

Resting state functional coupling between the ascending synchronising system, limbic system and the default mode network via theta oscillations

Parnesh Raniga^{1,2*}, Bryan Paton^{1,3,4*}, Gary F. Egan^{1,4}

¹ Monash Biomedical Imaging, Monash University, Melbourne, VIC 3800, Australia.

² The Australian eHealth Research Centre, CSIRO Health and Biosecurity, Herston, QLD 4029, Australia

³ School of Psychology, University of Newcastle, Callaghan, NSW 2308, Australia

⁴ ARC Centre of Excellence for Integrative Brain Function, Monash University, Melbourne, VIC 3800, Australia.

* *Equal First Authors*

Full Address of corresponding author:

Parnesh Raniga
Level 5 UQ Health Sciences Building
Royal Brisbane and Women's Hospital
Herston, Queensland 4029 Australia
Email Parnesh.Raniga@csiro.au

Abstract

In order to better understand dysfunction in dementia and psychiatric illnesses, the underlying neuronal systems that give rise to normal memory and cognitive processes need to be better understood. Based on electrophysiological recordings in animals, theta oscillations have been proposed as an intrinsic mechanism for the orchestration of memory functions, especially episodic and autobiographical memory. Theta oscillations are controlled by the ascending synchronising system, a set of nuclei in the pontine tegmentum and basal forebrain. At a network level, the default mode network has been shown to be responsible for episodic and autobiographical.

Using resting state fMRI data, we show using an ICA approach, seed based connectivity and dynamic causal modelling that the ascending synchronising system is coupled to the medial temporal lobe nodes including the hippocampus and parahippocampal gyrus and with the default mode network. Our results provide thus support the role of theta oscillations in memory function and coordination at a network level.

Keywords: Theta oscillations, default mode network, ascending reticular activating system, Alzheimer's disease, basal forebrain, episodic memory, autobiographical memory, memory.

Highlights:

- Resting state functional coupling between the DMN, MTL and ascending synchronising system.
- Theta oscillations may be the basis of this coupling given the role of these structures in control of theta.
- Theta oscillations have been implicated in memory, cognition and predictive coding.
- DMN, MTL and ASS are implicated in Alzheimer's disease.

Abbreviations

MRI : Magnetic resonance imaging
fMRI: functional magnetic resonance imaging
rs-fmri: resting state functional magnetic resonance imaging
PnO: Pontine nucleus oralis
SuM: Supra-mamillary nucleus.
MS: Medial septum
DB: Diagonal band of Broca.
VTA: ventral tegmental area
PCC: Posterior cingulate cortex
HC: Hippocampus
ARAS: Ascending reticular activating system
ASS: Ascending synchronising system
DMN: Default Mode Network
aMPFC: Anterior Medial Prefrontal Cortex
pIPL: Posterior inferior parietal lobule
NBM: Nucleus Basalis Mynert
DCM: Dynamic causal modelling
PHG: Parahippocampal Gyrus

1 Introduction

2

3 The neuronal systems underlying memory and related cognitive processes are of great
4 interest not only to further our understanding of how the brain works but also to better
5 understand dysfunction in disease states such as dementia and psychiatric illnesses.
6 In-vivo experiments using animal models of memory formation and retrieval, and
7 recent experiments in humans, have jointly pointed to brain oscillations in the theta
8 (Φ) frequency ranges (4-10 Hz in mice and 1-4 Hz in humans (Jacobs, 2014)) may
9 have a role in the synchronisation of distributed brain regions as a core mechanism of
10 memory. These putative oscillatory mechanisms are the most likely candidate for the
11 encoding and retrieval of short-term (Vertes, 2005), especially episodic (Burke et al.,
12 2014; Heusser et al., 2016), and autobiographical (Fuentemilla et al., 2014) memories.

13

14 While theta rhythms have mainly been associated with the hippocampi (HC), the same
15 rhythms can be observed in different regions of the cortex and are thought to be
16 responsible for orchestrating long range interactions for memory formation and
17 retrieval (Anderson et al., 2010; Fuentemilla et al., 2014; Mitchell et al., 2008). In
18 particular, the prefrontal cortex and the posterior cingulate cortex have been observed
19 to be entrained to hippocampal theta oscillation in humans (Anderson et al., 2010;
20 Fuentemilla et al., 2014; Kaplan et al., 2014), primates (Tsujimoto et al., 2006) and
21 mice (O'Neill et al., 2013) suggesting that theta entrainment may be a fundamental
22 neuronal mechanism in mammalian brains.

23

24 At a global network level, the default mode network (DMN), a set of brain regions
25 that are functionally connected when the brain is not engaged in an externally oriented
26 task, has been heavily implicated in episodic memory (see (Jeong et al., 2015) for a
27 recent review), autobiographical recall (Lin et al., 2016) and internal mentation
28 (Buckner, 2013). Indeed, resting state functional magnetic resonance imaging (rs-
29 fMRI) studies have shown recruitment of the hippocampus, entorhinal cortex and
30 medial temporal lobe structures into the DMN during memory retrieval (Andrews-
31 Hanna et al., 2010; Huijbers et al., 2011; Ward et al., 2014). Reports in literature of
32 overlaps between brain regions displaying theta oscillations and the nodes of the
33 DMN (Backus et al., 2016; Foster et al., 2013; Fuentemilla et al., 2014; Kaplan et al.,
34 2014) therefore raise the question of whether a more fundamental mechanism ties the
35 two (Foster and Parvizi, 2012).

36

37 Although theta oscillations are widely distributed in the brain, they have been shown
38 to arise from circuits in the ascending synchronising system (ASS) (Denham and
39 Borisyuk, 2000) in animal models. Tonic activity in the oral pontine reticular nucleus
40 (PnO) is converted to oscillatory activity in the supramamillary nucleus (SuM). The
41 SuM innervates the hippocampus directly and via the medial septum/ diagonal band
42 of Broca complex (MSDB) (Borhegyi et al., 1998). Cholinergic and GABAergic cells
43 from the medial septum show theta activity (Lee et al., 2005) and also regulate
44 hippocampal theta (Hangya et al., 2009; Teles-Grilo Ruivo and Mellor, 2013).
45 Moreover, dopaminergic innervation from the ventral tegmental area (VTA) to the

46 medial septum modulates the firing and bursting rates of MSDB neurons, which in
47 turn affect hippocampal theta activity (Fujisawa and Buzsáki, 2011; Orzel-
48 Gryglewska et al., 2015; Werlen and Jones, 2015). An overview of this network,
49 thought to elicit and modulate theta activity in the hippocampus is provided in Figure
50 1.

51
52 Theta oscillations are thought to be one of the core mechanisms in memory processes
53 (Düzel et al., 2010) including encoding, retrieval and autobiographical introspection.
54 Understanding the functional role of theta oscillations may enhance our understanding
55 of normal brain function and dysfunction in disease states such as Alzheimer's
56 disease. The pathologies of AD including atrophy in the medial temporal lobe (Grothe
57 et al., 2016), the basal forebrain (atrophy (Kerbler et al., 2015), tau pathology (Schöll
58 et al., 2016), and loss of cholinergic function (Mufson et al., 2008)) and beta-amyloid
59 build-up in the DMN (Buckner et al., 2005) exhibit anatomical patterns that overlap
60 with nodes showing theta oscillations. Moreover, the earliest known neurofibrillary
61 tangles are observed in the ascending reticular activating of which the ascending
62 synchronising system is a part (Braak et al., 2011).

63
64 While theta generation and modulation networks have been extensively studied in
65 animals, they are more difficult to study in humans due to the difficulty of in-vivo
66 electrophysiological measurements and the widespread nature of the network.
67 Electrophysiological recordings, due to their inherent local nature, have been limited
68 in mapping the theta activity at the network and global levels. Macroscopic
69 approaches such as EEG and MEG have shown the involvement of the DMN but do
70 not have the spatial resolution to resolve the synchronising network. We investigated
71 whether these synchronisation networks could be observed using high temporal and
72 spatial resolution resting state fMRI and if they were coupled to the default mode via
73 limbic nodes that have previously been shown to be coupled to the DMN. Identifying
74 these networks could provide evidence for the role of theta oscillations in
75 orchestrating dispersed cortical regions into extended brain networks supporting
76 memory function.

77
78 Using resting state data from 300 subjects from the Human Connectome Project (Van
79 Essen et al., 2013), we show using a group PCA-ICA approach that the PnO, VTA
80 and MSDB can be observed to be coupled with MTL structures and the DMN. Further
81 to this, we show with functional connectivity using seeds from the PnO, SuM, VTA
82 and MS, functional networks that are consistent with the DMN. We then use a
83 dynamic causal modelling (DCM) analytical approach to show that the DMN
84 incorporating the HC, MSDB, SuM, PnO and VTA is the most likely network given
85 the observed data. To our knowledge, this is the first report of the coupling between
86 the ASS including MSDB, MTL and DMN in humans using rs-fMRI and provides
87 evidence that theta oscillations may serve as a brain mechanism for coordinating these
88 disparate brain regions.

89

90 **2 Results**

91

92 **2.1 Group PCA-ICA**

93

94 A default mode network ICA component was isolated from the group based PCA-ICA
95 results based on visual inspection. The network for Band 1 (0.001-0.027 Hz) (see
96 Figure 2A and Supplementary Figure 1) showed a pattern consistent with the DMN
97 with functional connectivity observed between the posterior cingulate cortex (PCC),
98 anterior middle prefrontal cortex (aMPFC), and posterior inferior parietal lobule
99 (pIPL). Furthermore, limbic structures including the bilateral hippocampii (HC), the
100 retrosplinal cortex (RSP) and parahippocampal gyrus (PHG) were also observed. The
101 medial septum region was also functionally connected to the DMN along with the
102 nucleus basalis of Meynert (NBM), the latter only being connected in Band 1.

103

104 The network for Band 2 (0.027-0.07 Hz) (Figure 2B and Supplementary Figure 1)
105 showed similar patterns of functional connectivity as for Band 1. In the mid brain and
106 pontine tegmentum, two distinct but connected regions of functional connectivity
107 could be observed. The rostral region was identified to be the ventral tegmental area,
108 which is consistent with literature reports of functional connectivity between the VTA
109 and the DMN (Fujisawa and Buzsáki, 2011; Werlen and Jones, 2015) in animal
110 models and in fMRI (Tomasi and Volkow, 2014; Tompariy et al., 2015). The VTA
111 was also evident in Band 1. The adjacent activation region was more caudal and
112 dorsal, consistent with the location of the rostral portion of the pontis nucleus oralis
113 (PnO) (see Figure 3 for comparison with location of the PnO from the Harvard
114 Ascending Arousal Network Atlas (Edlow et al., 2012)). Functional connectivity with
115 only the rostral portion of the PnO is consistent with the literature on animal
116 stimulation for the elicitation of hippocampal theta (Vertes and Kocsis, 1997).

117

118 The mammillary bodies were functionally connected in both Band 1 and 2. Also, the
119 DMN in both Bands 1 and 2 had prominent activations of the midline thalamus with
120 activations in the Band 1 DMN being along the entire midline of the thalamus, but
121 restricted to a region just posterior of the thalamic adhesion in the Band 2 DMN. The
122 DMN results for Bands 3, 4 and 5 are not reported here, as the typical resting state
123 correlational analysis is limited to 0.01 to 0.1 Hz. Apart from the DMN structures
124 themselves, no other structures were observed to be coupled to the DMN at other
125 frequencies.

126

127 To cross-validate the results we performed global seed based analysis on a different
128 set of 100 subjects using seeds based on literature and the PCA-ICA results (see Table
129 2), and a frequency band typical of resting state data (0.01-0.1Hz).

130 **2.2 Seed based Connectivity**

131

132 Voxel based connectivity patterns for seed regions from the MSDB, PnO, SuM and
133 VTA are presented in Figure 4 (and also Supplementary Figure 2). Connectivity for
134 MSDB, PnO, SuM and VTA showed a profile consistent with regions composed of
135 the default mode, whilst the MSDB and VTA showed strong connectivity to DMN
136 regions as well as limbic regions including hippocampus and retrosplinal cortex.

137
138 The PnO showed a pattern of connectivity consistent with the DMN although the
139 activation was noisier than for the VTA and MSDB. The SuM connectivity pattern,
140 while showing regions overlapping with the DMN, was very noisy likely due to the
141 fact that the SuM is a very small region with a highly heterogeneous signal.

142
143 The connectivity of the NBM was consistent with that of the salience network with
144 functional connectivity observable across the cingulate sulcus and along the dorsal
145 anterior cingulate cortex. Strong functional connectivity was also observed with
146 bilateral insula (see Supplementary Figure 3).

147
148 Overall, the seed based functional network connectivity patterns mirror those
149 observed using the group PCA-ICA method, providing empirical replication of the
150 specific activity and in particular the correlated but wide spread activity in the DMN.
151 To determine if these results were an epiphenomena we fitted and inverted a series of
152 DCM models of increasing complexity with the aim of determining the best model
153 that could causally explain the observed functional connectivity.

154

155 **2.3 Dynamic Causal Modelling**

156

157 Although the functional connectivity measures are indicative of coupling between the
158 DMN, limbic nodes and the ASS, fitting a physiologically informed causal model of
159 the dynamic patterns of connectivity may be able to infer the true network topology
160 and the underlying physiological parameters. We fitted five different models (see
161 Figure 5) that included the DMN, limbic regions and the nodes of the ASS and
162 inverted the models using spectral DCM (Friston et al., 2014) in a group of 100
163 subjects. The models were compared using Bayesian Model Selection (Rigoux et al.,
164 2014).

165 The basic DCM model, model 1, included the cortical nodes of the DMN (Sharaev et
166 al., 2016). Model 2 increased the complexity of the DMN by inclusion of bilateral
167 hippocampi and the MSDB with reciprocal connections to all nodes. Model 3
168 included the nodes of the ascending synchronising system connected to the MSDB.
169 Model 4 removed the SuM as that region had the least consistent seed based
170 connectivity pattern. Model 5 was the most complex with the VTA connected to the
171 MSDB and the hippocampus based on anatomical connectivity in animal models.

172

173 Results of the DCM analysis showed that the log evidence of the five models were
174 $M1=2.5159e6$, $M2=2.5579e6$, $M3=2.5597e6$, $M4=2.5579e6$ and $M5=2.5795e6$.
175 Further, the results showed that the most likely model given the data from those
176 models tested is Model 5 (model posterior probability of 1.0). Model 5 included the

177 HC, MSDB and the theta generation nodes of the ASS (PnO, SuM and VTA)
178 connected to the DMN, could explain 90 ± 4 % of the variance in the data (see
179 Supplementary Figure 4 for boxplots of variance explained for all models). Also
180 Model 3 had higher log evidence and explained greater variance compared to Model 4
181 suggesting that the SuM may play a role in this coupled network.

182
183

184 **3 Discussion**

185

186 Our results provide the first in-vivo evidence of functional coupling between the
187 ascending synchronising system, limbic regions including the HC, PHG, MSDB and
188 the classical DMN. While the integration of MTL structures including HC and PHG
189 into the DMN has already been observed (Andrews-Hanna et al., 2010; Ward et al.,
190 2014) and the inclusion of the MSDB has been described (Greicius et al., 2003), the
191 coupling of the ASS together with the MTL and DMN in humans identified using rs-
192 fMRI is novel.

193

194 The results of the frequency specific group PCA-ICA showed typical patterns for
195 DMN connectivity across all frequency bands with the PnO observable only in Band 2
196 (0.027-0.7 Hz) and the NBM observable only in Band 1 (0.01-0.027 Hz). The MSDB
197 and VTA were prominent in both Bands 1 and 2. To cross-validate the coupling we
198 derived and to ensure that the coupling we saw was not an artefact of the group PCA-
199 ICA method (lower variance compared to standard ICA approaches) or of the
200 parameters we chose (low-dimensionality), we performed seed based, whole brain
201 connectivity analysis in a different subset of subjects. Functional connectivity from
202 the PnO, VTA and MSDB showed statistically significant patterns of connectivity
203 typical of the DMN. While the SuM showed similar but noisier patterns, clusters
204 concomitant with the pIPL were not present in the SuM results. It is possible, due to
205 the size of the SuM and the proximity of other nuclei that that the sampled signal was
206 too heterogeneous. However previous studies have observed a strong resting state
207 functional connectivity between the mammillary bodies and the HC (Blessing et al.,
208 2016).

209

210 Further cross-validation using DCM revealed that of the five models tested, the most
211 likely model given the data was one where the nodes of the ASS (including SuM, PnO
212 and VTA) and the limbic system (HC and MSDB) were coupled. The Bayesian
213 procedures used in the DCM model fitting balance the relative accuracy of a model
214 with the complexity of the same model, a form of Occam's razor. A model that has
215 many parameters can more closely fit the data but has poor generalisability, whereas a
216 more parsimonious model might fit the data slightly worse but can be readily applied
217 across many situations. In line with this accuracy versus complexity balance, the
218 inclusion of SuM resulted in a better model fit and greater explained variance even
219 when including the extra parameters (Model 3 vs. Model 4). This highlights the causal
220 role of the SuM in supporting the memory processes through theta based mechanisms
221 as has been suggested from animal studies.

222

223 While the hippocampus and medial temporal regions such as the entorhinal cortex,
224 parahippocampal regions are known to be the core regions for the retrieval of episodic
225 and working memory (Ritchey et al., 2015) and have been shown to be coupled to the
226 DMN (Andrews-Hanna et al., 2010; Ward et al., 2014), the neural mechanisms
227 underlying memory processes and coupling are not well understood. Oscillations in
228 neuronal firing over the theta frequency band, 4-10 Hz in mice and 1-4 Hz in humans
229 (Jacobs, 2014) have been proposed as a candidate mechanism for not only memory
230 function but long range communications in memory related neural circuits (Gollo et
231 al., 2011). In particular, theta oscillations have been shown to be relevant for memory,
232 both episodic and short term (Burke et al., 2014; Fuentemilla et al., 2014; Heusser et
233 al., 2016; Vertes, 2005). Not only are the distribution of the theta rhythms important,
234 but memory performance tracks the power of theta oscillations (Backus et al., 2016),
235 and coupling between the MTL and medial prefrontal cortex, in the theta range, has
236 been shown to be present in memory encoding and retrieval (Anderson et al., 2010;
237 Backus et al., 2016; Fuentemilla et al., 2014; Kaplan et al., 2014; Lin et al., 2016).

238

239 Whether theta oscillations are generated from a set of pacemaker neurons or are
240 intrinsic properties of the coupling of certain neuron populations (Buzsáki, 2002) is
241 unclear. Experiments on animal models have shown that theta power (Orzeł-
242 Gryglewska et al., 2015; Vertes and Kocsis, 1997; Werlen and Jones, 2015) and
243 subsequent memory performance appear to be modulated by a set of nuclei including
244 the PnO, SuM, VTA and MSDB, termed the ascending synchronising system
245 (Denham and Borisyuk, 2000). The functional coupling of these structures to the
246 DMN in rs-fMRI supports the hypothesis that theta oscillations are one of the
247 underlying mechanisms for episodic and autobiographical memory (Burke et al.,
248 2014; Buzsáki and Moser, 2013; Fuentemilla et al., 2014) and potentially the neuro-
249 biological substrate for long range coordination of memory interactions (Gollo et al.,
250 2011).

251

252 The findings also support the role of theta rhythms to contextualise prediction error
253 processing in medial temporal lobe structures coupled to cortical nodes of the DMN
254 via theta oscillations (Carhart-Harris and Friston, 2010; Carhart-Harris et al., 2014;
255 Friston, 2010). This coupling allows for the integration of primary sensory
256 information with memory and contextual information for higher order processing and
257 thus may form a substrate for the waking adult conscious experience. The slower theta
258 oscillations provide a context in which prediction error units can signal (via gamma
259 band bursts) discrepancies between predicted and actual sensory inputs. The roles of
260 this coupling is critical and its breakdown may underlie unusual and altered states of
261 consciousness, as seen in psychosis for example (Carhart-Harris and Friston, 2010;
262 Carhart-Harris et al., 2014).

263

264 Our observations about brainstem coupling to the DMN are however not new, with
265 two recent papers on intrinsic hippocampal functional connectivity (Bär et al., 2016;
266 Blessing et al., 2016) showing similar patterns of functional connectivity with medial
267 temporal lobe structures and also to the DMN. In particular, both these studies, in
268 different populations using different acquisition and processing paradigms, have

269 shown functional connectivity of the VTA, MSDB (labelled the subcallosal area) to
270 region in the brainstem labelled as the median raphe nucleus (MRN). The raphe nuclei
271 are the source of serotonin release in the brain with projections throughout the entire
272 brain (Wagner et al., 2016). Given that activation of the MRN tends to desynchronise
273 hippocampal theta activity and serotonin depletion tends to increase theta EEG power
274 and working memory function (López-Vázquez et al., 2014), we suspect that the
275 relevant brainstem region may be the PnO. Moreover, since in humans the PnO
276 surrounds the MRN the two regions can be easily misidentified due to partial volume
277 effects and motion at the resolution of typical functional MRI experiments (see
278 Supplementary Figure 5).

279
280 While nuclei such as the ventral tegmental nucleus of Gudden (VTNg) have been
281 thought to be a part of the limbic system and theta synchronising system (Kocsis et
282 al., 2001), the VTA as a node in this system has been recently proposed (Orzeł-
283 Gryglewska et al., 2015). In particular, the VTA is thought to help synchronise
284 cortical and subcortical interactions (Fujisawa and Buzsáki, 2011). In light of these
285 findings and our results, the VTA and dopamine may play a role in novelty detection
286 and long term potentiation for memory encoding (Lisman and Grace, 2005) and
287 working memory (Fujisawa and Buzsáki, 2011). Moreover, with evidence of phase
288 locking, where bursts of activity between two regions are synchronised, between the
289 VTA and hippocampal theta (Fujisawa and Buzsáki, 2011; Orzeł-Gryglewska et al.,
290 2015), the activation of the VTA with the DMN is consistent with our model. The
291 coupling between the hippocampus and the VTA has recently been shown to provide
292 context to rewarding experiences (Luo et al., 2011). Moreover, increased connectivity
293 between VTA and MTL regions has been linked to memory consolidation (Tompary
294 et al., 2015).

295
296 How can these rs-fMRI findings be interpreted? It is unlikely that the temporal
297 resolution and the slow response of the hemodynamic system would enable direct
298 observations of theta oscillations using rs-fMRI. However, unlike in mice and rats, the
299 power of theta oscillations in humans is not continuous but rather occurs in more
300 discrete bursts lasting about a second (Watrous et al., 2013). Hemodynamic coupling
301 of such bursts, reflecting envelope changes in theta oscillations would result in
302 detectable BOLD changes at around 0.1 Hz (Foster and Parvizi, 2012). This frequency
303 of BOLD fluctuations is at the upper edge of the usable spectrum of typical fMRI
304 studies (assuming a 2 s sample rate [TR]) but well within the spectrum of the data
305 used here. The coupling of the VTA and its hypothesised role in producing bursts of
306 theta activity also supports this notion (Fitch et al., 2006; Fujisawa and Buzsáki,
307 2011). Furthermore, the BOLD contrast has been shown to be most directly correlated
308 with power of high frequency local field potentials (Logothetis et al., 2001). Since
309 theta and gamma band oscillations are known to be coupled (Lisman and Jensen,
310 2013) and recent evidence shows this coupling is active in episodic sequence memory
311 (Heusser et al., 2016), it is likely that coupled gamma band oscillations would give
312 rise to the BOLD response changes in the low frequency ranges.

313
314 While this network has been observed previously, the number of subjects, length of
315 rs-fMRI acquisitions, quality of the data and the state of the art pre-processing method

316 have combined to produce the current results. The rs-fMRI acquisitions were acquired
317 for a duration of 15 mins per run which is not only longer than typical acquisitions but
318 also has higher temporal signal to noise due to the use of multi-band acquisition
319 protocol. Furthermore, the acquisitions were phase encoded left to right and not
320 anterior to posterior. This phase encoding scheme reduces the signal pileups and
321 dropouts in regions close to the air tissue interfaces such as the MSDB, the VTA and
322 mammillary bodies. Coupled with this, the standardised pre-processing pipeline
323 utilised in the HCP, along with a flip angle close to the Ernst angle, ensures that
324 confounds such as motion and cardiac and respiratory signals have a drastically
325 reduced influence on the signal of interest.

326
327 The coupling of the ASS, MTL and the DMN via theta oscillations in resting state has
328 implications not only for the understanding of how the brain functions normally but
329 also of how it is affected in neurological and psychiatric disorders. Pathological and
330 functional changes in the default mode have been observed in several disorders, most
331 prominently in Alzheimer's disease (Buckner et al., 2005) whereby amyloid beta
332 plaques form in regions overlapping the default mode (Grothe et al., 2016). Moreover,
333 neurofibrillary tangles and atrophy are more prominent in MTL structures with NFTs
334 initially appearing in the pontine tegmentum and midbrain followed by the entorhinal
335 and hippocampal cortices (Braak et al., 2011) and in the basal forebrain. Moreover,
336 theta oscillations have been observed to be selectively increased in mice models of
337 Alzheimer's disease and in humans, EEG signal in the theta range increases in MCI
338 and AD subjects (Hamm et al., 2015).

339
340 While in the current study, we have been able to show coupling between the default
341 mode network, medial temporal lobe structures and the ascending synchronising
342 system, our hypothesis that this was orchestrated by theta oscillations is speculative
343 based on prior work and we are unable to directly measure the oscillations using
344 fMRI. Also, while we cross-validated our PCA-ICA results using seed based global
345 connectivity, the resultant maps were noisy compared to the PCA-ICA maps and other
346 maps that have been produced prior although they clearly showed patterns consistent
347 with the DMN. This may be due to the lower smoothing (FWHM 4 mm) that we
348 employed and the size and heterogeneity of seed voxels. Nevertheless, this is a
349 potential shortcoming that we aim to further explore in future work.

350
351 The particular form of the DCM model used, spectral DCM, is based upon the cross-
352 spectral density between the various nodes of the fitted networks. The reasoning being
353 that the second order statistics, the cross spectral densities are all that are needed to
354 explain the coupling between the network nodes under steady state assumptions
355 (Friston et al., 2014). The switch from estimating hidden neuronal states from nodal
356 time series, where in the case of resting state fMRI data there are unknown connection
357 weights and an unknown number of network nodes and stochastic time series
358 fluctuations, to a problem of estimating the cross spectral densities and their
359 associated noise transforms the estimation problem into a deterministic one (Friston et
360 al., 2014). This switch also ensures a time and computationally efficient model
361 estimation process, especially in the case of this current study given the modest
362 number of networks, the density of the time series and the large number of

363 participants. One limitation of the spectral DCM is the steady state assumption
364 although this greatly improves the model evidence estimation process it means that
365 short lived fluctuations and modulations of connection strengths are not identifiable.

366
367 In conclusion, we have presented in first *in-vivo* results in humans showing coupling
368 between the ascending synchronisation system, the hippocampus and MTL structures
369 and the typical DMN nodes using rs-fMRI. This was done using a purely data-driven
370 approach, namely group PCA-ICA and confirmed using two different hypothesis
371 driven approaches namely seed based connectivity and dynamic causal modelling.
372 Our results add to the growing body of literature supporting the role of brain
373 oscillations in the theta frequency range as being the neurobiological basis of episodic
374 and autobiographical memory. Furthermore, we have discussed the potential role of
375 this coupled system in AD with differing pathologies affecting different parts of the
376 coupled system and the major impact of the disease being on memory, the system
377 hypothetically supported by this coupled system. In future work, we aim to explore
378 the implications of this coupling for neurological and psychological conditions.

379
380

381 **4 Materials and Methods**

382 **4.1 Subject Information**

383
384 Resting state fMRI data from 300 subjects from the human connectome project from
385 the S500 release was used in this study. The subjects were split into three groups each
386 of 100 subjects to cross-validate the three sets of analyses, namely: (i) the group PCA-
387 ICA, (ii) seed based connectivity, and (iii) dynamic causal. The rs-fMRI data was
388 processed by the minimal preprocessing pipeline as used in the Human Connectome
389 Project (Glasser et al., 2013). A single run of the rs-fMRI dataset from each subject
390 was used in this study. For all subjects, the first run, which was acquired with a phase
391 encoding from left to right was used. Ethics approval for the HCP project and protocol
392 was granted by the local Institutional Review Board at Washington University in St.
393 Louis. Full details on the HCP data set have been published previously (Van Essen et
394 al., 2013).

395

396 **4.2 MRI data**

397
398 The rs-fMRI data was processed by the HCP minimal preprocessing pipeline (Glasser
399 et al., 2013). Briefly, for rs-fMRI datasets, motion correction was performed and the
400 12 motion parameters were regressed out of the data. Image artefacts were removed
401 using an ICA based, machine learning technique (Griffanti et al., 2014). The rs-fMRI
402 dataset was registered to the MNI space.

403

404 **4.3 Band-Specific Group PCA-ICA**

405

406 The datasets of each subject from the first group of one hundred subjects was
407 bandpassed into five bands (Gohel and Biswal, 2015) [(0.01-0.027), (0.027-0.073), (
408 0.073-0.198), (0.198-0.5), (0.5-0.69)] Hz using the 3dBandpass program from the
409 AFNI suite (Cox, 1996). The bandpassed images were smoothed using a Gaussian
410 smoothing function with a FWHM of 5mm using SUSAN (Smith and Brady, 1997).

411

412 For each band, images of all the subjects (100 subjects) were fed into melodic (Smith
413 et al., 2014). A modified version of the program from FSL version 5.0.8 was used
414 whereby multicore computations were implemented for the PCA step of the
415 algorithm. All other steps and code remained identical. The number of extracted
416 components was fixed at 15 components to ensure that complete networks and not
417 partial networks were extracted.

418

419 **4.4 Seed based connectivity**

420

421 Regions of interest were created based on the work of Andrews-Hanna and coworkers
422 (Andrews-Hanna et al., 2010) with the ICA maps of the DMN extracted from the
423 group PCA-ICA. In all, 11 regions of the DMN and the nucleus basalis of Meynert
424 were created bilaterally as spheres of 6 mm radius. Regions for the medial
425 septum/vertical limb of the diagonal band of Broca (MSDB), supra mammillary
426 nucleus (SuM), pontis nucleus oralis (PnO) and the ventral tegmental area (VTA)
427 were created with their sizes and MNI coordinates presented in Table 2.

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429 Voxel based correlation analysis was undertaken for ROIs including the PnO, SuM,
430 MS, VTA and NBM. For each subject, a time-course corresponding to each region
431 was extracted using 3dmaskSVD. Following this, the rs-fMRI datasets were detrended
432 using 3dDetrend, bandpassed using 3dBandpass to a passband of 0.01 – 0.1 Hz and
433 smoothed using a Gaussian filter with a FWHM of 5 mm using 3dBlurToFWHM.

434

435 The extracted time-courses were correlated globally with the post-processed rs-fMRI
436 data. Whole brain correlation coefficients were tested for significance via a one sided
437 test using permutation testing and threshold free cluster extent (Smith and Nichols,
438 2009; Winkler et al., 2014). Testing was performed using the randomise tool from
439 FSL and fifty thousand permutations were performed. These steps were also applied
440 to the data for the second group of one hundred subjects.

441

442 **4.5 Dynamic Causal Modelling**

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444 Time courses were extracted from the rs-fMRI volumes using the ROIs from the seed
445 based connectivity analyses above.

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447 The DCM models were constructed based on the following assumptions:

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1. The basic default mode consisted of the PCC and aMPFC connected bilaterally and reciprocally. The pIPL regions were connected unidirectionally to the PCC and aMPFC regions ipsilaterally and connected reciprocally to each other as per the results of Sharaev and coworkers (Sharaev et al., 2016).
2. The hippocampus was connected to the PCC and aMPFC unidirectionally and hemispherically.
3. The MSDB was connected to all regions reciprocally.
4. The PnO was connected to SuM unidirectionally and the SuM was connected to the medial septum unidirectionally.
5. The VTA was connected to the MSDB and to the hippocampus unidirectionally.

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Based on these assumptions, five anatomical network models were constructed. Model 1 was the base model of the DMN (assumption 1). Model 2 included the hippocampus and medial septum (assumptions 1, 2, 3). Model 3 included the theta generation aspect of the ascending synchronising system but the VTA was not connected (assumptions 1,2,3,4). Model 4 was the same as Model 3 but with direct connectivity between the PnO and MS thereby excluding the SuM. Model 5 was the same as Model 3 but included the links between the VTA and MSDB and hippocampus. The five models are shown in Figure 5.

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The models were inverted using the spectral DCM method (Friston et al., 2014) and compared to each other based on Bayesian model selection as well as in terms of explained variance.

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6 Competing Interest

The authors declare no competing interests.

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Group	Number of Subjects	Age
PCA-ICA	100 (45 M)	29.2 ± 3.4
SBC	100 (37 M)	28.8 ± 3.6
DCM	100 (46 M)	28.9 ± 3.4

Table 1. Demographic information of the HCP subjects used in the study. Age of subjects is taken at the centre of the age range of the subject from the Human Connectome Project. For subjects in the over thirty-six years age range, the age was taken to be thirty-six years.

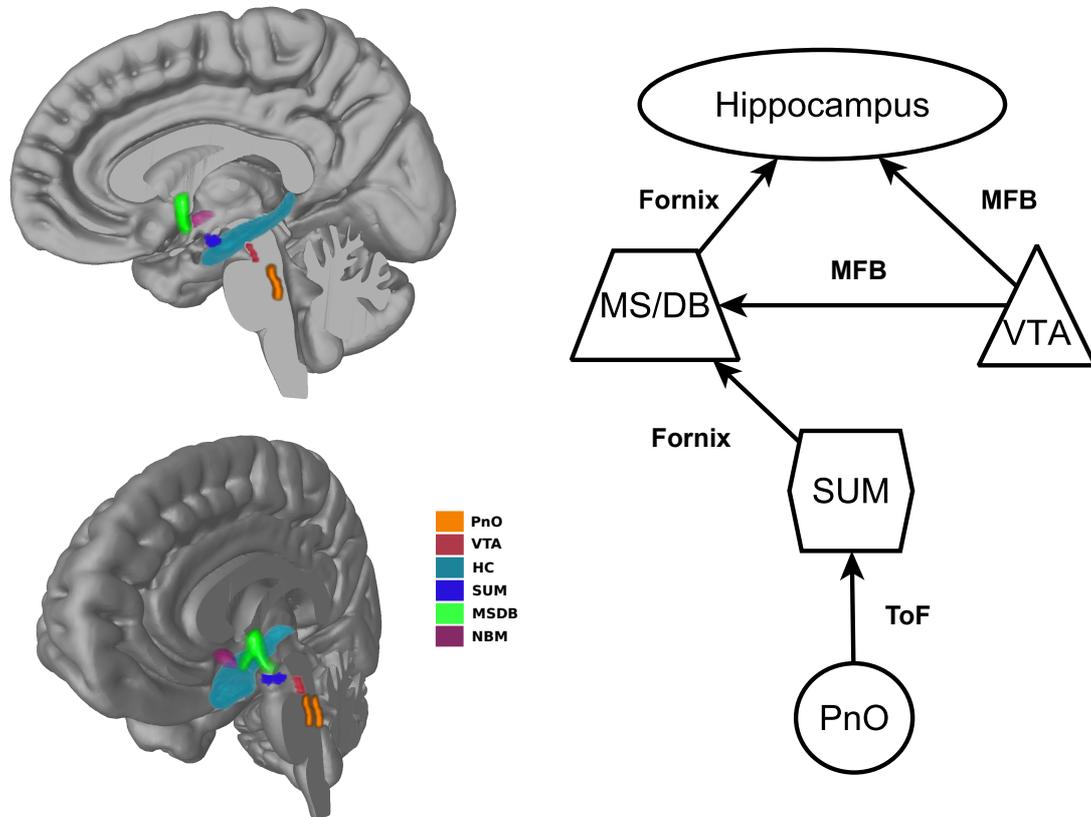


Figure 1 Simplified schematic representation of the parts of the ascending synchronising system implicated in the generation and maintenance of the theta rhythm (right panel) and 3D rendering of those structures in a canonical brain (left panels). Known fiber bundles connecting the regions are labelled on the schematic. These include the tract of Forel (ToF), the fornix and the medial forebrain bundle (MFB).

Region Name	Region Abbreviation	Size	MNI Coordinates
Posterior Cingulate Cortex	PCC	6 mm Sphere (905 mm ³)	8 -56 26
			-8 -56 26
Anterior Medial Prefrontal Cortex	aMPFC	6 mm Sphere (905 mm ³)	6 52 -2
			-6 52 -2
Posterior inferior parietal lobule	pIPL	6 mm Sphere (905 mm ³)	44 -74 32
			-44 -74 32
Medial Septum	MS	6 mm Sphere (905 mm ³)	0 8 -12
Hippocampus	HC	6 mm Sphere (905 mm ³)	26 -20 -14
			-24 -20 -16
Supra mammillary nucleus	SuM	4 mm Sphere (268 mm ³)	0 -8 -14
Ventral tegmental Area	VTA	ROI (432 mm ³)	0 -22 -20
Pontis nucleus oralis	PnO	ROI (256 mm ³)	0 -32 -22
Nucleus Basalis Mynert	NBM	6 mm Sphere (905 mm ³)	22 4 -12
			-22 4 -12

Table 2. Regions of interests used in the seed based connectivity and dynamic causal modelling, their sizes and MNI coordinates. Where bilateral ROIs were used, both left and right coordinates are provided. Spheres with a 6mm radius were used for all regions except the supra mammillary nucleus where a 4mm sphere was used to avoid signal spill over and the VTA and PnO where the ROIs were voxel masks extracted from the PCA-ICA analysis.

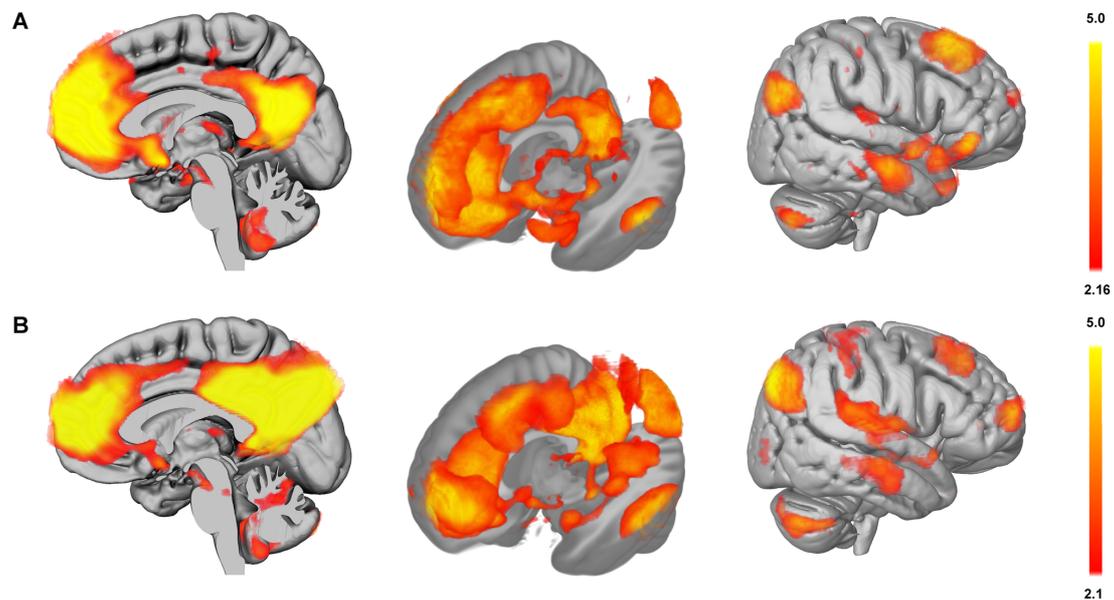


Figure 2 The default mode network as observed in Band 1 (0.01-0.027 Hz) (A) and Band 2 (0.027-0.07 Hz) (B). Overlays are thresholded z maps for the components as produced by melodic from FSL. In Band 1, the medial septum/diagonal band of Broca complex, ventral tegmental area and midline thalamus are connected to the default mode and the hippocampus. In Band 2, the medial septum/diagonal band of Broca complex, ventral tegmental area, pontine nucleus oralis and midline thalamus are connected to the default mode and the medial temporal lobe.

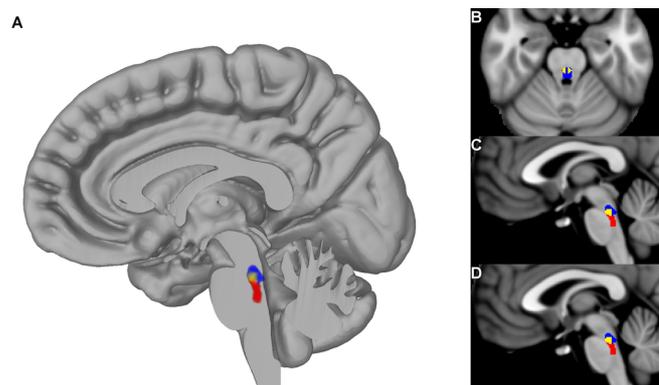


Figure 3 PnO ROI as defined from the group PCA-ICA (shown in blue), ROI from the Harvard Ascending Arousal Network (AAN) atlas (shown in red) and overlap in yellow shown in a 3D rendering (A), axial section B (MNI coordinates Z=-24), sagittal sections C (MNI coordinates X=-1) and D (MNI coordinates X=2).

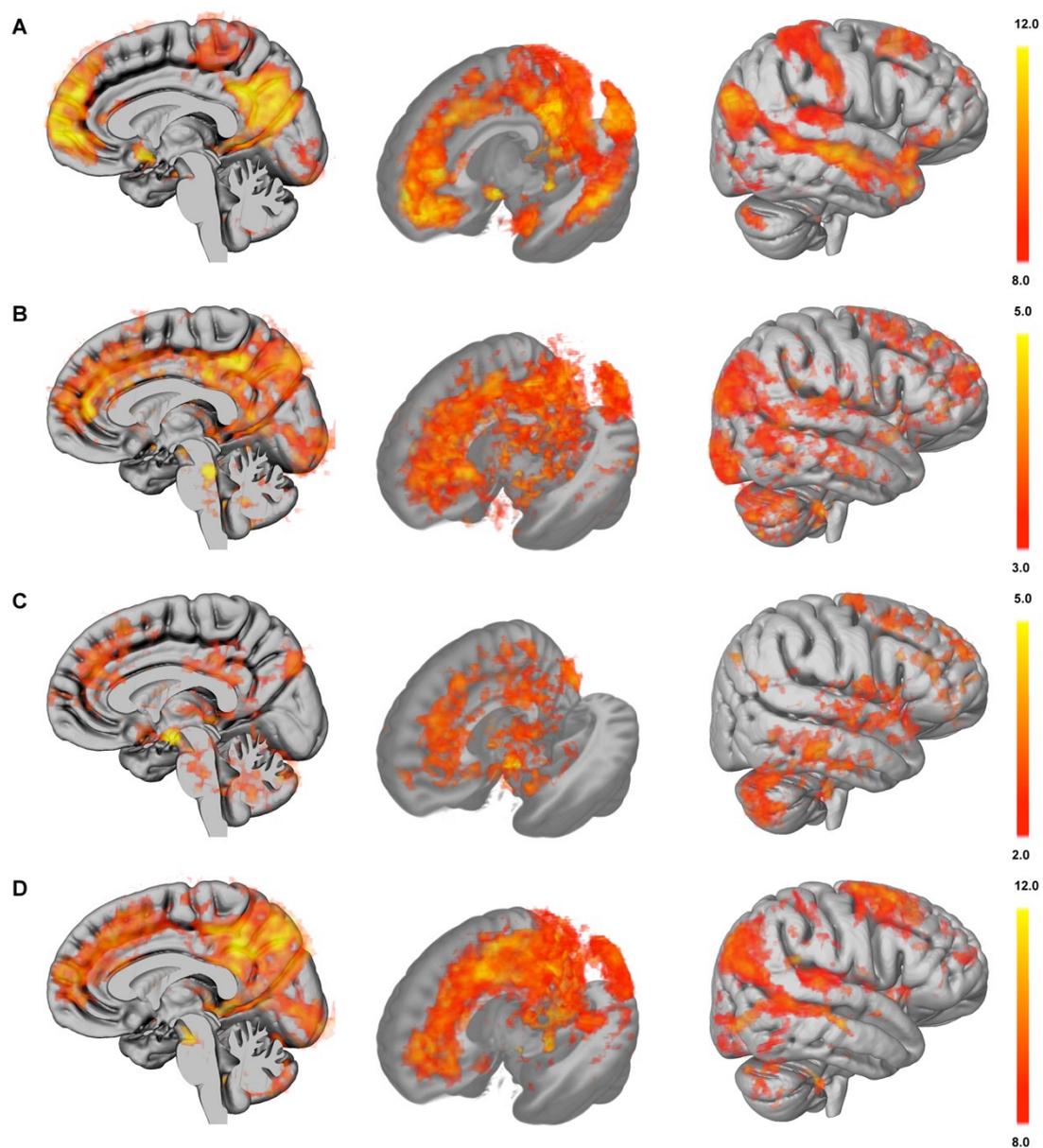


Figure 4 Seed based connectivity. T-scores are displayed for (A) MSDB, (B) PnO, (C) SuM and (D) VTA. All voxels displayed are significant at $p < 0.05$ using fsl-randomise permutation tests and threshold free cluster enhancement, however higher thresholds are used in the display to show relevant details.

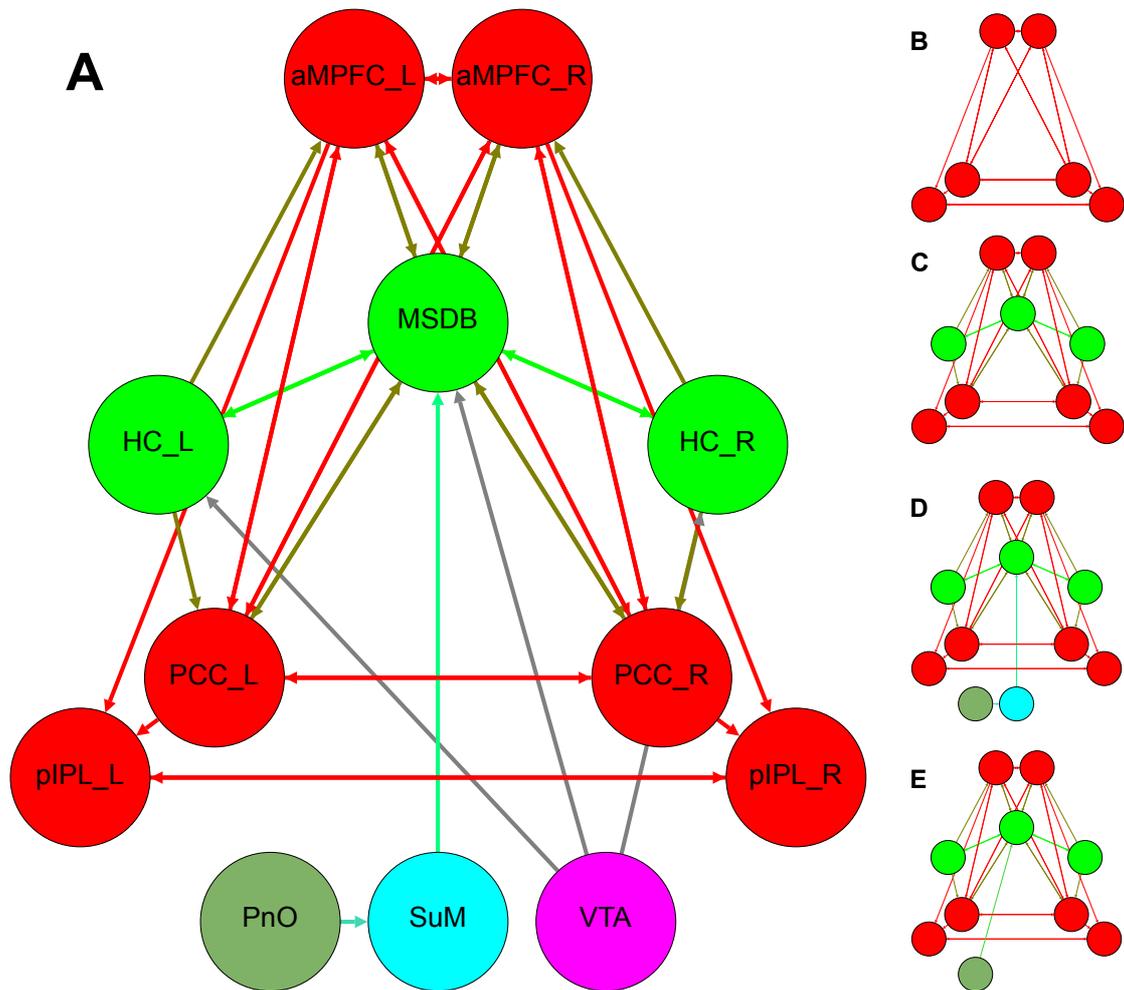
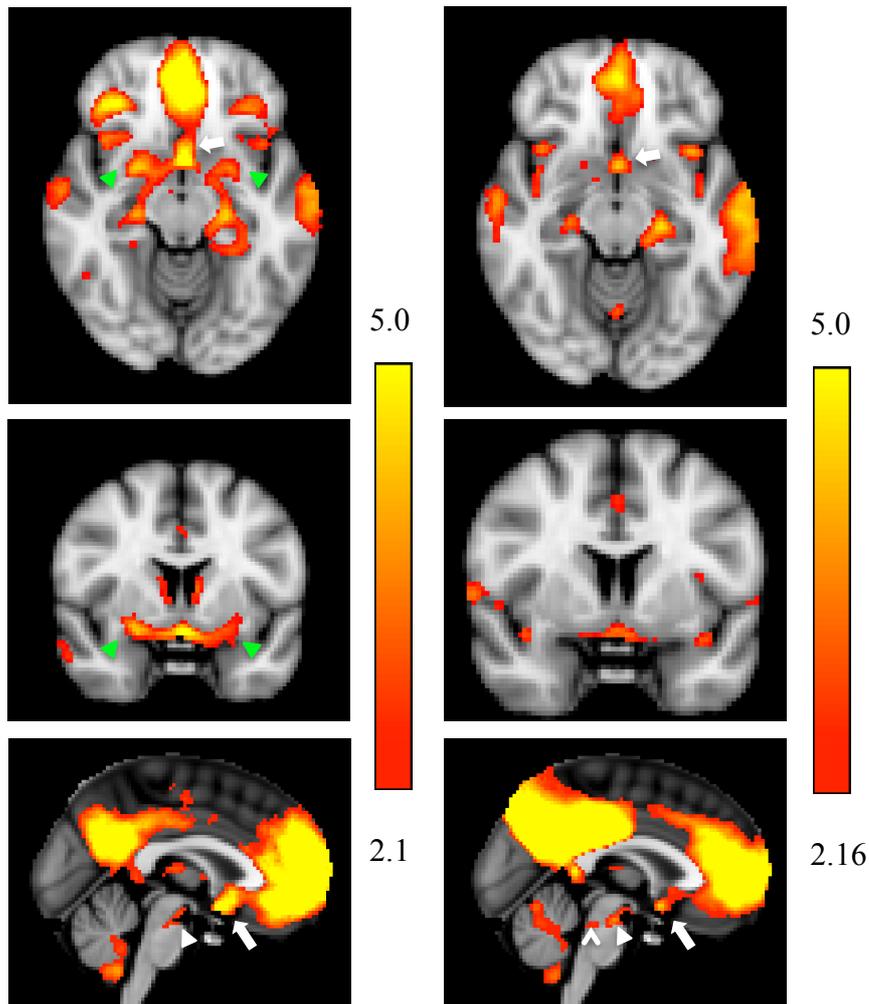
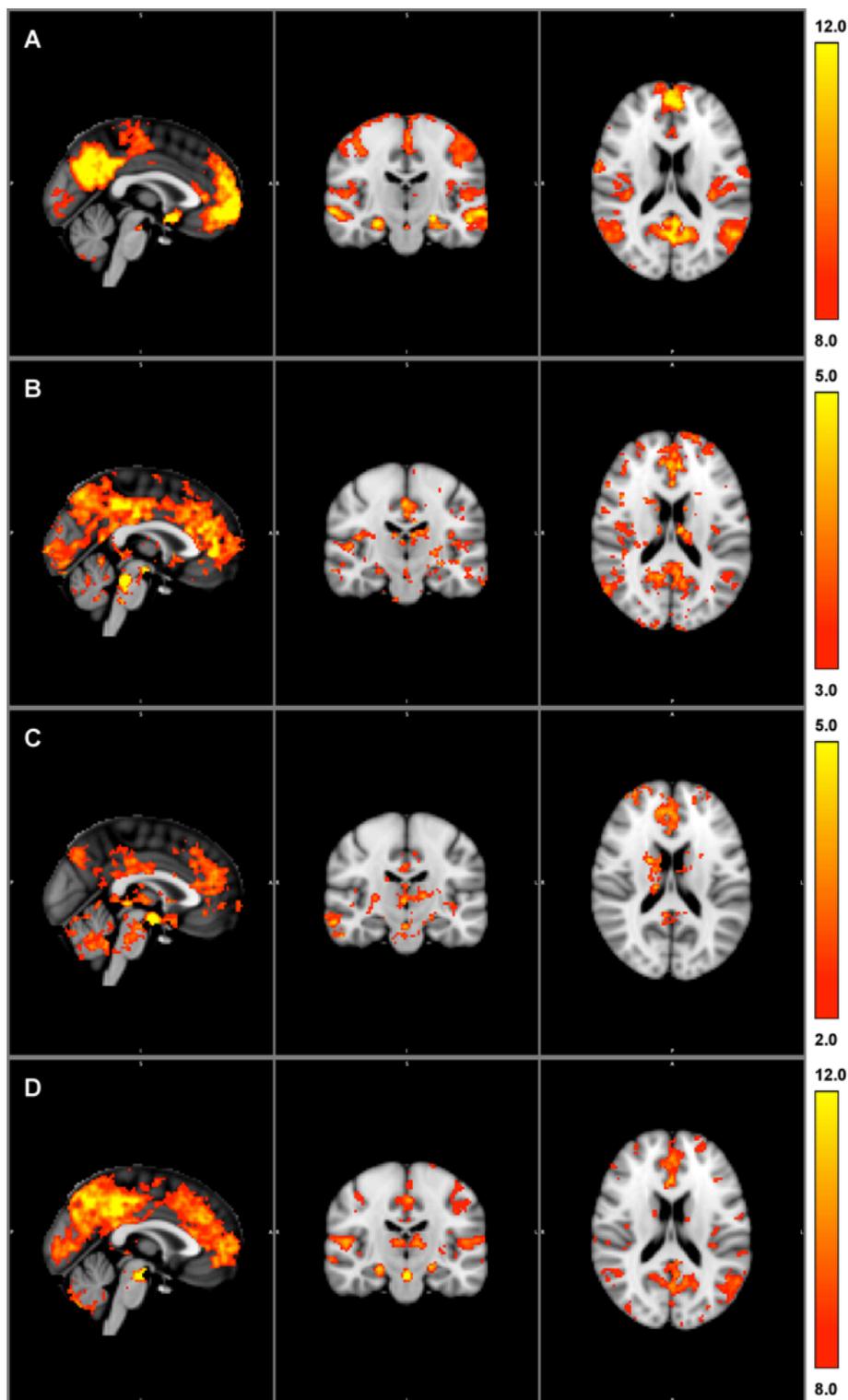


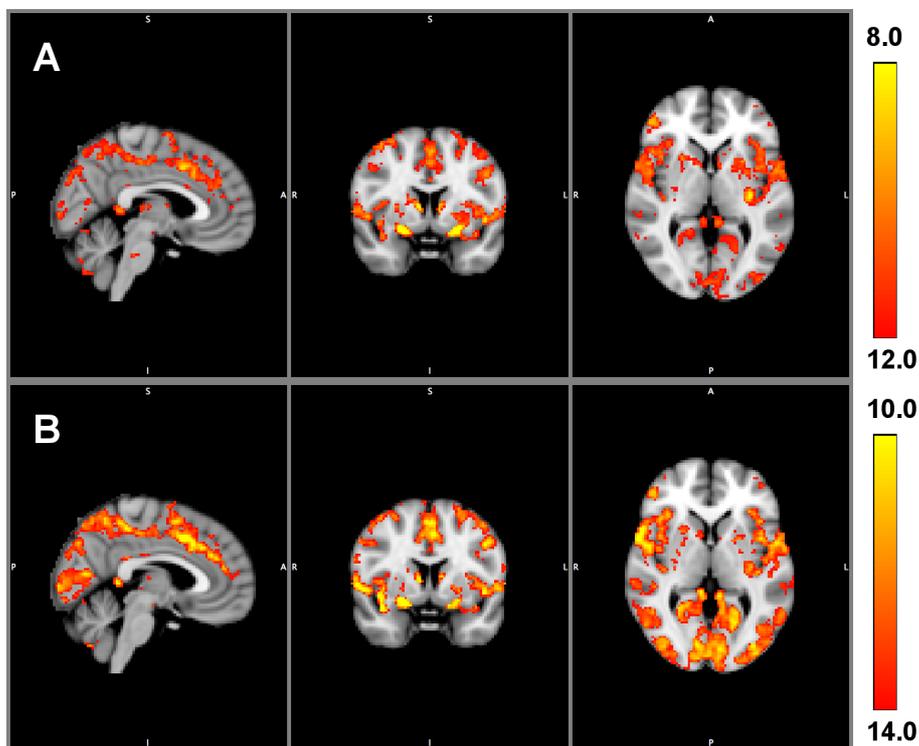
Figure 5 The models tested as part of the DCM analyses. Nodes belonging to the classical default mode are shown in red, those belonging to the limbic system are shown in green, the PnO is shown in olive, the SuM is shown in turquoise and the VTA in purple. The models are of increasingly greater complexity with Model 1 (B) including only the classic default mode (red nodes), Model 2 (C) including the DMN and limbic nodes (red + bright green nodes) and Model 3 (D) including the DMN, limbic structures and ascending synchronising system sans the VTA (red, bright green, olive and turquoise nodes). Model 4 (E) proposes a connection between the PnO and the MSDB (red, bright green, olive nodes) and Model 5 (A) includes the VTA as connected to the limbic structures.



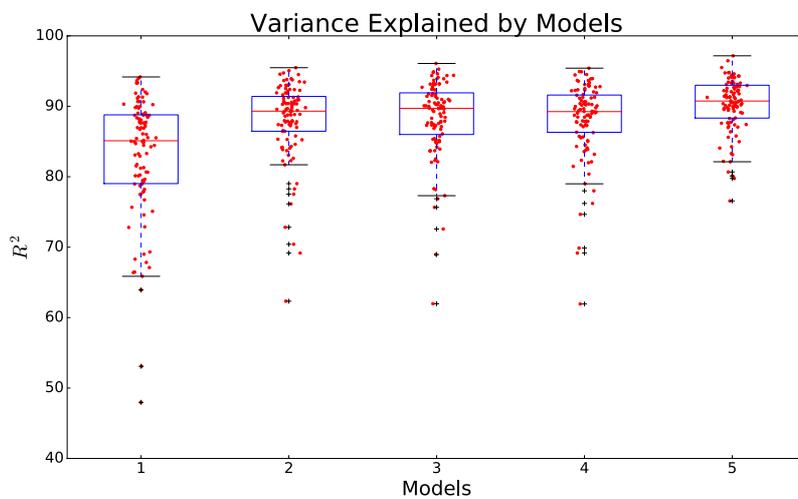
Supplementary Figure 1 Cortical and subcortical structures that are a part of the default mode at Band 1 (0.001-0.027 Hz) left column and Band 2 (0.027-0.073 Hz) right column. Axial slices ($z = -12\text{mm}$), coronal slices ($y = 4\text{mm}$) and sagittal slices ($x = 0\text{mm}$) in the MNI coordinate system illustrate known cortical regions including the hippocampus and the para-hippocampus cortex and medial regions in the thalamus but also ventral tagmental area in the midbrain (white arrowhead), the medial septum in the forebrain (white arrow), the nucleus basalis of Meynert (NBM) (green arrowheads) and the pontine nucleus oralis (PNO) (red arrowhead)



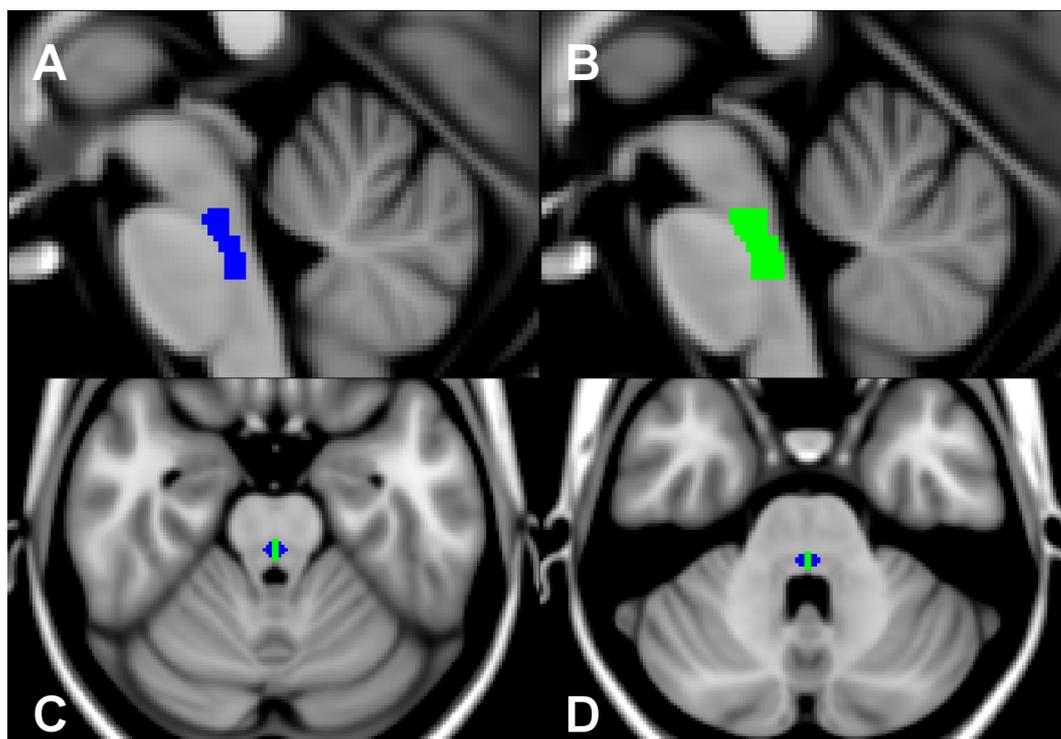
Supplementary Figure 2 Seed based connectivity profiles using the MSDB (A), PnO (B), SuM (C) and VTA (D) as seeds. Slice positions are X=0, Y=-18 and Z=18 mm in MNI coordinates. A Overlays are the t-values for significant voxels ($p < 0.05$) computed using fsl-randomise with threshold free cluster enhancement, however higher thresholds for the t-values are used in the display to show relevant details.



Supplementary Figure 3 Seed based connectivity profiles using the Basal forebrain Left (A) and Right (B) as seeds. Overlays are the corrected t-values computed using randomise with threshold free cluster enhancement. All voxels displayed are significant at $p < 0.05$ using fsl-randomise permutation tests and threshold free cluster enhancement, however higher thresholds are used in the display to show relevant details. Slice positions are X=4, Y= 4 and Z = 2 mm in MNI coordinates.



Supplementary Figure 4 Boxplots of the explained variance for the DCM analyses. Model 1 is the basic DMN including PCC, aMPFC and pIPL. Model 2 includes basic DMN and MS + HC. Model 3 includes basic DMN, MS, HC, SuM and PnO. Model 4 includes basic DMN, MS, HC and PnO. Model 5 is the complete model.



Supplementary Figure 5 Serial sagittal sections ((A) $x=2$ (B) $x=1$) through the MNI single subject template showing the relative positions of the PnO (blue) and MRN (green) as delineated in the Harvard AAN atlas. Axial sections ((C) $z=-32$ and (D) $z=-24$) show the encapsulation of the MRN by PnO.