Improved Correspondence of Resting-State Networks After Macroanatomical Alignment

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Abstract: Resting state brain activity, as measured with functional magnetic resonance imaging (fMRI) in the absence of stimulation, is widely investigated in clinical, pharmacological, developmental and cross-species neuroscience research. However, despite the general and broad interest in understating the nature of resting state networks (RSNs), there has not been a thorough investigation into the relationship between these functional networks and their adherence to underlying brain anatomy. We acquired resting state fMRI data from 10 subjects and extracted individual and group RSN maps respectively using independent component analysis (ICA) and self organising group-level ICA (sog-ICA). Cortex based alignment (CBA), an advanced surface based alignment technique which uses individual curvature information to align individual subjects' brains to a dynamic group average, was used to maximise anatomical correspondence across subjects. Cross subject spatial correlations of the RSN maps (independent components) were carried out with and without CBA. Seven RSNs, which are amongst the most reported and studied networks, were identified. We observed a systematic gain in the spatial correlation in all of them following CBA, although this gain was not uniform across RSNs. The observed increase in similarity of the functional RSNs after anatomical alignment illustrates that these functional networks are indeed related to underlying macroanatomical features. Moreover, our results demonstrate that by correcting for individual anatomical differences, advanced surface based alignment techniques increase the overlap of corresponding resting state networks across subjects, thereby providing a useful means to improve resting state group statistics with no need for substantial smoothing. *Hum Brain Mapp* 35:673–682, 2014. © 2012 Wiley Periodicals, Inc.

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INTRODUCTION

Interest in the brain activity during a 'task free' functional magnetic resonance imaging (fMRI) experiment has increased substantially in recent years. What started with a serendipitous finding that there is remarkable similarity in activation patterns whilst a subject is 'at rest' [Raichle et al., 2001; Raichle and Snyder, 2007], has sparked research by a myriad of groups. Resting-state (RS) brain activity is now investigated in clinical research [Mohammadi et al., 2009; Rombouts et al., 2005], developmental research [Fransson et al., 2007] and even cross-species

Additional Supporting Information may be found in the online version of this article.

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research [Mantini et al., 2011; Rilling et al., 2007] amongst other fields. Despite the ever-increasing interest in RS activity and the default mode network (DMN) in particular, the degree to which functional resting-state networks (RSNs) correspond with macroanatomical landmarks has not been thoroughly investigated. Insights into this relationship are pertinent seeing that these intrinsic connectivity networks are often defined based on their spatial proximity to cortical landmarks; in fact a seminal review of RS research stated that the DMN is ‘anatomically defined’ [Buckner et al., 2008]. Besides the DMN, some of the most frequently investigated RSNs include frontoparietal (FPN), auditory (AUD), sensory-motor (SMN), visual (VIS), superior parietal (SPN) and self-referential (SRN) networks. Some recent work suggests that default mode activity may represent the brain cycling through its possible repertoire of configurations of these functional networks [Deco et al., 2011; Senden et al., 2012].

Although the debate over the functional relevance of RSNs continues, methods to label and extract these networks continue to be developed. One of the simplest approaches used for mapping RSNs is seed-based cross correlation, where a known node of the respective network is selected as a seed region of interest and all other nodes of the network are revealed through their linear correlation to the seed [Biswal et al., 1995]. Another very popular approach uses independent component analysis [ICA; Hyvarinen and Oja, 2000]. ICA has been shown to be a useful method to apply to RS data [see, e.g., Damoiseaux et al., 2006; Esposito et al., 2009; Greicius et al., 2004; Mantini et al., 2007; van de Ven et al., 2004], as it is a completely data-driven technique which is able to successfully separate several RSNs without the need to define seed regions. RSNs obtained by ICA, and, particularly the most widely studied RSN, the DMN, have been revealed with a high degree of within- and between-subject consistency [Damoiseaux et al., 2006; De Luca et al., 2005; Esposito et al., 2009; Mantini et al., 2007; Meindl et al., 2010; Smith et al., 2009].

Previous work addressing the question of the relationship between structure and function of RSNs has mostly focused on measures of anatomical connectivity. The spatially separate nodes of RSNs are, by definition, functionally connected, however this does not necessarily imply that there are direct anatomical connections between the nodes of the network. There have been a number of studies that have investigated whether these functionally connected regions are also anatomically connected via fibre tracts, as reconstructed by diffusion tensor imaging [Damoiseaux and Greicius, 2009; van den Heuvel et al., 2009]. The evidence from these studies generally indicates that these functionally connected RSNs are also structurally connected but not in all cases, for example no direct anatomical connections could be found between two of regions of the DMN [Greicius et al., 2009].

Our approach for examining structural–functional relationships focuses on investigating the consistency of net-

works with respect to macroanatomical landmarks. After largely removing macroanatomical variability, a gain in the overlap of RSNs across subjects is expected when these functional networks ‘respect’ anatomical landmarks. To evaluate this, we employ a surface-based, curvature-driven alignment technique subsequently called cortex-based alignment (CBA), to largely reduce macroanatomical variability across subjects [Fischl et al., 1999; Goebel et al., 2006]. CBA utilises the geometric properties inherent in the convoluted human neocortex and uses individual convex/concave curvature gradients to align the gyral/sulcal folding pattern across subjects. It has previously been shown that advanced macroanatomical alignment procedures can lead to increased spatial correspondence of functional areas [Argall et al., 2006; Fischl et al., 1999; Frost and Goebel, 2012].

Recently, we showed that, by reducing intersubject macroanatomical variability through curvature-driven alignment, a concomitant reduction in spatial variability of discrete functional areas is observed indicating the degree of cortical structure–function relationship [Frost and Goebel, 2012]. This article uses the same logic but applies it to RSN functional connectivity distributions as obtained by ICA decompositions and cortical projections of these component maps as opposed to discrete specialised functional areas (e.g., fusiform face area, parahippocampal place area, frontal eye fields, etc.). This article examines the spatial variability of RSNs in healthy subjects, before and after advanced macroanatomical alignment. We expect that intersubject spatial variability of RSN cortical maps will be reduced following macroanatomical alignment, resulting in more sensitive group statistics over RSN cortical maps. We expect, however, that the potential gains in the intersubject spatial similarities of the networks will be relatively modest (compared with, e.g., task-evoked regionally focused activations). In fact, because RSN activity is normally highly distributed over the entire cortex, any increase in overlap of the RSN layouts will mainly be a reflection of alterations occurring at the ‘fringe’ (border) of these distributions, i.e., in a small fraction of the overall network pattern.

MATERIALS AND METHODS

Participants

Ten healthy subjects (four female and six male) with a mean age of 31.3 (range 25–46) were scanned as part of a larger project [Frost and Goebel, 2012].

Data Acquisition

Two hundred and forty-two volumes of RS data were acquired after 30 min of functional scans consisting of visual area localisers, the data of which is not included in this article. Participants were instructed to close their eyes

but remain awake. The projection screen was darkened to provide a relaxing environment, free of all visual stimuli. All participants confirmed that they did not fall asleep during the RS scan

fMRI Scanning Parameters

All subjects were scanned with a Siemens 3T head only scanner (Magnetom Allegra, Siemens Medical Systems, Erlangen, Germany). A standard echoplanar-imaging sequence (repetition time [TR] = 2 s field of view = 224 mm × 224 mm, matrix size = 64 × 64, and echo time [TE] = 30 ms) with a voxel size of 3.5 mm³. Each volume consisted of 32 slices, covering the whole brain. A high-resolution structural scan (voxel size, 1 mm × 1 mm × 1 mm) was also collected for each subject using a T1-weighted three-dimensional (3D) ADNI sequence [TR, 2,050 ms; TE, 2.6 ms; 192 sagittal slices].

Data Analysis

Analysis was carried out using the BrainVoyager QX v2.3 software package (Brain Innovation, Maastricht, The Netherlands).

Functional preprocessing

The first two functional volumes of the RS scan were removed to allow T1 saturation to stabilise. The remaining 240 volumes underwent a series of preprocessing steps. Slice scan time correction was performed using sinc interpolation to correct for the interleaved slice acquisition. Motion correction was performed using a 3D rigid-body transformation of each volume to the first volume: motion was first detected using trilinear interpolation and then corrected using sinc interpolation. To remove scanner related linear and nonlinear drifts a temporal high-pass filter with cut-off set to three cycles per time-course was applied. Functional images were normalised in Talairach space. Finally, data was spatially smoothed, using a Gaussian kernel of 5 mm FWHM and temporally smoothed with a Gaussian kernel of 2 s FWHM.

Anatomical preprocessing and alignment

High-resolution T1-weighted images of each participant were normalised in Talairach space. This operation included the definition of the landmarks AC (anterior commissure), PC (posterior commissure) and the borders of the cerebrum; the defined subject-specific landmarks were then used to rotate each brain in the AC–PC plane followed by piecewise, linear transformations to fit each brain in the common Talairach ‘proportional grid’ system [Talairach and Tournoux, 1980]. Cortical surface representations were created using an automatic segmentation tool [Kriegeskorte and Goebel, 2001]. Individual curvature maps were then derived from the extracted cortical

meshes. CBA was then performed by first carrying out a rigid alignment to a randomly chosen target subject, followed by a nonlinear morphing alignment to a dynamic group average curvature map. This proceeds from a coarse to fine level where, during the early phase, smoothed curvature maps are used to align the gross anatomical features (Central sulcus, Sylvian fissure, cingulate sulcus, etc.); as the alignment algorithm progresses, more detailed curvature information is included to maximise macroanatomical correspondence across the whole cortex [Frost and Goebel, 2012; Goebel et al., 2006]. CBA results in the creation of files describing the nonlinear mapping of each subject’s reconstructed cortex from normalised (Talairach) subject space, to the macroanatomically aligned group space. These vertex-level mapping files are also used to transform the functional data (individual RS maps) to the group aligned space.

Single subject and group ICA

The preprocessed and Talairach normalised RS data for each individual subject was analysed using a standard ICA technique, which has been shown to be a robust data-driven method for extracting RSNs [van de Ven et al., 2004]. A plug-in for the BrainVoyager QX 2.3 software (Brain Innovation, Maastricht University, Maastricht, The Netherlands), which implements the fastICA algorithm [Hyvarinen and Oja, 2000] was used. Before ICA was performed, principal component analysis was applied to reduce data dimensionality to 30 [Esposito and Goebel, 2011]. The ICA algorithm then computed 30 spatially independent components. Another plug-in, self-organizing group ICA (sogICA), was used to automatically match and cluster components across subjects based on linear correlations between components [Esposito et al., 2005]. As the time-courses of any two components from different RS scans cannot be assumed in phase, we only used the spatial similarities (computed as the correlations between the ICA maps and not the temporal similarities, i.e., the correlations between the ICA time-courses). In more detail, sogICA implements a hierarchical clustering algorithm which operates with the constraint that each subject has to contribute one component per cluster. Here, all 300 components (30 per subject and 10 subjects) were clustered, resulting in 30 clusters. To assess the quality of the produced clusters, the within-cluster similarities and the cluster ‘silhouettes’ [Rousseeuw, 1987] were calculated and plotted for the selected clusters. The cluster silhouettes allow one to assess how much a given member is ‘well clustered’, with higher positive values pointing to little doubt about its assignment and lower negative values pointing to a possible misclassification.

Statistical analysis

After ICA maps were extracted from the individual RS data and components matched across subjects, a linear

correlation analysis was carried out to measure spatial similarity across subjects after projection of the RSN maps onto a common cortical space. To this end, seven individual ICA maps, from those clusters comprising the most studied RSNs, were taken from each subject and projected to the individual cortical surface. From the individual surface, the RSN maps of each subject were then transferred to a common average cortical surface using a point-by-point correspondence, and spatially correlated with the homologue RSN maps from all other subjects undergoing the same cortical mapping procedure. These correlations, as well as their mean and standard deviation across all subjects, were calculated for both unaligned and cortex-based aligned common spaces, using all cortical map points on the 'average' surface mesh, amounting to ~80,000 spatial observations. Aligned surface maps were created using the output of the CBA algorithm to transform the RSN maps to the macroanatomically aligned space.

To assess the stability of the obtained results, a slightly different approach was additionally used, where each network map of each subject was correlated with the group average network map in both aligned and nonaligned surface space. For display purposes, group RSN cortical maps were obtained from 1-sample *t*-statistic maps in the common cortical space using both unaligned and cortex-based aligned maps, and thresholded at $P = 0.05$ (uncorrected).

RESULTS

From the sogICA analysis, seven RSN components were identified that were highly similar to those reported in previous ICA-based RS-fMRI studies. These RSN components could be functionally categorized by the Talairach coordinates of the most active subregions [for reference, see, e.g., the table presented by Allen et al., 2011] and were labelled as DMN, FPN, AUD, SMN, VIS, SPN and SRN [Damoiseaux et al., 2006; Mantini et al., 2007]. Figure 1 gives an overview of the seven RSN group maps obtained without and with CBA as well as cross-subject correlations of the RSN maps before and after alignment. All other clusters were discarded as their component members mostly contained artefact or noise components as well as lower silhouette values indicating suboptimal clustering (see also Supporting Information A).

In the subsequent correlation analyses, we observed a generalised increase in the correlation of all RSNs after the application of CBA (see Fig. 2). The subjectwise correlation, obtained by correlating the maps of each subject to all other subjects, of the DMN maps increased from 0.33 without to 0.35 after alignment whereas that of the FPN maps increased from 0.25 to 0.29. These gains, however, were modest and not statistically significant ($P > 0.05$). The average correlation of SMN maps increased from 0.06 to 0.14. The VIS component maps increased from an average correlation of 0.08–0.20. AUD maps increased from

0.09 to 0.16. The SPN maps displayed the largest gain from 0.05 before alignment to 0.21 after alignment. Finally, the SRN maps increased from an average correlation of 0.07–0.12. Apart from the DMN and FPN cases, all these gains were statistically significant ($P < 0.05$).

Figure 3 reports the silhouette plots of the seven RSN maps before and after alignment. It indicates that the cluster qualities improved for all RSNs and all subjects with only a few exceptions concerning the least representative subjects.

When correlation coefficients were calculated examining the spatial similarity of each subject's individual network maps with the group average of that network, we also observed an increase in similarity, albeit on a more modest scale. Table I shows mean correlation levels for all RSNs based on this approach. Obviously, when correlating an individual's map to the group average, the correlation levels were much higher independent of the alignment approach. For instance, the smallest correlation value (obtained for the AUD component unaligned = 0.44) was still higher than the strongest correlation of subject-to-subject correlations (DMN aligned = 0.35). In addition, the difference between the nonaligned and aligned conditions was diminished when compared with the cross-subject correlations. However, six of the seven RSNs (with the sole exception of SRN) still resulted in being more highly correlated to the group mean after alignment than before alignment thus suggesting the same systematic albeit modest effect of CBA increases on the spatial similarity of the RSNs.

Despite the fact that visual differences between the group RSN maps before and after alignment are subtle, on close inspection one can see the effect of cortical alignment on these maps. Figure 4 shows two group RSN maps, the SPN and the AUD network, both are shown unaligned and aligned using CBA. Some clear differences are visible between the maps of the AUD network, such as the gain in group level 'activation' revealed through more areas showing stronger values (brighter yellow) after CBA. This is coupled with an increased spatial coherency of the functional maps after anatomical alignment, most obviously characterised with more focused activation in the superior temporal sulcus and the angular gyrus. One can see in the AUD network that the improvement is visible in planum temporale and the superior temporal sulcus, which are two secondary auditory regions crucial for auditory processing [Belin et al., 2002; Binder et al., 2000]. As for the SPN, the improvement is most visible in the lateral intraparietal sulcus, a region involved in saccadic eye movement control and imagery and spatial attention [Corbetta, 1998; Culham et al., 2001].

DISCUSSION

Using the combination of single-subject ICA to extract individual RSN maps, and sogICA, to match RSN maps and cluster them into groups, we were able to extract the

Figure 1.

An overview of the seven resting-state networks. Group maps are shown unaligned on the left and aligned with CBA on the right. The box plots display the correlation values of the spatial similarity between subjects in both unaligned and CB-aligned space. The central plots to the left (1) display correlations before alignment and the plots to the right (2) display correlations after alignment. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Figure 2.

Bar graph depicting the average correlation values for seven resting-state networks. Correlations were computed by correlating the map of each network of each subject to the same network of all other subjects in a pairwise manner. This was done in both nonaligned and cortex-based aligned surface space.

functional maps of the seven most consistent and widely studied RSNs in all our subjects. All seven RSNs examined in this study exhibited higher intersubject correlations and

better clustering after CBA application. This can be interpreted as evidence that the RSNs are intrinsically bound to the underlying macroanatomical cortical boundaries

Figure 3.

Silhouette plots of the clusters where higher values indicate better clustering and lower values indicate possible misclustering. Silhouette values are higher after CBA (2) than without curvature alignment (1). [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

TABLE I. Mean correlation values of spatial similarity between individual subject and group maps

RSN	Not aligned	CB aligned
DMN	0.63	0.65
FPN	0.54	0.60
SMN	0.45	0.46
VIS	0.47	0.53
AUD	0.44	0.47
SPN	0.51	0.54
SRN	0.45	0.45

Displays mean correlation values of individual subject maps to group average maps of the same resting-state network.

and that macroanatomical (cortex-based) alignment co-registers RSNs better than standard volumetric normalisation. More specifically, by performing a purely anatomically (curvature) driven alignment, we observed systematic, albeit weak, gains in the spatial similarity of the RSN maps across subjects.

Not all of the networks, however, saw the same gain in similarity when comparing spatial correlation coefficients between the nonaligned and the aligned network maps. In fact, the RSNs with strongest (prealignment) intersubject correlation benefited least from CBA and, at the same time, the added value of CBA was most evident amongst the RSNs with lower SNR, which makes detailed effects of alignment difficult to interpret.

The spatially most consistent RSN was the DMN. Along with its clearly pronounced spatial profile, easily distinguishable on visual inspection, the DMN is the RSN which has the strongest structural–functional relationship, in other words, the functionally defined DMN is highly related to macroanatomical boundaries, i.e., cingulate sulcus, angular gyrus, superior temporal sulcus and occipitoparietal sulcus. Interestingly, although the DMN was also ranked as the ‘most similar’ network in terms of spatial correlations, both before and after alignment, we observed that it gained the least in terms of increase in correlation of the network maps. One must note that, even before applying CBA, the DMN is more highly correlated than any other RSN map.

Figure 4.

Group maps of the AUD and the SPN RSNs. On the left are the unaligned group maps of the AUD RSN (A) and the SPN (C). On the right is the group map of the AUD RSN after CBA (B) and SPN (D) also after the data were aligned using CBA. Key differences between aligned and nonaligned maps have been

highlighted in circles. For the AUD and the angular gyrus and superior temporal sulcus sees the clearest sharpening and for the SPN maps a clear gain is seen in the superior parietal lobule. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

The absence of a large gain in correlation after macroanatomical alignment is likely due to the high baseline (i.e., volumetric prealignment) level of intersubject correlation. In contrast, this could be also due to the fact that, compared with other RSNs, the DMN maps are less noisy in, and less variable across, all subjects, thereby reducing the net gain of anatomical alignment.

It is interesting to note that the two RSNs which had the most significant gains in spatial cross-subject correlation were the SPN and VIS network maps. The parietal and occipital lobes in particular are known to have high variability in the organization and orientation of sulci and gyri, such as the calcarine sulcus, lateral occipital sulcus and the intraparietal sulcus, in standardised (Talairach) space across subjects [Frost and Goebel, 2012; Perrot et al., 2011; Thompson and Toga, 1996]. By applying the CBA algorithm, thereby effectively minimising this intersubject macroanatomical variability, we observed a significant increase in the spatial similarity of these RSN maps, as measured by increased spatial correlation between all subject pairs. That we were able to reduce the spatial variability in these two RSNs, whose underlying anatomy is highly variable, is further evidence that the functionally defined maps are intrinsically related to the underlying anatomical structure.

We observed a large difference between correlations of subjects when they are correlated to the group average map of each RSN compared with when these are computed in a pairwise fashion to the map of each other subject. This finding is easily understood as the mean network maps already contain information from each subject. A subsequent correlation of a single subject to that group will, of course be higher than a correlation to another individual subject. It is striking however that even for correlations to the group mean map we observe a systematic improvement after CBA although the gain in spatial correlation between nonaligned and CBA aligned maps is modest. Furthermore, the construction of a group average network map, by its very nature, does not reveal areas of intersubject variability but reflects the most consistent areas across subjects. The goal of this research however is to investigate to what extent this intersubject variability is due to differences in individual macroanatomy. By focusing on the difference between nonaligned and aligned cross-subject correlations, we can observe the effect of the morphology of the underlying anatomy on the spatial layout of functional networks. As we observed postalignment gains across all the studied networks it seems that RSNs correspond to cortical macroanatomy.

Due to the distributed and widespread nature of RSN maps, it is difficult to observe the correspondence between functional activations and their adherence to underlying macroanatomical structures (sulci and gyri) in the maps themselves. Moreover, as a consequence of these aspects, gains in overlap of functional maps are strongest at the fringes of these maps and, therefore, visual differences can be quite subtle. Nonetheless clear examples can be found

where the gains in spatial correspondence, as measured by increases in spatial correlation, are coupled with visible differences on the functional network maps. Two such examples, the SPN and the AUD network, demonstrate that, after anatomical alignment, the functional maps not only gain in group level activation strength but also the improved spatial correspondence of anatomy leads to increased ‘sharpening’ of these two functional maps. This is most clearly observed by the increased group level ‘adhesion’ to underlying anatomical boundaries, such as the superior parietal lobule in the case of the SPN and the angular gyrus and superior temporal sulcus for the AUD network maps (see Fig. 4). It should be made clear however that, owing to the fact that we are concerned here with functional networks and not discrete functional areas, this ‘sharpening’ of the activated RSNs cannot always be expected to accompany increased spatial correspondence. In contrast to task-based fMRI, where the activity in a given region depends only on the signal in that region, RSNs represent a distributed functional connectivity, thereby more or less ‘activity’ in a given region depends not only on the signal in that region but also on the signal in other regions of the network.

It is also important to note here that, as well as the sharpening of functional maps and a decrease in the ‘extent’ of the activity due to better macroanatomical alignment, we also observed other instances of increased spatial correlation in the absence of a shrinking of the extent of the activated network which might be expected. This is due to the intrinsically distributed nature of the RSN patterns. As spatial correlations were computed over the entire cortical space, including both ‘more involved’ and ‘less involved’ cortical regions, whereas any improvement in pattern similarity by CBA would only result in an increase in the average spatial correlations, the spatial extent of this activity (as obtained by setting a threshold to the group maps) can show two seemingly opposing effects. First, with an increase in the average spatial correlations, the spatial extent of this activity may become more focal and the extent therefore decreases as the distance between activated anatomical features is decreased through alignment. In contrast, minimising macroanatomical alignment also allows more vertices to surpass the threshold and therefore increase the extent of the network.

The findings presented here mirror our previous work, which investigated the relationship between structure and function of specialised areas in the cortex using fMRI [Frost and Goebel, 2012]. Although in that study we focused on examining the effect of macroanatomical alignment on discrete functional areas as typically considered for a region of interest analysis (fusiform face area, hMT+, lateral occipital cortex, frontal eye fields, Broca’s area, etc.), here we have focused on the relationship between structure and function in widespread, distributed functional networks. A similar pattern of results have emerged in both data sets. First that, in the majority of cases, a reduction in anatomical variability has resulted in an increase in spatial similarity of functional areas/networks. Second,

not all areas or networks benefit from macroanatomical alignment to the same extent suggesting that the degree of structural–functional correspondence is not uniform across the cortex.

It is worth noting that the size of the intersubject correlations was modest, and that, even when significantly increased after cortical alignment, these remained small, suggesting that only a minimal fraction of the total variance in the RSN patterns can be ascribed to the anatomical variability. In general, there are several factors of functional, physiological and demographic nature, which, beside anatomical variability, could equally explain the intersubject variance of the RSN patterns for example, the individual levels of previous music exposure [Kay et al., 2012; Luo et al., 2012], motor exercise [Vahdat et al., 2011] and creativity [Takeuchi et al., 2012], as well as the caffeine [Rack-Gomer et al., 2009] and alcohol [Esposito et al., 2010] blood concentrations, and the different genders [Filippi et al., 2012]. It is indeed the highly ‘plastic’ behaviour of the RSN patterns that has made their study attractive in the clinical research.

The results of this study provide some interesting insights into how one might improve group statistics. It is clear in any group brain imaging study that there is a reduction in spatial sensitivity stemming from the fundamental differences in cortical folding patterns across subjects. Although a common technique used to account for this unwanted variability for functional averaging is to utilise spatial smoothing kernels, this approach sacrifices spatial resolution, which is not tolerable for high-resolution studies that are increasingly performed in the context of both ultrahigh field acquisition and multivariate pattern analysis [see, for example. De Martino et al., 2011].

Our results presented here illustrate that a minimal but distinct gain in spatial overlap can be achieved in group studies by improving the macroanatomical correspondence across subjects. Furthermore our results demonstrate that the used surface based, curvature-driven alignment technique effectively increases spatial similarity of the seven major RSNs considered in this article. This is strong evidence that these intrinsic functional networks are systematically related to specific macroanatomical structures.

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