

A Resting State Network in the Basal Ganglia

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Introduction. In the resting state the brain undergoes slow (0.01-0.1 Hz) fluctuations in functionally related networks of brain regions. Approximately 10 such Resting State Networks (RSNs) have been discovered over the past decade [1][2][3]. Increasing power over previous studies using high field, a short repetition time and a large number of subjects, combined with group Independent Component Analysis, we uncover a previously unreported network. The co-localisation of some resting state networks and physiological signal sources has previously been noted (e.g. [4]). We introduce a method for distinguishing between the two on the basis of temporal features and show that this network groups with resting state networks charted in the literature.

Materials and Methods. Twenty-six subjects underwent 5 minutes of low spatial resolution (LR) relatively high temporal resolution (TR=1s) whole-brain EPI on a 3T Bruker Medspec scanner (3.2x3.5x4 mm voxels, TE=28ms, 18 AC-PC-aligned slices) under typical resting state conditions. Twenty-one subjects also performed a high spatial resolution (HR) run, with low temporal resolution (TR=3.5s).

Analysis. Images were preprocessed (slice timing correction, motion correction, template registration, no spatial smoothing). Four groups of data were analysed with two group-ICA tools. The groups of data were 1: LR data, all 26 subjects 2: LR data, subgroup 1 of 13 subjects, 3: LR data, subgroup 2 of 13 subjects, 4: HR data, all 21 subjects. Preprocessed time-series were analysed with FSL's Melodic 3.0 [5] and Group ICA of FMRI Toolbox (GIFT) [6]. In MELODIC, multi-session temporal concatenation was employed in order to find common spatial patterns without assuming consistency in the temporal response between subjects. Component time courses from the GIFT analysis were analysed in MATLAB for spectral content (fraction of power below 0.058 Hz to the total) and dynamic range in normalized power spectra (maximum – minimum).

Results. As well as previously-known resting state networks we find an unreported network. The components identified here and the percentages of the total variance they explain in the data are listed in Table 1. RSNs are labeled following Ref [3] with the addition of L,R,A,P if the network was split into two subcomponents left-right or anterior-posterior. The labels have been incremented past those listed in Ref [3] in the order of strength in this analysis. The new network was reproducible across subjects, being present in the analyses of subgroups (groups 2 and 3) and across runs, being present in group 4 (high resolution data). It can be seen to be cleanly restricted to the basal ganglia (Figure 1, thresholded above P<0.05). It is continuous, fully incorporating symmetrically the striate nuclei (pallidum, putamen and caudate nuclei), extending inferiorly to the amygdaloid complexes. Plotting the measures of spectral content and dynamic range of the time-courses shows the known RSNs to be well separated from physiological components (Fig.2). The component we report here clusters clearly with known RSNs.

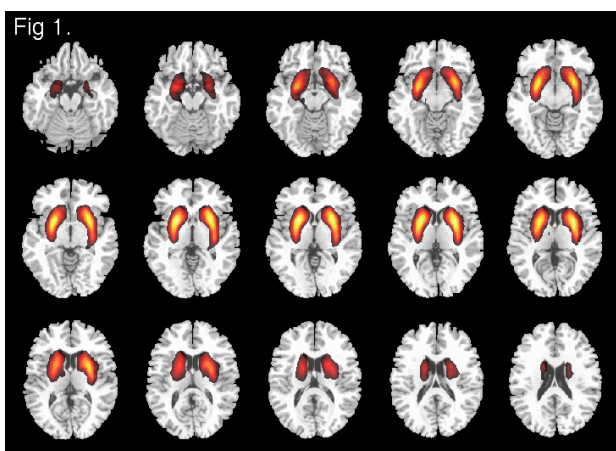
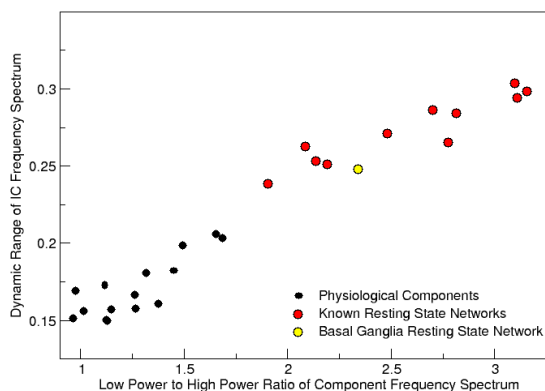


Fig 2.



Discussion. RSNs are attracting increasing attention for the insight they may explain in the data are listed in Table 1. RSNs are attracting increasing attention for the insight they may explain in the resting state of the brain, as important potential confounds in fMRI and – because they have been found to be disturbed in many neurological and psychiatric pathologies – as the possible source of the behavioral disturbances suffered in a wide range of disorders such as Alzheimer's and schizophrenia. This basal ganglia RSN may attract attention for all of these reasons. For instance, despite the fact that neurovascular reactivity is very high in all deep grey nuclei, BOLD signal changes related to cognitive tasks is more inconsistently detected in the basal ganglia. It is possible that congruent oscillatory BOLD signal in these areas could interfere in classical subtraction fMRI experiment designs. The basal ganglia and thalami have been traditionally related to spontaneous oscillations of brain electrical activity, so that spontaneous BOLD signal oscillation would have been expected in the same areas. As the basal ganglia are known to be affected in pathologies such as Parkinson's disease, it will be interesting to investigate if this network functions normally in those patients.

Table 1.

Label	Descriptor	Label in Refs {[1],[2],[3]}	Rank	%var
RSN6		{H,(d),}	7	5.34
RSN4L	Dorsal pathway(L)	{C,(h),RSN4}	10	3.99
RSN2B	Default Mode (post)	{B,(e),RSN2}	13	3.71
RSN7		{E,(a),}	15	3.25
RSN5	Ventral pathway	{,RSN5}	16	2.99
RSN8		{F,,}	17	2.34
RSN9		{[C,D], [(g),(h)],RSN4}	21	1.61
RSN3	Sensorimotor	{I,(c),RSN3}	27	0.94
RSN4R	Dorsal pathway(R)	{D,(g),RSN4}	28	0.93
RSN1	Visual	{A,(b),RSN1}	29	0.91
RSN2A	Default Mode (ant)	{B,(f),RSN2}	32	0.64
RSN11		{J, (f)}	39	0.25
RSN12	Basal Ganglia		41	0.20

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[1] Damoiseaux et al. (2006) PNAS 103(37):13848 [2] Beckmann et al. (2005) Philos Trans R Soc Lond B Biol Sci. 29:360 [3] De Luca et al. (2006) NI. 2006 Feb 15;29(4):1359. [4] Shmueli et al. (2007) NI. 38:306 [5] Beckmann et al. (2005). NI 25(1):294. [6] V. D. Calhoun et al (2005). NI (25) 527.