and within-group effects in activation likelihood estimation meta-analyses. Hum. Brain Mapp. 33, 1–13.
Turner, J.A., Laird, A.R., 2012. The cognitive paradigm ontology: design and application. Neuroinformatics 10, 57–66.
van den Heuvel, M., Mandl, R., Hulshoff, Pol, 2008. Normalized cut group clustering of resting-state fMRI data. PLoS One 3, e2001.
Van Essen, D.C., Ugurbil, K., Auerbach, E., Barch, D., Behrens, T.E., Bucholz, R., Chang, A., Chen, L., Corbetta, M., Curtiss, S.W., Della Penna, S., Feinberg, D., Glasser, M.F., Harel, N., Heath, A.C., Larson-Prior, L., Marcus, D., Michalareas, G., Moeller, S., Oostenveld, R., Petersen, S.E., Prior, F., Schlaggar, B.L., Smith, S.M., Snyder, A.Z., Xu, J., Yacoub, E., WU-Minn HCP Consortium, 2012. The Human Connectome Project: a data acquisition perspective. Neuroimage 62, 2222–2231.
Yarkoni, T., Poldrack, R.A., Nichols, T.E., Van Essen, D.C., Wager, T.D., 2011. Large-scale automated synthesis of human functional neuroimaging data. Nat. Methods 8, 665–670.
Zald, D.H., McHugo, M., Ray, K.L., Glahn, D.C., Eickhoff, S.B., Laird, A.R., 2013. Meta-analytic connectivity modeling reveals differential functional connectivity of the medial and lateral orbitofrontal cortex. Cereb. Cortex (in press).