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66 Co-activation based parcellation of the human frontal pole

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ABSTRACT

Historically, the human frontal pole (FP) has been considered as a single architectonic area. Brodmann's area 10, 013 in the frontal lobe with known contributions in the execution of various higher order cognitive processes. How- 28 ever, recent cytoarchitectural studies of the FP in humans have shown that this portion of cortex contains two 29 distinct cytoarchitectonic regions. Since architectonic differences are accompanied by differential connectivity 30 and functions, the frontal pole qualifies as a candidate region for exploratory parcellation into functionally dis- 31 crete sub-regions. We investigated whether this functional heterogeneity is reflected in distinct segregations 32 within cytoarchitectonically defined FP-areas using meta-analytic co-activation based parcellation (CBP). The 33 CBP method examined the co-activation patterns of all voxels within the FP as reported in functional neuroimag- 34 ing studies archived in the BrainMap database. Voxels within the FP were subsequently clustered into sub- 35 regions based on the similarity of their respective meta-analytically derived co-activation maps. Performing 36 this CBP analysis on the FP via k-means clustering produced a distinct 3-cluster parcellation for each hemisphere Q14 corresponding to previously identified cytoarchitectural differences. Post-hoc functional characterization of clus- 38 ters via BrainMap metadata revealed that lateral regions of the FP mapped to memory and emotion domains, 39 while the dorso- and ventromedial clusters were associated broadly with emotion and social cognition processes. 40 Furthermore, the dorsomedial regions contain an emphasis on theory of mind and affective related paradigms 41 whereas ventromedial regions couple with reward tasks. Results from this study support previous segregations 42 of the FP and provide meta-analytic contributions to the ongoing discussion of elucidating functional architecture 43 within human FP. 44

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Q15 Introduction

The frontal pole (FP) of the human brain, often referred to as BA 10, is situated in the most rostral curvature of the cerebral cortex. During hominid evolution, this region experienced a differential reorganization in apes and humans, and subsequently encompasses a significantly larger proportion of the cortex in humans than in other species (Öngür et al., 2003; Semendeferi et al., 2001, 2011). This region continues to develop deep into adolescence in humans and has been shown to play a crucial

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http://dx.doi.org/10.1016/j.neuroimage.2015.07.072 1053-8119/© 2015 Elsevier Inc. All rights reserved. role in a diverse range of higher order cognitive functions, including 58 many adapted behaviors claimed to be "human-specific" (Duncan, 59 2010; Kovach et al., 2012; Ramnani and Owen, 2004; Waskom et al., 60 2014).

Anatomical definition of the FP was guided by a combination of postmortem human and nonhuman primate histology and cytoarchitectural 63 studies. Brodmann's (1909) classic cytoarchitectural definition of BA 10 64 encompassed a wide area of 6-layer granular isocortex located on the 65 rostral surface of the frontal lobe as well as the contiguous region 66 along the medial wall of the hemisphere. Brodmann's definition (as 67 adopted by Talairach and Tournoux, 1988) has been widely employed 68 in neuroimaging and neuropsychological research. However, treatment 69 of the anatomically defined FP as a single homogenous area, without respect to its' functional properties, likely masks a more detailed regional 71

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specificity within the rostral frontal cortex. Furthermore, functional 7273 boundaries of this region have been highly variable across studies, leading to inconsistencies in their resultant functional properties. In-74 75deed, a recent cytoarchitectural study of the FP in humans (Bludau et al., 2014) showed that the frontopolar cortex contains two distinct 76 cytoarchitectonic regions. This mapping study distinguished between 77 78a region on the rostral surface of the frontal lobe that they labeled 79area Fp1, and an area located along the mesial surface of the superior 80 frontal gyrus that they labeled Fp2. Cytoarchitecturally, Fp1 shows 81 higher cell density in layer II and in lower parts of layer III, and a broader 82 layer IV than area Fp2. Thus, in a region that was once thought to be 83 cytoarchitecturally homogeneous (Dumontheil et al., 2008), we now have evidence to the contrary, which suggests that there may be func-84 85 tionally discrete sub-regions of the FP.

In addition to using cytoarchitectural differences to subdivide a 86 region, it is also possible to distinguish cortical areas based on their pat-87 terns of connectivity. For example, fiber tracing studies in the marmoset 88 89 and the macague monkey have indicated that areas within the FP possess different anatomical connection patterns (Burman et al., 2011; 90 Petrides and Pandya, 2007). These connectional differences are further 91 supported by diffusion tensor imaging (DTI) findings in humans that in-92dicate that the FP can be divided into sub-regions based on connection 93 94patterns (Liu et al., 2013). Using a clustering procedure, Liu performed a connectivity-based parcellation and defined three subregions of the 95 frontopolar cortex and neighboring transitional area of the extreme ros-96 tral orbitofrontal cortex. 97

It is also possible to parcellate regions based on differences in 98 99 functional connectivity patterns. Connectivity-based parcellation techniques can be applied to resting-state fMRI data to identify sub-100 regions within an ROI based on differences in voxel-wise time-series 101 correlations between the seed and the whole-brain. Most previous 102103efforts to identify functional distinctions within sub-regions of the FP 104 were carried out, however, before quantitative coordinate-based meta-analytic methods were made available (Christoff and Gabrieli, 1052000; Gilbert et al., 2006, 2010). More recently, a robust and task-106 dependent approach for investigating connectivity between brain 107 regions has emerged with the advent of meta-analytic connectivity 108 109 modeling (MACM) (Eickhoff et al., 2010; Laird et al., 2009b; Robinson et al., 2010). This technique mines the co-activation patterns reported 110 across hundreds of published neuroimaging studies archived in the 111 BrainMap database (http://brainmap.org) in order to determine the 112 113 task-based functional connectivity of brain regions. This data-driven parcellation technique provides a complementary approach toward 114 the delineation of cortical modules (Muhle-Karbe et al., 2014). The 115 methodology is motivated by the notion that the function of a brain 116 region is ultimately constrained by its connections with other areas 117 118 (Passingham et al., 2002) known from monkey and cat axonal tracing, which implies that functional units should be distinguishable based on 119the dissimilarity of their connections. Bludau et al. provided a prelimi-120nary MACM in which they tested whether FP areas defined by prob-121abilistic locations of FP1 and FP2 showed different patterns of co-122123activation. Their results showed definite regional differences, however 124they did not test whether a parcellation based on task-based functional connectivity follows similar contours as their cytoarchitecturally de-125fined areas. 126

Although structure and function are closely related in brain architec-127128ture, there is not necessarily a one-to-one relationship between them. Instead, it is possible for differential functional zones to exist even 129within an area that shares gross similarities in cytoarchitecture. This 130occurrence has been noted in previous studies examining the prefrontal 131 cortex (Duncan and Owen, 2000), but has yet to be explicitly studied 132across a range of cognitive processes within the FP. To further investi-133 gate the task-based functional connectivity of the FP, we conducted 134co-activation based parcellation (Eickhoff et al., 2011; Johansen-Berg 135et al., 2004) in conjunction with MACM. This allowed us to test whether 136 137 regional differences in the whole-brain functional co-activation patterns of the FP enable identification of discrete subdivisions of the re-138gion. These frontopolar sub-regions were then functionally character-139ized by means of forward and reverse inference to determine their140behavioral profiles according to the BrainMap taxonomic classification141system.142

Methods

Region of interest	t definition	144
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The region of interest (ROI) for each hemisphere encompassed the 145 two cytoarchitectonic areas of BA 10; the lateral frontopolar area 1 146 (FP1) and the medial frontopolar area 2 (FP2) as defined by Bludau 147 et al. (2014). A detailed description of the analyses carried out to iden- 148 tify the cytoarchitectonic organization of the FP can be found in 149 Bludau et al. (2014). In summary, observer-independent detection of 150 cytoarchitectonic borders was performed via histological analysis 151 of 10 post-mortem human brains. To this end, histological sections 152 $(\text{thickness} = 20 \,\mu\text{m})$ containing the frontal polar region were digitized 153 with an in-plane resolution of 1.02 µm per pixel. Gray-level index (GLI; 154 Wree et al., 1982) images of these slices were then calculated, thus 155 providing a means for identification of the cytoarchitectonic organiza- 156 tion for the region (e.g. identification of the borders for each cellular 157 layer within the cortex, volume fraction of cells within cellular layers). 158 A sliding window procedure was used for border detection along the 159 cortical ribbon, which compared adjacent groups of profiles against 160 each other (Schleicher and Zilles, 1990; Schleicher et al., 1999, 2000, 161 2005, 2009). 162

The frontopolar areas were 3D-reconstructed using linear and non- 163 linear transformation algorithms (Hömke, 2006), and normalized to 164 the T1-weighted single-subject template of the MNI (Montreal Neuro- 165 logical Institute; Evans et al., 2012; Evans et al., 1992). From there, a **Q16** maximum probability map (MPM) of Fp1 and Fp2 was created that 167 assigned the cytoarchitectonic area of each voxel with the highest prob- 168 ability in the reference space of the MNI template (Amunts et al., 2005; 169 Eickhoff et al., 2005, 2006). This allowed the inclusion of only those 170 voxels into the ROI where the frontal polar fields had been more likely 171 found than any other brain region in histological examination (Fig. 1A). 172

Taking into consideration that the FP includes a midline region along 173 the medial wall of the rostral frontal lobe, we separated the initial search 174 region into two independent ROIs for the right and left hemispheres. 175 This was done to ensure that resultant parcellation solutions would 176 not contain cross-hemispheric clusters. The MPM of the right and left 177 FPs was thresholded and reformatted into two binary masks, where **Q17** voxels within the ROI were assigned a value of 1 and all other voxels a 179 value of zero. The resultant left hemisphere ROI consisted of 3020 180 voxels, while the resultant right hemisphere ROI consisted of 2777 181 voxels (voxel size: $2 \times 2 \times 2 \text{ mm}^3$) (Fig. 1B).

Data processing outline

Once the boundaries of our ROIs (the right and left FPs) were 184 established, a meta-analytic connectivity map was created for each 185 voxel within each ROI. These voxel-wise MACMs assigned the probability of co-activation of each remaining voxel in the brain with the 187 seed-voxel based on the thousands of experiments archived in the BrainMap database. Next, voxels within the ROI were grouped together 189 (via k-means clustering) based on the similarities of their MACM coactivation maps. The stability and consistency of k-means cluster solutions were assessed using a combination of different cluster stability 192 metrics to identify an optimal parcellation solution.

A second MACM was performed using each cluster within the optimal parcellation solution as independent seed regions. This step in our analysis yielded a whole-brain co-activation map for each cluster within the right and left FPs. Lastly, functional characterization of each cluster was assessed by testing for significant overrepresentation of taxonomic 198

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