Differential medial temporal lobe and default-mode network functional
connectivity and morphometric changes in Alzheimer's Disease

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11   **Abstract**

We report group level differential detection of medial temporal lobe resting-state functional

connectivity disruption and morphometric changes in the transition from cognitively normal

to early mild cognitive impairment in an age-, education- and gender-matched 105 subjects

Alzheimer's Disease Neuroimaging Initiative dataset. In mild Alzheimer's Disease, but not

early mild cognitive impairment, characteristic brain atrophy was detected in FreeSurfer

estimates of cortical thickness and subcortical and hippocampal subfield volumes. By

contrast, functional connectivity analysis detected earlier significant changes. In early mild

cognitive impairment these changes involved medial temporal lobe regions of

transentorhinal, perirhinal and entorhinal cortices (associated with the earliest stages of

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content/uploads/how_to_apply/ADNI_Acknowledgement_List.pdf.

neurofibrillary changes in Alzheimer's Disease), hippocampus, parahippocampal gyrus and

temporal pole, and cortical regions comprising or co-activated with the default-mode

network, including rostral and medial prefrontal cortex, anterior cingulate cortex,

precuneus and inferior temporal cortex. Key findings include: a) focal and bilaterally

symmetric spatial organization of affected medial temporal lobe regions; b) mutual

hyperconnectivity bilaterally involving ventral medial temporal lobe structures (temporal

pole, uncus); and c) dorsal medial temporal lobe hypoconnectivity with anterior and

posterior midline default-mode network nodes. These findings position medial temporal lobe

resting state functional connectivity as a candidate biomarker of an Alzheimer's Disease

pathophysiological cascade, potentially in advance of clinical biomarkers, and coincident

with biomarkers of the earliest stages of Alzheimer's neuropathology. Our results indicate

that medial temporal lobe resting-state functional connectivity should be further investigated

as a potential biomarker in the diagnosis of Alzheimer's Disease.

Highlights

- Functional connectivity change seen before structural change in Alzheimer's Disease

- Medial temporal lobes mutually hyper-connect in mild cognitive impairment

- Medial temporal lobe and default mode network decouple in mild cognitive impairment

- Loci of functional change in hippocampi are focal with bilaterally symmetric features

- Nonmonotonic functional connectivity changes in Alzheimer's Disease progression

Keywords: hippocampus; medial temporal lobe; hyperconnectivity; hypoconnectivity

Abbreviations: ADNI = Alzheimer's Disease Neuroimaging Initiative; CA = cornu ammonis;

CDR = clinical dementia rating; CDRSB = clinical dementia rating, sum of boxes; CDT = cluster

determination threshold; CN= cognitively normal; CSF = cerebrospinal fluid; D = dementia;

DMN = default-mode network; EPI = echo-planar image; FWHM = full width half maximum;

ICA = independent components analysis; ICV = intra-cranial volume; MCI = mild cognitive

impairment; MMSE = mini-mental state examination; MTL = medial temporal lobe; PCC =

posterior cingulate cortex; PHG = parahippocampal gyrus; rsfMRI = resting-state functional

MRI; ROI = region of interest;

Running Title: Alzheimer's Disease medial temporal lobe functional connectivity and

morphometric changes

56   1. Introduction

In late-onset Alzheimer's Disease, neuropathologies may cumulate for decades before possible

though not inevitable clinical manifestation. Diagnostic guidelines (Albert, 2011; Jack, 2011a;

McKhann, 2011; Sperling, 2011) and a research framework (Jack, et al., 2018) for cognitively

normal (CN), mild cognitive impairment (MCI), and Alzheimer's Disease individuals, consider

multiple neuroimaging modalities including amyloid β and tau tracers, markers of metabolic

activity (FDG PET), and morphometry (MRI). An hypothesized Alzheimer's Disease

pathophysiological cascade links these neuroimaging modalities together with cerebrospinal

fluid (CSF) markers for amyloid β and tau to the Alzheimer's Disease clinical progression (Jack,

2011b, 2013).

The hypothesis tested in this investigation was that functional connectivity disruption can be

detected in the early MCI group. Disruption of functional connectivity in Alzheimer's Disease

has been observed in the default-mode network and other resting-state networks in resting-state

functional MRI (rsfMRI) (Greicius, et al., 2004; Buckner, et al., 2005; Sorg, et al., 2007;

Sperling, et al., 2010; Zhou, et al., 2010; Jones, et al., 2011; Jones, et al., 2012, 2016; Brier, et

al., 2012; Ward, et al., 2014; Cai, et al., 2015; Dillen, et al., 2017). However, such observations

have not broadly impacted clinical practice (Woo, et al., 2017).

The purpose of the present study is thus to compare functional biomarkers using functional

connectivity analysis of resting-state fMRI, with structural imaging biomarkers serving as a

reference baseline. The experimental design is a group-level analysis of an Alzheimer's Disease

Neuroimaging Initiative (ADNI) population containing clinically-defined cognitively normal,

early MCI and mild Alzheimer's dementia subgroups. We observed cortical thinning,

subcortical volume loss, and whole hippocampal and hippocampal subfield volume loss, in the

mild Alzheimer's Disease subgroup, but not in the early MCI group. A group-level pairwise

region of interest (ROI) analysis was used to assess functional connectivity changes. *A priori*,

the first element in each ROI pair (the "anchor ROI") was in the medial temporal lobe (MTL)

identified by a method described below. The reason to anchor each ROI pair in the MTL was

that it is in the MTL perirhinal cortex (Brodmann Areas 35 and 36) and, specifically, the

transentorhinal region (Brodmann Area 35) that the neurofibrillary changes associated with

Alzheimer's Disease start and then, in a progression with disease stages, appear in entorhinal

cortex (Brodmann Area 28), hippocampus and temporal cortex, association cortices, and

ultimately primary sensory cortices (Braak and Braak, 1985, 1991). The ROI position of the

second element in each identified ROI pair was determined in a data-driven method described

below. The combination of *a priori* and data-driven approach directly linked functional

connectivity analysis to focal regions of earliest neuropathology in Alzheimer's Disease.

We report evidence that functional connectivity changes occur in the CN to early MCI transition

in the absence of structural imaging findings. The progression of observed CN to MCI

functional connectivity changes was further evaluated by comparing the mild Alzheimer's

Disease and CN groups. We conclude that rsfMRI functional connectivity analysis of MTL may

provide a complementary approach to established neuroimaging and other biomarkers within a

model of Alzheimer's Disease pathophysiology (Jack, 2013) and an Alzheimer's Disease

research framework (Jack, et al., 2018).

2. Materials and Methods

Data used in the preparation of this report were obtained from the Alzheimer's Disease

Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu). The ADNI project was launched

in 2003 as a public-private partnership, led by Principal Investigator Michael Weiner, MD. The

primary goal of ADNI has been to test whether serial magnetic resonance imaging, positron

emission tomography, other biological markers, and clinical and neuropsychological assessment

can be combined to measure the progression of mild cognitive impairment and early Alzheimer's

Disease.

2.1. Participants

The participants in this report were a subset of the ADNI 2 experimental sub-study on resting

state fMRI functional connectivity (rsfMRI) (Jack, et al., 2008; Weiner, et al., 2015). The ADNI

2 rsfMRI studies available for download on the Laboratory of Neuro Imaging (LONI) website in

September 2016 consisted of 886 scan pairs (structural MRI, rsfMRI) from 220 participants. We

subjected scans to a rigorous multistage preprocessing and quality assurance procedure described

in further detail below and summarized in Supplemental Figure 1. The procedure yielded a 105

participants cross-sectional study dataset.

Table 1 summarizes participant demographics and metadata. Participants were assigned to one

of three clinical categories: CN; early MCI; and mild Alzheimer's Disease. Clinical assignments

adhered to ADNI 2 protocols (publicly available on the adni.loni.usc.edu website). The three

clinical groups were balanced for age (*P = 0.56*), education (*P = 0.95*) and gender (*P = 0.22*).

The effect of clinical group was significant for Clinical Dementia Rating (CDR) (*P < 0.001*),

Clinical Dementia Rating Sum-of-Boxes (CDR-SB) (*P < 0.001*), Mini-Mental State

Examination (MMSE) (*P < 0.001*), and APOEε4 (*P = 0.007*).

Table 1. Study participant demographics and metadata.

	CN n = 32	MCI n = 39	AD n = 34	P value
Age (Mean, SD)	74.2 (5.5)	72.5 (6.8)	73.4 (7.2)	0.56[b]
Female (n, %)	18 (56)	22 (56)	13 (38)	0.22[a]
Education (Mean, SD)	16 (2.2)	16 (2.5)	17 (2.6)	0.95[b]
CDR (Median, Min, Max)	0 (0, 0)	0.5 (0.5, 0.5)	0.5 (0.5, 1.0)	<0.001[b]
CDR-SB (Median, Min, Max)	0 (0, 0)	1.0 (0.5, 3.0)	2.5 (0.5, 7.0)	<0.001[b]
MMSE (Median, Min, Max)	29.5 (27, 30)	29 (27, 30)	25 (20, 26)	<0.001[b]
APOEε4=2 (n, %)	1 (3)	4 (10)	9 (26)	0.007[a]

[a](Chi-square test); [b](ANOVA);
AD = Alzheimer's Disease; CDR = clinical dementia rating; CDR-SB = clinical dementia rating sum-of-boxes,
CN = cognitively normal; MCI = mild cognitive impairment; MMSE = mini-mental state examination; SD =
standard deviation;

2.2. Image acquisition

The present analysis focuses on two of the up to eight scans obtained during a typical ADNI 2

subject visit. These are the high-resolution T_1-weighted 3D whole brain structural scan (Scan #2

in the protocol) and the resting state functional scan (Scan #4 in the protocol). Structural and

rsfMRI scans were acquired with 3T MRI scanners of a single manufacturer (Philips Medical

Systems: Achieva, Ingenia, Ingenuity, Intera) from 14 unique sites in two configurations

(MULTI-COIL; SENSE-HEAD), and fifteen (15) different software versions (3.2.1 or higher).

Structural scans were acquired with a T_1-weighted sagittal magnetization-prepared rapid gradient

echo (MP-RAGE) sequence, with 1.2 mm right/left, 1.0 mm anterior/posterior and 1.0 mm

superior/inferior resolution. RsfMRI scans were acquired with a T_2-weighted gradient echo

planar imaging sequence with repetition time/echo time, 3000/30, flip angle, 80º, 48 axial slices,

and 64 x 64 in-plane matrix yielding an isotropic 3.3 mm voxel size. Phase-directions varied:

anterior-posterior, N = 16; posterior-anterior, N = 86; missing values = 4. Only two temporal

slice order sequences were included in this study dataset: a) ascending 48 planes (odd, even),

N=98; and b) descending 48 planes (even, odd), N=7. RsfMRI scans were of two durations: a)

140 TRs ("resting state", N=91); and b) 200 TRs ("extended resting state", N=14). Additional

image acquisition protocol details can be found on the public adni.loni.usc.edu website.

2.3. Image processing

Structural images and rsfMRI images were downloaded from LONI either in DICOM format

(and locally converted using dcm2nii) or in 4DNIfTI format (DICOM to NIfTI conversion

performed by LONI). Preprocessing and data analysis were performed using a combination of

FreeSurfer (Dale, et al., 1999), Analysis of Functional Neuroimages (AFNI) (Cox, 1996), and

"home-grown" analysis implemented in R and *tcsh* shell scripts. The AFNI Version was

AFNI_17.1.03 (2-May-2017). The FreeSurfer version was V6.0 run in the Amazon Cloud on

Ubuntu 14.04. The R version was Version 3.4.3 (30-Nov-2017). The AFNI Python script

uber_subject.py was used to generate a preprocessing shell script which was manually edited.

Structural image analysis with FreeSurfer 6.0

Subcortical and hippocampal subfield segmentation, and cortical parcellation (surface area,

thickness and volume) were obtained with FreeSurfer Version 6.0 image analysis suite, which is

documented and freely available for download online (http://surfer.nmr.mgh.harvard.edu/) (Dale,

et al., 1999). FreeSurfer default settings were applied via the "recon-all" command.

Functional MRI analysis with AFNI

The rsfMRI echo-planar image (EPI) preprocessing sequence consisted of the following steps

using AFNI: a) alignment of EPI centers to a standard atlas (MNI_avg152T1); b) elimination of

the first ten (10) EPIs; c) outlier detection and de-spiking; d) application of time-shift correction;

e) alignment to the least motion distorted volume; f) alignment to the anatomical image and warp

to a standard space (MNI_avg152T1); g) generation of anatomical and EPI masks; h) application

of spatial smoothing (FWHM = 4.0mm); i) scaling voxel time series to a mean of 100; j)

generation of demeaned motion parameters and motion parameter derivatives; k) generation of

motion "censor" masks (motion limit = 0.3); l) generation of ventricle (Vent) and white-matter

(We) segmentation masks from FreeSurfer segmentation and parcellation results; and m)

deconvolution with 12 regressors (6 regressors + 6 motion derivatives). The process yielded a

4D residual error volume that served as input to the next stage of volumetric and correlation

analysis. Global signal regression (GSR) was not performed. Bandpass filtering was performed

in the final ROI pairwise analysis stage as discussed below.

Table 2 lists pre-processing stage group-level statistical summaries obtained from AFNI

@ss_review_basic. There were no significant differences between groups for average censored

motion, maximum censored motion and the average fraction of TR frames censored for excess

motion. Group average temporal signal-to-noise values were in excess of 170 with standard

deviation in the range 16-19, indicating good overall input EPI signal levels. The values did not

differ significantly across groups. Finally, the group average Dice coefficient, which measures

the extent of overlap between the anatomical and EPI brain masks, was in excess of 0.88 with

standard deviation in the range, 0.012-0.015, indicating good overall anatomical – EPI

alignment. The values did not differ significantly across groups.

177   **Table 2.** Group-average pre-processing statistics.

	CN n = 32	MCI n = 39	AD n = 34	P value[a]
Avg. Censored Motion (Mean, SD)	0.095 (0.02)	0.091 (0.02)	0.091 (0.02)	0.63
Max. Censored Motion (Mean, SD)	0.473 (0.11)	0.508 (0.13)	0.506 (0.14)	0.46
Censor Fraction (Mean, SD)	0.09 (0.06)	0.08 (0.06)	0.10 (0.07)	0.56
Avg. TSNR (Mean, SD)	179 (16)	178 (19)	180 (16)	0.85
Global Correlation (Mean, SD)	0.022 (0.01)	0.022 (0.01))	0.023 (0.01)	0.91
Dice Coefficient (Mean, SD)	0.888 (0.01)	0.891 (0.02)	0.890 (0.01)	0.69
[a](ANOVA); AD = Alzheimer's Disease; CDR = clinical dementia rating; CDR-SB = clinical dementia rating sum-of-boxes, CN = cognitively normal; MCI = mild cognitive impairment; SD = standard deviation; TSNR = temporal signal-to-noise.				

2.4. Image quality assurance

The initial database consisted of 886 rsfMRI scans (and their paired structural images) from 220

subjects. An R package "ADNIMERGE" contained MRI and rsfMRI quality assessments (e.g.,

comments by ADNI quality reviewers) and related data (e.g., rsfMRI slice order) stored in the

tables "mayoadirl_mri_imageqc" and "mayoadirl_mri_fmri", respectively. The 886-scan set was

reduced to 673 scans (n=196) by rejecting all scans that did not conform to the slice order

sequences listed above, or failed visual inspection in the FSL viewer, or contained any reviewer

comment in either of the available pair of comment fields. Comments typically referenced

motion or clinical findings.

The rsfMRI EPI preprocessing sequence, with motion-limit set to 0.3, was applied to each of the

673 structural-rsfMRI pairs. The global signal was analyzed as an initial screen for excessive

motion. Scans were rejected if the global average time-series amplitude value fell outside the

range 96-104 or if the standard deviation of the global average time series exceeded 2.0. This

gross motion screening procedure reduced the analysis database to 507 structural-rsfMRI pairs

(n=190 subjects).

The 507 scan pairs database was further screened using statistics generated by the AFNI-based

preprocessing pipeline. Scans were marked for rejection according to the following criteria: a)

DICE coefficient < 0.78; b) censor fraction > 0.21; c) maximum censored displacement > 1.00;

d) average TSNR > 400 or average TSNR < 100; e) degrees of freedom left < 100; and f) global

correlation < 0.10. 206 scan pairs from 106 subjects met these quality assurance criteria. Where

multiple candidate scan pairs were present for a given subject, the latest available pair was

selected. 80% of the final dataset consisted of scans obtained from subjects who were on at least

their second ADNI 2 study visit. The final study database consisted of 105 structural-functional

scan pairs from 105 subjects. ANOVA confirmed that preprocessing quality measures were

matchead across the three diagnostic groups. See Table 2.

2.5. ROI seed and ROI pairs of interest identification

ROI seeds for ROI pairwise functional connectivity analysis were identified by an hybrid *a*

priori data-driven method. The procedure was applied independently in left and right

hemispheres. To bootstrap the ROI seed selection procedure, FreeSurfer subcortical

segmentations were used to define the global 3D bounding box for the hippocampus and MTL.

A grid of 6mm-spaced coordinates within the bounding box formed the input candidate ROI seed

pool. Input candidate seeds were retained subject to the conditions that the mask for a 6mm

radius spatial sample (33 voxels) centered on the ROI seed was 100% contained within the

global anatomical brain mask, and not greater than 50% overlap with either of the global

ventricle or global white matter masks obtained during pre-processing. The qualifying set of

6mm radius input ROI masks were summed (AFNI *3dMask*) and visually inspected

(Supplemental Figure 2). For each subject and for each input ROI mask, the average time series

was computed and retained using AFNI *3dmaskave*.

To obtain candidate ROI pairs for analysis, we performed for each input candidate ROI the

following group-level procedure. First, the average time series computed and stored in the

preceding step, was used to compute the Fisher z-transformed Pearson correlation coefficient

with every other voxel in the subject 4D image (AFNI *3dfim+*). Computation was restricted to

those voxels contained within the global brain mask generated during AFNI baseline

processing). Second, a group-level, one-way, three-factor (CN, MCI, Dementia) 3D ANOVA

(AFNI *3dAnova*) was conducted and the 3D volume of F statistics was retained. Third, a 3D

cluster analysis (AFNI *3dclust*) was performed on the F statistic 3D volume and for each

qualifying cluster a candidate ROI mask of a 6mm spatial sample located at the cluster center of

mass was retained. Qualifying clusters were those with threshold F-statistic ($F \geq 3.086$; $p \leq 0.05$,

uncorrected) and minimum cluster size ($N_C = 20$). These parameters were permissive by design.

Fourth, only those candidate ROIs were retained for which the mask was 100% contained within

the global brain mask (not including the brainstem and cerebellum) and did not have greater than

50% overlap with either the global ventricle or global white matter masks. Fifth, qualifying

candidate ROI masks were visually inspected. Sixth, the ROI seed list was pruned to retain only

those MTL ROI seeds (the anchor ROIs in ROI pairs of interest) that generated candidate ROIs

through the F-statistical map analysis. Finally, individual subject average time series for the

final F-statistic map-driven ROI masks were computed and stored.

The above ROI identification procedure yielded ROI "pairs of interest" in which the anchor

element in each ROI pair was a left (right) hemisphere MTL ROI. The second element (non-

anchor) in each ROI pair was the corresponding F-statistic map-driven ROI whose position was

determined by the data. For example, in an ROI pair of interest whose anchor element was in

left MTL, the position of the second ROI could lie in ipsilateral or contralateral hemisphere,

including MTL. For the left hemisphere, 22 MTL ROI seeds formed the anchor MTL element in

50 ROI pairs of interest (see Supplemental Figure 3). For the right hemisphere, 38 MTL ROI

seeds formed the anchor MTL element in 82 ROI pairs of interest (see Supplemental Figure 4).

A cluster analysis (AFNI *3dclust*) of the sum of non-anchor ROI masks showed that they

comprised a restricted subset of brain regions. For left hemisphere, there were 31 clusters with a

maximum of three ROI masks in overlapping anatomical positions. For right hemisphere, there

were also 31 clusters with a maximum of five ROI masks in overlapping anatomical positions.

Findings in the present study described in detail below are with respect to these anchor MTL and

non-anchor ROI pairs of interest.

2.6. ROI time series quality assurance

Individual ROI residual time series were band-pass filtered (4th order Butterworth, $f = \{0.01,$

$0.1\}$) and averaged, and a subjected to a final quality assurance check for outliers. The 3rd-130th

(of the original 140 or 200 TRs) time series elements were retained as the candidate final ROI

time series. A subject ROI time series was excluded from group-level analysis if any of the

following conditions were true: a) the time series was constant; b) the time series standard

deviation, $\sigma > 20.0$; or c) the fraction of time points with values greater than the outlier threshold

θ exceeded 5%. The outlier threshold was set as $\theta = \mu + 3\sigma$, where μ was the time series average

value.

2.7. ROI pairwise correlation analysis

ROI pairs were subjected to group-level correlation analysis and ANOVA. The core statistical

method was one-way, three-factor (clinical group) ANOVA, with *post hoc t* tests applied

pairwise (between factors) only for significant ANOVA tests. Correction for large-scale

multiple testing was implemented through False Detection Rate (FDR) correction (Benjamini &

Hochberg, 1995) and permutation repeated measures (N = 5000) (Nichols and Holmes, 2002;

Efron, 2010; Eklund, et al., 2016).

2.8. Assignment of anatomical position to an ROI coordinate

ROI seed coordinates were mapped to anatomical locations by analyzing the output of the AFNI

whereami output. The AFNI *whereami* tool maps an input coordinate to anatomical position

with respect to a multiplicity of atlases. To assign an anatomical label we used the "Focus

Point", and "Within 2mm" or "Within 4mm" outputs from the Talairach-Tournoux, MNI (Macro

Labels, N27), and MNI (Cytoarchitectonic Max Probability Maps) and checked for consistency.

Results were visually confirmed.

3. Results

3.1. Cortical thinning in group-level AD-CN and AD-MCI contrasts, but not in the MCI-CN

contrast

The effect of clinical category on cortical thinning was evaluated using one-way, three-factor

ANOVA on estimates of cortical thickness from 34 cortical regions per hemisphere (68 total)

(Supplemental Table 1; Supplemental Figure 5). An FDR corrected (*q=0.1, N=68 tests*)

ANOVA F statistic critical *p* value threshold, $p_F^* = 0.032$, identified 23 significant tests. For

significant ANOVA tests only, *post hoc* pairwise *t* tests were computed and FDR-corrected

(*q=0.1, N=23 tests*) per contrast and gave critical *p* value thresholds: MCI-CN ($p_{MCI,CN}^*$=0.006);

AD-CN ($p_{D,CN}^*$=0.037); and AD-MCI ($p_{D,MCI}^*$=0.022). There were twenty-one significant AD-

MCI comparisons and fifteen significant AD-CN comparisons. Effect sizes, measured by

Cohen's *d*, were in the range $0.6 \leq d \leq 1.0$. There were two significant positive MCI-CN

comparisons (left and right paracentral lobule). All AD-MCI and AD-CN contrasts were

negative. There were no significant negative MCI-CN comparisons.

3.2. Subcortical volume changes in group-level AD-CN and AD-MCI contrasts, but not in the

MCI CN contrast

The effect of clinical category on subcortical volumes was evaluated using one-way, three-factor

ANOVA on estimates of subcortical volumes from 8 cortical regions per hemisphere (16 total)

(Supplemental Table 2; Supplemental Figure 5). An FDR-corrected (*q=0.1, N=16 tests*) one-

way three-factor ANOVA F statistic *p* value, $p_F^* = 0.012$, identified eight significant tests. For

the significant ANOVA tests only, *post hoc* pairwise *t* tests were computed and FDR-corrected

(q=0.1, *N=8 tests*) per contrast: AD-CN ($p^*_{D,CN}$ = 0.004); and AD-MCI ($p^*_{D,MCI}$ = 0.031). There

were eight significant AD-CN contrasts; and six significant AD-MCI contrasts. Cohen's *d*

values were in the range $0.3 \le d \le 1.1$. All significant pairwise comparisons for ventricles (e.g.,

inferior lateral ventricle) were positive and all significant pairwise contrasts for subcortical

structures (e.g., whole hippocampus) were negative. With an FDR rate $q = 0.1$, by design set to

be liberal, no *p* value fell below the FDR-corrected value (*N=8 tests*) in the MCI-CN contrast,

which indicated no significant MCI-CN comparisons.

3.3. Hippocampal subfield volume reduction in group-level AD-CN and AD-MCI contrasts,

but not the MCI-CN contrast

Hippocampal subfields (11 per hemisphere) were analyzed similarly as above and all twenty-two

ANOVA tests were significant, FDR corrected p value (*q=0.1, N=22 tests*), p^*_F = 0.032

(Supplemental Table 3). *Post hoc* pairwise *t* tests detected twenty-two significant AD-CN

comparisons ($p^*_{D,CN}$ = *0.029, N=22 tests*), and eighteen significant AD-MCI comparisons ($p^*_{D,MCI}$

= *0.077, N=22 tests*). Effect sizes, measured as Cohen's *d*, were at least "strong" and above,

with left hemisphere effect scores uniformly higher than the right hemisphere (left: $0.9 \le d \le 1.1$;

right: $0.7 \le d \le 0.86$). All significant AD-MCI and AD-CN hippocampal sub-field pairwise

contrasts were negative. For the MCI-CN contrast no *p* value was below the FDR-corrected

value (*q=0.1, N=22 tests*).

3.4. Significant pairwise ROI functional connectivity changes in the MCI-CN group-level

contrast

The effect of clinical category on group average ROI pairwise functional connectivity was

evaluated using one-way, three-factor ANOVA in separate analyses for the left hemisphere (50

ROI pairs of interest comprising 50 hypotheses, or simultaneous tests) and for the right

hemisphere (82 ROI pairs of interest comprising 82 simultaneous tests). For the left hemisphere,

an FDR-corrected (q=0.05, N=50 tests) ANOVA F statistic critical p value threshold, p_F^* =

0.026, identified 28 significant tests (Supplemental Table 4). For the significant ANOVA tests

only, *post hoc* pairwise *t* tests were computed and FDR-corrected (q=0.05, N=28 tests)

independently per contrast: MCI-CN ($p_{MCI,CN}^*$ = 0.0168); AD-CN ($p_{D,CN}^*$ = 0.0214); and AD-

MCI ($p_{D,MCI}^*$ = 0.0364). Of the 28 significant ANOVA comparisons, there were ten significant

post hoc MCI-CN *t* test comparisons (*post hoc* pairwise *t* test $p < p_{MCI,CN}^*$). Results are

summarized in Table 3. Six of the ten MCI-CN comparisons were positive (indicating

hyperconnectivity) with Cohen's effect size d, $0.52 \le d \le 0.92$. Four of the ten were negative

(indicating hypoconnectivity) with Cohen's d, $0.52 \le d \le 0.79$.

Table 3. Left MTL ROI - ROI pairwise significant MCI - CN comparisons[4].

Anatomical Region(s)		ANOVA (1-way, 3-levels) FDR p^*=0.026, q=0.05, n=50			Group Average Fisher Z Value			MCI-CN FDR p^*=0.0168		AD-CN FDR p^*=0.0214		AD-MCI FDR p^*=0.0364	
MTL ROI	ROI	F	p	p*	CN	MCI	AD	p	d	p	d	p	d
ROI pair hyper-connectivity MCI vs CN													
L: Uncus, A36, Hipp (EC)	L: A38	11.3*	0.00004	0.0000	-0.03	0.18	0.24	**<0.001**	**0.92**	**<0.001**	**1.09**	0.1488	0.25
L: Hipp (CA, FD)	R: A38	8.7	0.00034	0.0010	0.05	0.13	0.23	**0.0156**	**0.52**	**<0.001**	**1.01**	0.0138	0.52
L: A35, A36, Hipp (SUB, CA)	R: Uncus, A28, A36	7.0*	0.00145	0.0018	-0.04	0.14	0.04	**<0.001**	**0.83**	0.0406	0.42	0.0162	0.51
L: Hipp (CA)	R: A10, A47	6.3	0.00252	0.0032	-0.08	0.05	-0.08	**0.0016**	**0.66**	0.4716	0.02	**0.0006**	**0.80**
L: A27, Hipp (FD, CA, SUB)	R: A10, A11	5.6	0.00489	0.0056	0.00	0.08	-0.04	**0.0168**	**0.52**	0.1380	0.27	**0.0012**	**0.74**
L: Uncus, A36, A28, Hipp (SUB)	L: A34	4.4	0.01515	0.0188	-0.06	0.08	0.06	**0.0042**	**0.65**	**0.0096**	**0.57**	0.3524	0.09
ROI pair hypo-connectivity MCI vs CN													
L: Hipp (FD, CA, SUB), Ling. G.	L+R: Precuneus	5.8	0.00424	0.0040	0.20	0.05	0.09	**0.0002**	**0.79**	**0.0050**	**0.63**	0.2098	0.19
L: A35, A36, Hipp (SUB, CA)	L+R: Precuneus	4.6	0.01187	0.0122	0.21	0.08	0.10	**0.0034**	**0.68**	**0.0142**	**0.56**	0.3586	0.09
L: A28, A35, Hipp (SUB, EC, CA)	R: A45, A47	4.5	0.01291	0.0104	0.08	-0.05	0.07	**0.0098**	**0.58**	0.4490	0.04	**0.0040**	**0.64**
L: Caudate tail, Hipp (CA, FD)	L+R: ACC	3.8	0.02570	0.0260	0.12	0.01	0.06	**0.0016**	**0.71**	0.0622	0.38	0.1258	0.27
ACC = anterior cingulate cortex; AD = Alzheimer's disease; CA = cornu ammonis; CN = cognitively normal; EC = entorhinal cortex; FD = dentate gyrus; FDR = false detection rate; Hipp = hippocampus; Ling. G. = lingual gyrus; MCI = mild cognitive impairment; MTL = medial temporal lobe; ROI = region of interest; SUB = subiculum; *(Significant at FDR q = 0.01).													

328 For the right hemisphere, an FDR-corrected (q=0.05, N=82 tests) ANOVA F statistic critical p

329 value threshold, p_F^* = 0.0102, identified 17 significant MCI-CN comparisons (Supplemental

330 Table 5). For the significant ANOVA tests only, *post hoc* pairwise *t* tests were computed and

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[4] Supplemental Information Table 6 (Worksheet MCI-CN_Detail) provides additional details, including ROI MNI coordinates.

FDR-corrected ($q=0.05$, *N=17 tests*) independently per contrast: MCI-CN ($p^*_{MCI,CN} = 0.027$);

AD-CN ($p^*_{D,CN} = 0.0034$); and AD-MCI ($p^*_{D,MCI} = 0.0278$). Of the 17 significant ANOVA

comparisons, there were 13 significant *post hoc* MCI-CN *t* test comparisons (*post hoc* pairwise *t*

test $p < p^*_{MCI,CN}$). Results are summarized in Table 4. Nine of the 13 MCI-CN comparisons

were positive (indicating hyperconnectivity) with Cohen's effect size d, $0.45 \le d \le 0.95$. Four

of the 13 were negative (indicating hypoconnectivity) with Cohen's d, $0.57 \le d \le 0.73$.

Table 4. Right MTL ROI - ROI pairwise significant MCI - CN comparisons[5].

Anatomical Region(s)		ANOVA (1-way, 3-levels) FDR p*=0.0102, q = 0.05, n = 81			Group Average Fisher Z Value			MCI - CN *post hoc t* test FDR p*=0.027		AD - CN *post hoc t* test FDR p*=0.003		AD - MCI *post hoc t* test FDR p*=0.028	
MTL ROI	ROI	F	p	p*	CN	MCI	AD	p	d	p	d	p	d
ROI pair hyper-connectivity MCI vs CN													
R: Uncus, A28, Hipp (CA, SUB)	L: Uncus, EC, A38	11.6*	0.00003	0.0000	-0.12	0.04	0.05	**0.0000**	**0.95**	**0.0000**	**1.14**	0.4620	0.02
R: A36, Hipp (CA, FD)	R: A9, A10	8.7*	0.00032	0.0002	-0.05	0.09	-0.08	**0.0000**	**0.89**	0.2916	0.14	**0.0006**	**0.82**
R: A20, Uncus, Hipp (EC, SUB, CA)	L+R: A25., L: A11	7.8*	0.00069	0.0004	-0.12	0.04	-0.05	**0.0000**	**0.91**	0.0462	0.42	**0.0116**	**0.55**
R: A27, Hipp (FD, CA)	R: A11, A10	6.9	0.00152	0.0014	-0.04	0.06	-0.06	**0.0056**	**0.64**	0.2870	0.14	**0.0000**	**0.81**
R: Caudate, Hipp (CA, FD)	R: A9, A10	6.8	0.00163	0.0014	-0.08	0.07	-0.06	**0.0016**	**0.75**	0.3180	0.11	**0.0006**	**0.77**
R: Hipp (CA, SUB, FD)	R: A11, A10	6.6	0.00204	0.0016	-0.05	0.05	-0.06	**0.0034**	**0.67**	0.3732	0.08	**0.0004**	**0.82**
R: Uncus, A28, A34, Hipp (EC)	R: A44, A45	6.5	0.00228	0.0036	-0.06	0.08	0.11	**0.0024**	**0.70**	**0.0006**	**0.85**	0.2704	0.14
R: A35, A36, Hipp (SUB, CA)	R: A11	5.4	0.00611	0.0088	-0.09	0.04	-0.04	**0.0012**	**0.77**	0.1060	0.31	**0.0278**	**0.46**
R: Uncus, A34, Amyg, Hipp (EC)	R: A11	4.7	0.01134	0.0102	-0.01	0.06	-0.06	**0.0270**	**0.45**	0.1468	0.26	**0.0016**	**0.70**
ROI pair hypo-connectivity MCI vs CN													
R: A30, Hipp (FD, CA)	L: SMA	7.0	0.00145	0.0010	0.12	-0.01	0.14	**0.0020**	**0.73**	0.3148	0.11	**0.0016**	**0.75**
R: Uncus, A28, A35, Hipp (EC)	L+R: A10	6.4	0.00232	0.0012	0.14	0.03	-0.03	**0.0088**	**0.57**	**0.0002**	0.81	0.0930	0.32
R: Amyg, Hipp (CA)	R: A38, A21	5.9	0.00386	0.0052	0.15	0.04	0.17	**0.0030**	**0.63**	0.3686	0.08	**0.0010**	**0.78**
R: Hipp (CA, FD, SUB)	L+R: A11	5.8	0.00405	0.0048	0.02	-0.10	0.02	**0.0012**	**0.70**	0.4836	0.01	**0.0016**	**0.69**

ACC = anterior cingulate cortex; AD = Alzheimer's disease; Amyg = amygdala; CA = cornu ammonis; CN = cognitively normal; EC = entorhinal cortex; FD = dentate gyrus; FDR = false detection rate; Hipp = hippocampus; MCI = mild cognitive impairment; MTL = medial temporal lobe; ROI = region of interest; SMA = supplemental motor area; SUB = subiculum; *(Significant at FDR q =

3.5. *Parcellation of functional connectivity changes of left MTL in the group-level MCI-CN contrast*

341 The positions of left MTL anchor ROI masks for significant ROI pairs of interest in the MCI-CN

342 contrast are shown in sagittal section (Figure 1 (top)) and coronal section (Figure 3 (left)).

343 Positions of the corresponding non-anchor paired ROIs are discussed next and shown in

344 Supplemental Figure 6. The spatial organization of the ten MTL anchor ROI masks was

345 analyzed using AFNI *3dclust* which identified three clusters oriented along a ventral-medial to

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[5] Supplemental Information Table 6 (Worksheet MCI-CN_Detail) provides additional details, including ROI MNI coordinates.

dorsal-lateral axis in the left MTL. First, in the ventral medial cluster, in the area of the

hippocampal head, the most medial anchor ROIs were positioned in the parahippocampal gyrus

(uncus), and Areas 35 and 36, and were ipsilaterally hyperconnected with a more rostral non-

anchor ROI positioned in Area 34. More laterally in this cluster, anchor ROI positions

progressively shifted to Area 28, hippocampus (subiculum and CA) and parahippocampal gyrus.

Functional connectivity changes with paired non-anchor ROIs consisted of hyperconnectivity

with ROIs in ipsilateral and contralateral Area 38, and hypoconnectivity with a contralateral ROI

positioned laterally in Area 45 and 47.

A second cluster of MTL anchor ROI masks, lateral and dorsal to the ventral medial cluster, was

positioned in its medial subregion in the hippocampus (subiculum, CA), and in its lateral

subregion in the hippocampus (CA) in the region of the caudate tail and parahippocampal gyrus.

The anchor ROI in this cluster was hyperconnected with its paired non-anchor ROI positioned in

contralateral lateral Area 10 adjacent to Area 47.

Last, in the dorsal cluster of anchor ROI masks, its medial subregion was positioned in Area 36

and hippocampus (CA, FD, subiculum), and in its lateral subregion in hippocampus (CA) in the

region of the caudate tail and parahippocampal gyrus. Functional connectivity changes in this

subzone included: a) an anchor ROI hyperconnected with a contralateral non-anchor ROI

positioned in lateral Area 10/11; b) an anchor ROI hypoconnected with a non-anchor ROI

located in precuneus; c) an anchor ROI hypoconnected with a non-anchor ROI located in anterior

cingulate cortex; and d) an anchor ROI simultaneously hyperconnected with a contralateral non-

anchor ROI located in the region of uncus, Area 28 and 36, and hypoconnected with a non-

anchor ROI located in precuneus.

In summary, in the left hemisphere, for the identified significant ROI pairs in the MCI-CN

contrast, the anchor MTL ROIs clustered within focal subregions of entorhinal and perirhinal

areas, hippocampus, and parahippocampal gyrus. The spatial pattern of functional connectivity

changes with corresponding non-anchor ROIs suggested that MTL subzones were: a) ventrally,

bilaterally hyperconnected, including uncus and Area 38; b) dorsally and laterally,

simultaneously hyperconnected and hypoconnected with distinct non-overlapping contralateral

lateral frontal cortical regions; and c) over an extended dorsal and lateral zone, hypoconnected

with midline regions associated with anterior and posterior default-mode network (DMN) nodes.

3.6. Parcellation of functional connectivity changes of right MTL in the group-level MCI-CN

contrast

The position of right MTL anchor ROI masks for significant ROI pairs of interest in the MCI-CN

contrast are shown in sagittal section (Figure 2 (top)) and coronal section (Figure 3 (left)).

Positions of the corresponding non-anchor paired ROIs are discussed next and shown in

Supplemental Figure 7. The spatial organization of the 13 MTL anchor ROI masks was analyzed

using AFNI *3dclust* which identified two clusters oriented along a ventral-medial to dorsal-

lateral axis. In the first cluster, near the head of the hippocampus, in its medial subregion,

anchor ROIs were positioned in the uncus, and Areas 28, 34, 35 and 36. Anchor ROI positions

in the middle and lateral subregions progressively shifted to the hippocampus (subiculum, FD

and CA). Pairwise functional connectivity with corresponding non-anchor ROIs consisted of an

interleaved pattern of hyperconnectivity and hypoconnectivity with small regions of overlap. In

the medial subregion, immediately adjacent anchor ROIs were either hyperconnected with an

ipsilateral lateral non-anchor ROI in Area 44 and 45, or hypoconnected bilaterally with a non-

anchor ROI in Area 10 at the midline. In the middle subregion there was a zone of

hypoconnectivity with an ipsilateral non-anchor ROI in the region of Area 38 and 21.

Immediately lateral to this hypoconnected anchor ROI, were a pair of anchor ROIs that were

hyperconnected with non-anchor ROIs positioned in contralateral uncus, Area 38 and 28. In the

most lateral subregion, anchor ROIs were hyperconnected bilaterally with a non-anchor ROI in

the region of Area 11 and 25 at the midline.

The second cluster of anchor ROIs, dorsal to the first, was characterized by multiple immediately

adjacent anchor ROIs with a distinct distribution of functional connectivity with corresponding

non-anchor ROIs. In its medial extent, anchor ROIs in this cluster were positioned in Area 35,

36 and hippocampus (CA, FD, subiculum) and in its lateral extent in hippocampus (CA, FD) in

the region of the caudate tail, but not parahippocampal gyrus. In the medial extent of this cluster

of anchor ROIs, functional connectivity changes with non-anchor ROIs consisted of

hyperconnectivity with an ipsilateral lateral ROI positioned in Area 10 and 11. In the lateral

extent of this cluster of anchor ROIs, there was hyperconnectivity with an ipsilateral lateral non-

anchor ROI whose position shifted to that of Area 9 and 10. In the medial subzone of this cluster

of anchor ROIs, there was functional hypoconnectivity with a corresponding paired non-anchor

ROI positioned in contralateral supplemental motor area (SMA) and in its lateral extent

hyperconnectivity bilaterally with a non-anchor ROI positioned in Area 11 at the midline.

In summary, in the right hemisphere in the transition from CN to MCI, the spatial pattern of

pairwise functional connectivity changes between anchor MTL and non-anchor ROIs suggests

that MTL subzones were: a) ventrally, hyperconnected with contralateral uncus and Area 38 and

hypoconnected with ipsilateral anterior Area 38; b) hyperconnected with ipsilateral lateral frontal

cortex; and c) hypoconnected with frontal cortical zones at the midline in regions adjacent to or

associated with anterior DMN midline nodes.

3.7. Significant pairwise ROI functional connectivity changes in the AD-CN group-level

contrast

In the left hemisphere, an ROI pair was significant for functional connectivity changes in the

AD-CN contrast for *post hoc* pairwise *t* test critical *p* value threshold less than the FDR-

corrected, $p^*_{D,CN} = 0.0214$, (*q=0.05, N=28 tests*). There were 21 significant AD-CN comparisons

(Supplemental Tables 4 and 6). The MTL anchor ROI mask positions are shown in Figure 1

(bottom) and Figure 3 (right), and non-anchor ROI mask positions are shown in Supplemental

Figure 8. Comprising the 21 significant comparisons were: a) nine hyperconnected pairs,

Cohen's d, $0.52 \leq d \leq 0.86$, median=0.75; and b) 12 hypoconnected pairs, Cohen's d, $0.7 \leq d \leq$

0.86, median=0.64. There were more than twice as many AD-CN significant comparisons

(N=21) as there were MCI-CN significant ROI comparisons (N=10). There were 1.5 times as

many hyperconnected ROI pairs ($N_{AD-CN}=9$ vs $N_{MCI-CN}=6$) and 3.0 times as many hypoconnected

ROI pairs ($N_{AD-CN}=12$ vs $N_{MCI-CN}=4$). Six of the nine significant hyperconnected and ten of the

twelve significant hypoconnected ROI pairs were not significant in the MCI-CN contrast.

Despite the increase in numbers of significant ROI pairs, the overall spatial organization of MTL

ROI positions was similar to that of the MCI-CN contrast. The greater number of co-located

anchor ROIs preferentially distributed in the ventral medial and dorsal lateral ROI clusters.

A striking feature in the AD-CN contrast was individual anchor MTL ROIs which formed

multiple significant ROI pairs. Fourteen left hemisphere MTL ROIs comprised the anchor ROI

in 21 significant ROI pairs. This was compared to nine MTL anchor ROIs that formed 10

significant ROI pairs in the MCI-CN contrast. In the AD-CN contrast, six MTL ROIs comprised

the anchor element in two significant ROI pairs. The most common combination (four of six)

was one hyperconnected pair and one hypoconnected pair. For example, an anchor ROI in

ventral MTL (Area 35) was hyperconnected with a non-anchor ROI located contralateral Area 38

and simultaneously hypoconnected with a non-anchor ROI in the region of the orbital gyrus at

the midline. As a second example, an anchor ROI in the dorsal MTL in hippocampus (CA) was

hyperconnected with a contralateral non-anchor ROI located in the region of uncus and

entorhinal cortex, and simultaneously hypoconnected with a non-anchor ROI in contralateral

lateral inferior temporal gyrus. In the single case of an anchor MTL ROI having two

hypoconnections, an anchor ROI positioned in hippocampus (CA) adjacent to the

parahippocampal gyrus, was hypoconnected with a non-anchor ROI located in precuneus at the

midline and hypoconnected with a non-anchor ROI located in the contralateral lateral frontal

cortex in Area 45 immediately adjacent to Area 47. Last, in the single case of an anchor MTL

ROI having two hyperconnections, an anchor ROI positioned in the region of Areas 28, 25, 36

and uncus, was *bilaterally* hyperconnected with a non-anchor ROI located in Area 38.

In the right hemisphere, ROI pairwise tests were significant for functional connectivity changes

in the AD-CN contrast with a *post hoc* pairwise *t* test critical *p* value threshold less than the

FDR-corrected, $p^*_{D,CN}$ = 0.0034, (*q=0.05, N=17 tests*). There were six significant comparisons

(Supplemental Tables 5 and 6). The MTL anchor ROI mask positions are shown in Figure 2

(bottom) and Figure 3 (right) and the paired non-anchor ROI mask positions are shown in

Supplemental Figure 9. Four of the six AD-CN comparisons were positive indicating

hyperconnectivity with Cohen's effect size *d*, $0.7 \leq d \leq 1.14$. Two of these four significant

comparisons were also significant in the MCI-CN contrast, indicating persistence of effect with

disease progression: hyperconnectivity with contralateral uncus; and hyperconnectivity with

ipsilateral Area 44 and 45. Two of these four significant comparisons were not significant in the

MCI-CN contrast with the following characteristics: a) both MTL anchor ROIs were positioned

in the region of the head of the hippocampus, entorhinal cortex and uncus; b) one (dorsal) was

hyperconnected with a contralateral non-anchor ROI located in lateral Area 10; and c) the other

(ventral) was hyperconnected with an ipsilateral non-anchor ROI located in medial Area 11

(nearly at the midline). Last, for two of the six significant AD-CN ROI pairs, neither of which

was significant in the MCI-CN comparison, the pairwise functional connectivity change was

hypoconnectivity (Cohen's d, $0.77 \leq d \leq 0.81$). The anchor ROIs in these pairs were positioned

in the region of the head of the hippocampus, entorhinal cortex and uncus. One (dorsal) was

hypoconnected with a non-anchor ROI located in Area 10 at the midline; the other (ventral) was

hypoconnected with a non-anchor ROI located in ipsilateral lateral A10 adjacent to A46.

Summarizing left and right hemisphere jointly, the spatial pattern of functional connectivity

changes from CN to D reflected a combination of consolidation, progression, and reversion of

the changes observed in the CN to MCI contrast. First, there were not anchor ROIs positioned in

additional MTL subzones. Second, additional significant ROIs in the AD-CN contrast clustered

preferentially in the region of the head of the hippocampus, entorhinal cortex and uncus,

compared to the wider distribution in the MCI-CN contrast. Third, significant AD-CN non-

anchor ROIs were positioned within similar cortical regions (e.g., lateral frontal cortex, midline

regions) as in the MCI-CN contrast or in additional regions (e.g., right inferior temporal cortex).

Last, a combination of reversion and consolidation was evident in the absence in right

hemisphere in the AD-CN contrast of the more dorsal cluster of ROIs present in MCI-CN

contrast.

3.8. MCI-CN functional connectivity changes may persist or revert in the group-level AD-CN

contrast

In the AD-CN contrast there were functional connectivity changes that persisted or were

transient compared to the MCI-CN contrast. In the left hemisphere for three of six MCI-CN

hyperconnected ROI pairs and for two of four MCI-CN hypoconnected ROI pairs, the functional

connectivity change persisted or was amplified in the AD-CN contrast. In the right hemisphere,

however, only two of nine MCI-CN hyperconnected ROI pairs and for one of four MCI-CN

hypoconnected ROI pairs, did the functional connectivity change persist. Examples of persistent

effects included: a) left MTL and its ipsilateral and contralateral hyperconnectivity with Area 38;

b) left MTL hypoconnectivity bilaterally with anterior cingulate cortex and precuneus; and c)

right MTL hypoconnectivity bilaterally with Area 10 at the midline. Of the set of ROI pairs with

persistent functional connectivity changes in the MCI-CN and AD-CN contrasts, only one ROI

pair was monotone, i.e., significant in all three contrasts MCI-CN, AD-CN, and AD-MCI. For

this progressively hyperconnected ROI pair, the MTL ROI element was positioned in left MTL

in the region of Areas 28, 35, 36 and uncus, and the second element was in a contralateral region

with focal point in Area 38. In contrast, for three of six hyperconnected and for two of four

hypoconnected significant MCI-CN ROI pairs in the left hemisphere, and in all but three of 13

significant ROI pairs in the right hemisphere, the changes reversed course such that there was no

significant difference in the AD-CN contrast.

In summary, there were monotonic and non-monotonic, transient and persistent changes in

functional connectivity between the identified ROI pairs in the AD-CN contrast compared with

the MCI-CN contrast. The enduring changes observed across the CN, MCI and D progression

include mutual bilateral hyperconnectivity between MTL and Area 38, and hypoconnectivity of

left and right MTL with anterior and posterior regions immediately adjacent to or associated with

midline DMN nodes.

3.9. Sensitivity analysis

In preliminary studies, we assessed by spot-checking the sensitivity of the detection of

statistically significant (one-way, three-factor ANOVA ROI pair) functional connectivity

comparisons to changes in preprocessing parameters. The results reported in this study were

obtained with FWHM = 4.0 mm spatial smoothing in the AFNI preprocessing stage. Smoothing

with FWHM = 6.0 mm or FWHM = 8.0 mm and FDR q = 0.05, eliminated the observation of

significant ANOVA trials. In such cases, we did not proceed to the 5000 permutation repeated

measures test (although we observed anecdotally using a 1000 permutation repeated measures

test that a few significant tests were observed). Similarly, present results were obtained using an

ROI defined as the 6.0 mm radius volume centered at a given source or target ROI seed.

Expansion to an 8.0 mm radius volume eliminated the observation of significant ANOVA tests.

In any of the above tests, when we relaxed the FDR q value, for example, to $0.05 \leq q \leq 0.20$,

progressively greater numbers of significant ANOVA tests were observed. These preliminary

observations drove the decision to proceed with FWHM = 4.0 mm and ROI volume radius = 6.0

mm where, with a conservative FDR q = 0.05.

We assessed the reproducibility of the reported results under repeated measures with different

random number generator seeds in the 5000-trial permuted repeated measures. We completed

two additional 5000-trial runs for the left hemisphere data and found that for the MCI-CN

contrast (the only contrast analyzed in detail) there were comparable numbers of significant tests

and same, adjacent or overlapping ROI pairs with comparable F statistic values to those reported

here. The remaining pairs were typically in positions adjacent to or overlapped those reported.

We determined the impact of an even more conservative FDR value $q = 0.01$ on the reported

pairwise ROI functional connectivity results. For the left hemisphere, the FDR corrected F

statistic p value was ($p_F^* < 0.0018$) and there remained nine significant ANOVA tests. For the

significant ANOVA tests only, *post hoc* pairwise t tests were computed and FDR-corrected ($q =$

0.01, N =9 tests) independently per contrast: $p_{MCI,CN}^* = <0.0001$; $p_{D,CN}^* = 0.0052$; $p_{D,MCI}^* =$

0.0014. There were no significant hypoconnected ROI pairs. There were two significant

hyperconnected MCI-CN pairs and these are shown in Table 3 marked with an asterisk. For the

right hemisphere, the FDR corrected F statistic p value was ($p_F^* < 0.0006$) and there remained

five significant ANOVA tests. For the significant ANOVA tests only, *post hoc* pairwise t tests

were computed and FDR-corrected ($q = 0.01$, N =5 tests) independently per contrast: $p_{MCI,CN}^* =$

<0.0001; $p_{D,CN}^* = 0.0018$; $p_{D,MCI}^* = 0.0008$. There were no significant hypoconnected ROI pairs.

There were three significant hyperconnected MCI-CN pairs and these are shown in Table 4

marked with an asterisk. In summary, the impact of an even more conservative FDR value q =

0.01 on reported MCI-CN significant comparisons is that the findings of hypoconnected ROI

pairs are not conserved; the findings of hyperconnected ROI pairs are conserved. For the D-CN

contrast, findings are confirmed, although with reduced numbers, in that there remain significant

comparisons in left and right hemisphere representing hyperconnected ROI pairs and

hypoconnected ROI pairs.

4. Discussion

We report evidence that disruption of task-free resting state network functional connectivity is

present before the Alzheimer's Disease pathophysiological stage at which neurodegeneration has

sufficiently progressed to be detected. The results were obtained by comparing resting-state

fMRI connectivity with an automated analysis of standard (1mm) structural T1 MRI as cortical

thinning, subcortical structural volume reduction and hippocampal subfield volume reduction.

An anatomically bootstrapped, data-driven procedure identified statistically significant

comparisons in resting state functional networks having edges where one node was in the MTL

and the other was at anatomical locations corresponding with DMN nodes. Further, we observed

a diversity of effects of Alzheimer's Disease progression on ROI pairwise functional

connectivity, including complex patterns of hypoconnectivity *and* hyperconnectivity across the

MCI-CN and AD-CN transitions confirming that the effect of Alzheimer's Disease progression

on functional connectivity is more complex than simply there being monotonic loss or gain of

functional connectivity.

4.1. Structural imaging findings provide an important control for functional connectivity

findings

A key structural MRI finding in Alzheimer's Disease is cortical atrophy (thinning and volume

loss) that correlates with symptom severity and has a demonstrated diagnostic and prognostic

value (Braak and Braak, 1991; Fan, et al., 2008; Davatizikos, et al., 2009; Lerch, 2005; Jack, et

al., 2008; Dickerson, et al., 2009; Misra, et al., 2009; Miller-Thomas, et al., 2016). This finding

was reproduced here (Supplemental Table 1) and served as an important control for functional

connectivity analysis. We hypothesized that the anatomical locations of the cortical ROIs

observed in our functional connectivity analysis would correspond with previously demonstrated

spatial patterns of cortical thinning. Indeed, the anatomically boot-strapped data-driven method

employed in the present study identified significant MCI-CN cortical ROI anatomical positions

in areas known to be most vulnerable to cortical thinning. These included the rostral medial

temporal cortex, temporal pole and superior frontal regions, but not the inferior temporal cortex.

Significant functional connectivity changes involving inferior temporal cortex were however

observed in the AD-CN contrast. The absence of statistically significant cortical thinning in the

MCI-CN contrast suggests that the observed functional connectivity changes may not solely be

accounted for as a reflection in MTL of mechanisms arising in cortical regions.

The present study also reproduces key findings of hippocampal volume and hippocampal

subfield volume loss with Alzheimer's Disease progression (Hyman, et al., 1984; Braak and

Braak, 1991; Jack, et al., 1992, 1998; Schuff, et al., 2009; Boutet, et al., 2014; Sorensen, et al.,

2016; Wolk, et al., 2017). The confirmation of expected significant volume loss and significant

functional connectivity changes in the AD-CN contrast provides a control for the present MCI-

CN and AD-CN findings.

The absence of significant reduction in whole hippocampus volume and hippocampal subfield

volumes in the MCI-CN contrast reported above is with respect to a widely available benchmark:

up-to-date automated analysis (FreeSurfer) of research quality T1-weighted scans (1.0 x 1.0 x 1.0

mm^3). We do not conclude that there are no morphometric changes taking place

contemporaneously with the CN to MCI transition. Wolk, et al. (2017), analyzed high resolution

(~0.4 x 0.4 x 2 mm^3) T2-weighted MRI scans orthogonal to the long axis of the hippocampus at

autopsy. They reported significant group-level reduction of MTL subfield volumes (e.g., Area

35, perirhinal cortex) in the CN to early MCI transition where whole hippocampus volumes were

not significantly different. In a feasibility study of an *in vivo* approach, Boutet, et al., (2017)

used 7T MRI to detect hippocampal subfield volume changes in an AD–CN contrast. These

studies, together with present results, indicate the potential of dual functional and high-resolution

morphometric biomarkers for detecting the earliest stages in the Alzheimer's Disease

pathophysiology.

4.2. Comparison to prior work

With respect to our functional connectivity findings, five published reports are of particular

relevance (Grecius, et al., 2004; Jones, et al, 2011; Brier, et al., 2012; Ward, et al., 2014; Dillen,

et al., 2017). Grecius, et al., (2004) performed a pairwise group-level (healthy control (N=14) vs

very mild or mild Alzheimer's Disease (N=13)) independent components analysis (ICA) and

ROI analyses of steady-state DMN connectivity during a simple sensorimotor task in a cohort

drawn from the Washington University Alzheimer's Disease Research Center. Key findings

were: a) prominent bilateral coactivation of the hippocampus with DMN in both clinical groups;

and b) disruption of hippocampal – PCC connectivity in the Alzheimer's Disease group. Dillen

et al., (2017) performed a within-group and between-group analysis of hippocampus and DMN

node functional connectivity analysis in a cohort drawn from an outpatient population at the

Memory Clinic Cologne Julich (healthy control (N=25), subjective cognitive decline (SCD)

(N=28); and prodromal Alzheimer's Disease (N=25)). Significantly, they reported a decoupling

of hippocampus with posterior cortical DMN nodes in both SCD and prodromal Alzheimer's

Disease groups.

Brier, et al., (2012) performed a cross-sectional analysis of five task-free resting state networks

(RSN), including DMN, in a cohort drawn from the Knight Alzheimer's Disease Research

Center at Washington University in St. Louis. Subjects were assigned to one of three groups

according to CDR scores 0 (cognitively normal, N=386), 0.5 (very mild AD, N=91), and 1.0

(mild AD, N=33). The study reported summary measures of intranetwork and internetwork

steady-state correlation structure based on Fisher z-transformed pairwise Pearson correlation

analysis of ROI seed-based average time series. While not uniformly statistically significant, the

conclusion was that there was group-level progressive loss of intranetwork and internetwork

connectivity. The study also reported results of the effect of clinical group (CN, MCI,

Alzheimer's Disease) on ROI pair-wise functional connectivity between PCC and eight other

DMN nodes. For two ROI pairs (PCC – medial prefrontal cortex; PCC –left inferior temporal

lobe) there was a statistically significant reduction of connectivity in the CDR 0.5 group

compared to the CDR 0 group. Present results confirm the Brier, et al. observation of ROI pair-

wise functional connectivity loss in the MCI-CN comparison. They also extend the Brier, et al.

results. First, where Brier, et al., utilized a single ROI seed to estimate midline DMN structures

(e.g., PCC, thalamus), the present study utilized an anatomically bootstrapped data-driven

method that identified distinct left and right ROI seeds in these structures. The result was a more

fine-grained ROI pair-wise analysis which led to the observation of widespread left- and right-

hemispheric MTL hyperconnectivity ventrally together with disconnection with midline DMN

and DMN coactivated regions. Second, by design, the present study included hippocampus and

other MTL structures in the analysis and presented evidence that these structures are involved in

the loss of functional connectivity in the MCI-CN comparison.

Jones, et al. (2011) performed group-level functional connectivity analyses of task-free steady-

state DMN connectivity in cohorts drawn from the Mayo Clinic Alzheimer's Disease Research

Center and Mayo Clinic Study of Aging. Age-related changes in DMN functional connectivity

were analyzed using an ICA approach in a cognitively normal cohort (N=341). The age-related

changes consisted of differential effects in anterior and posterior DMN connectivity: a) anterior

DMN showed both increases and decreases in connectivity within the frontal lobe; and b)

posterior DMN showed a pattern of predominantly but not exclusively decreases in connectivity.

An age-matched CN and Alzheimer's Disease group analysis using both ICA and seed-based

ROI approaches concluded that DMN connectivity changes in Alzheimer's Disease represent an

acceleration of the same aging pattern observed in the control sample. The present study

complements these findings by providing additional detailed parcellation of changes in MTL,

separately analyzed in left and right hemisphere.

Ward, et al., (2014), in their study comparing resting state data and an associative memory

encoding task, concluded that the parahippocampal gyrus is the primary hub of the DMN in the

MTL during resting state. Their report ends with the suggestion that measuring PHG

connectivity may provide a biomarker of early Alzheimer's Disease. The present study,

although motivated by a different hypothesis (that functional connectivity changes temporally

precede detection of significant neurodegeneration) and using an entirely independent analysis

method (anatomically bootstrapped, data-driven method), provides quantitative evidence in

support of the Ward, et al., suggestion. We observe evidence of functional disconnection

bilaterally between posterior cortical DMN nodes (anterior cingulate cortex, precuneous) and

parahippocampal gyrus as part of a larger pattern of disruption involving anterior and posterior

DMN, and subcortical structures including hippocampus and parahippocampal gyrus.

4.3. Limitations

Limitations of the present study relate to the study population, the imaging data and

preprocessing methods. First, by excluding participants with other neurological injury or

findings, the study population was not representative of a general age-matched clinical

population. Second, the effect of the "penciling artefact", found in ADNI image data in left

lateral frontal cortex, on functional connectivity measures is unknown and introduces uncertainty

in the interpretation of present results. For example, there was a multiplicity of significant ROI

pairs between right MTL and ipsilateral lateral frontal cortex. There was not a comparable

finding in the left hemisphere, whereas there were bilateral findings with respect to midline

ROIs. Third, the present study applied in the pre-processing stage an atlas (AFNI: MNIavg152)

derived from younger brains than used in this study which could inject systematic error into the

data. Similarly, the FreeSurfer parameters were the default set which may be sub-optimal given

the population comprising this study. Last, there is not a consensus regarding the use or non-use

of GSR (Murphy and Fox, 2017) and the present study did not apply GSR. The reasoning was

two-fold. First, given the "penciling artefact" in ADNI data, it was problematic whether and

how to obtain a viable global signal estimate. Second, the preprocessing procedure estimated

and removed motion confounds and the ROI identification procedure applied ventricle and white

matter masks to minimize the influence of non-grey matter signals. However, any global or

large-scale regional neuronal fluctuations would not be controlled in this procedure.

4.4. Translational considerations

A challenge in the consideration of functional connectivity biomarkers is that there are in clinical

use well-established semi-quantitative structural biomarkers of Alzheimer's Disease (Fazekas, et

al., 1987; Scheltens, et al., 1992; Wahlund, et al., 2001). These methods have been extended in

clinical practice and medical research to include T1-based quantitative semi-automated and

automated methods for mild cognitive impairment and Alzheimer's Disease diagnosis, tracking

and prognosis (Dale, et al., 1999; Chupin, et al., 2009; Davatzikos, et al., 2009; Leung, et al.,

2010; Leung, et al., 2013; Misra, et al., 2016; Schuff, et al., 2009; Sorensen, et al, 2016).

The development of semi-automatic and automatic derivation of resting-state functional

connectivity biomarkers for Alzheimer's Disease classification is comparatively new (Grecius, et

al., 2004; Sepulcre, et al., 2017; and Wiepert, et al., 2017). First, Grecius, et al., (2004) applied a

goodness-of-fit test between an ICA-derived PCC-based or whole DMN-based templates and

individual subject images to classify Alzheimer's Disease or healthy ageing individuals. Second,

Wiepert, et al., (2017), proposed a network failure quotient (NFQ). The measure combined the

increases and decreases in DMN subsystem connectivity with Alzheimer's Disease progression

into a single statistic. The authors demonstrated that the statistic ("trained" in an ADNI cohort)

had the greatest effect size in differentiating CN and AD in a distinct cohort (Mayo Clinic).

Last, Sepulcre, et al., (2017) applied graph theory methods to demonstrate distinct associations

between functional connectivity changes in cognitively normal aging brains and cortical patterns

of *in vivo* tau and amyloid β positron emission tomography imaging. A remaining challenge is

to fully characterize classification sensitivity and specificity of functional connectivity

biomarkers compared to CSF-derived, plasma-derived and *in vivo* and structural imagine

modalities.

4.5. Conclusion

The contribution of the present study in the context of established structural and emerging

resting-state functional connectivity biomarkers is four-fold. First, we demonstrated that

functional connectivity changes were detected where structural changes were not yet in evidence

using widely available imaging clinic resources. Second, we measured functional connectivity

changes anchored in the MTL structures directly implicated in the earliest stages of Alzheimer's

Disease. Third, we observed a complex pattern of changes: monotonic and non-monotonic, and

persistent and reverting patterns of hyperconnectivity and hypoconnectivity, in a spatial

organization closely related to the default-mode network. Last, we adopted a multi-modal

functional-structural approach and demonstrated differential potential clinical value of resting-

state functional connectivity biomarkers in Alzheimer's Disease diagnosis, tracking and

prognosis.

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7. Figures

Figure 1. Position in the left hemisphere sagittal plane (4mm stride) of anchor MTL ROI

elements of significant ROI pairs of interest in the MCI – CN contrast (top) and D – CN contrast

(bottom). Shown are ROI masks for the 6-mm radius volume centered at the ROI seed. In both

contrasts, ROIs group in a ventral anterior subzone and a dorsal posterior subzone. There is

progressive change that may correlate with disease progression. In the D – CN contrast, there

are more significant ROI pairs of interest collectively whose anchor MTL ROIs cover a larger

extent of the MTL compared to MCI – CN. In addition, there is an increase in the number of

individual MTL ROIs that form multiple significant ROI pairs in which one pair is of type

hypoC and the other hyperC. Positions of the ROI paired with each MTL ROI shown are

summarized in Table 3, their MNI coordinates are listed in Supplemental Tables 4 and 6, and

corresponding image maps are shown Supplemental Figures 6 and 7. The direction of ROI pair

functional change is color-coded for hyperconnectivity (*red*), hypoconnectivity (*blue*), and

simultaneous hyperconnectivity and hypoconnectivity (*green*).

Figure 2. Position in the right hemisphere sagittal plane (4mm stride) of anchor MTL ROI

elements of significant ROI pairs of interest in the MCI – CN contrast (top) and D – CN contrast

(bottom). Shown are ROI masks for the 6-mm radius volume centered at the ROI seed. In the

MCI - CN contrasts, but not the D – CN, ROIs group in a ventral anterior subzone and a dorsal

posterior subzone. In the D – CN contrast, the dorsal posterior ROI cluster is not present,

indicating that there may be a class of ROI pairwise functional connectivity changes that persist

and those that are associated specifically with the CN to MCI transition. Positions of the ROI

paired with each MTL ROI shown are summarized in Table 4, their MNI coordinates are listed

in Supplemental Tables 5 and 6, and corresponding image maps are shown Supplemental Figures

8 and 9. The direction of ROI pair functional change is color-coded for hyperconnectivity (*red*),

hypoconnectivity (*blue*), and simultaneous hyperconnectivity and hypoconnectivity (*green*).

Figure 3. Coronal series showing the position of anchor MTL ROI elements of significant MCI

– CN contrast ROI pairs (a) and D – CN contrast (b) ROI pairs. Shown are the anchor MTL ROI

masks consisting of a 6-mm radius volume centered at the anchor MTL ROI seed. The direction

of ROI pair functional change is color-coded for hyperconnectivity (*red*), hypoconnectivity

(*blue*), and simultaneous hyperconnectivity and hypoconnectivity (*green*).

8. Supplemental Material - Tables

1. **Supplemental Information Table 1 (Cortical Thickness ANOVA Results).** Excel table containing the ANOVA F statistic and *p* value, *post hoc* pair-wise *t* statistic and *p* value, pair-wise Cohen's *d*, group average, and group average standard error, for 68 cortical region thickness estimates.

2. **Supplemental Information Table 2 (Subcortical Segmentation ANOVA Results).** Excel table containing the ANOVA F statistic and *p* value, *post hoc* pair-wise *t* statistic and *p* value, pair-wise Cohen's *d*, group average, and group average standard error, for 16 hippocampal subfield volume estimates.

3. **Supplemental Information Table 3 (Hippocampal Subfields ANOVA Results).** Excel table containing the ANOVA F statistic and *p* value, *post hoc* pair-wise *t* statistic and *p* value, pair-wise Cohen's *d*, group average, and group average standard error, for 22 subcortical structure volume estimates.

4. **Supplemental Information Table 4 (Left Hemisphere ANOVA Raw Results).** Excel tables containing left significant ROI pairs of interest, their ANOVA sample F statistic and *p* value, repeated measures permuted F statistic and *p* value, permutation estimated *post hoc* pair-wise *t* test *p* value, pair-wise Cohen's *d*, and group averages.

5. **Supplemental Information Table 5 (Right Hemisphere ANOVA Raw Results).** Excel tables containing right significant MCI-CN contrasts, their ANOVA sample F statistic and *p* value, repeated measures permuted F statistic and *p* value, permutation estimated *post hoc* pair-wise *t* test *p* value, pair-wise Cohen's *d*, and group averages.

6. **Supplemental Information Table 5 (Left and Right Tabulated ANOVA Results).** Excel tables containing right significant MCI-CN and AD-CN and AD-MCI contrasts, their ANOVA sample F statistic and *p* value, repeated measures permuted F statistic and *p* value, permutation estimated *post hoc* pair-wise *t* test *p* value, pair-wise Cohen's *d*, and

936   group averages, and including MNI coordinates. Tables correspond to Tables 3 and 4 in

937   the main text.

9. Supplemental Material - Figures

1. **Supplemental Figure 1.** Resting-state fMRI processing block diagram.

2. **Supplemental Figure 2.** Spatial distribution in left (right) ROI masks sampled from within the global left (right) MTL 3D "bounding box".

3. **Supplemental Figure 3.** Spatial distribution of ROI masks (each corresponding to the center of mass of an F statistic cluster) identified by 3D ANOVA with a left MTL anchor ROI.

4. **Supplemental Figure 4.** Spatial distribution of ROI masks (each corresponding to the center of mass of an F statistic cluster) identified by 3D ANOVA with a right MTL anchor ROI.

5. **Supplemental Figure 5.** Progression of cortical thinning in representative regions and subcortical structure volume with clinical group. ANOVA results are shown in table format in Supplemental Tables 1-3.

6. **Supplemental Figure 6. MCI-CN (left MTL anchors).** Spatial distribution of the non-anchor ROI masks (where the anchor ROI mask was in left MTL) for the 10 significant ROI pairwise comparisons in the MCI-CN contrast.

7. **Supplemental Figure 7. MCI-CN (right MTL anchors).** Spatial distribution of the non-anchor ROI masks (where the anchor ROI mask was in right MTL) for the 10 significant ROI pairwise comparisons in the MCI-CN contrast.

8. **Supplemental Figure 8. AD-CN (left MTL anchors).** Spatial distribution of the non-anchor ROI masks (where the anchor ROI mask was in left MTL) for the 21 significant ROI pairwise comparisons in the AD-CN contrast.

9. **Supplemental Figure 9. AD-CN (right MTL anchors).** Spatial distribution of the non-anchor ROI masks (where the anchor ROI mask was in right MTL) for the 6 significant ROI pairwise comparisons in the AD-CN contrast.

Functional Connectivity Processing Stream

AD = Alzheimer's Disease; AFNI = Analysis of Functional Neuroimages; CN = Cognitively Normal; FDR = False Detection Rate; fMRI = functional Magnetic Resonance Imaging; MCI = Mild Cognitive Impairment; MNI = Montreal Neurological Institute; MTL = Medial Temporal Lobe; MRI = Magnetic Resonance Imaging; ROI = Region of Interest; rsfMRI = resting-state fMRI; SD = Standard Deviation; SUMA = Surface Mapping; V = Ventricles; WM = White Matter

rsfMRI

MRI

1) FreeSurfer V6.0

2) AFNI SUMA_Make_Spec_FS 12/30/16

3) AFNI afni_proc.py v5.15 (drop 1st N frames, despike, time shift, align, warp (MNI), registration, blur (4.0mm), scale, regression (6 motion, 6 first derivative motion), fast anaticor

4) ROI Identification (Shell Scripts + AFNI: 3dfim+, 3dcalc, 3dANOVA)

5) ROI-Pair Analysis (R) (band-pass filter individual ROI time series, quality check (tests on amplitude, SD, fraction "bad" samples), ANOVA, repeated measures, permutation analysis

Parcellation

Cortical Thickness

Subcortical Volumes

HPC Subfield Volumes

WM Mask

V Mask

Residual Time Series (4D Volumes)

Statistics (e.g., Motion, Censor Fraction, DICE)

4a) Candidate ROI seed pool (obtained by anchoring candidate ROI seeds in L or R hemisphere MTL bounding box and using one-way three-factor 3dANOVA F statistic to identify significant clusters in whole brain); prune seed list based on cluster size (20) and min. separation distance (6mm)

4b) Final ROI Seed Pool Time Series

Apply one-way three-factor ANOVA with permutation repeated measures and FDR correction to test significance of the effect of diagnostic label (CN, MCI, D) on ROI pair-wise Z-transformed Pearson correlation coefficient

Spatial distribution in left (right) ROI masks sampled from within the global left (right) MTL 3D "bounding box".

Sum of MTL ROI masks (voxel values set to 0 (not included) or 1 (included)) used as the *starting point* for the MTL ROI identification procedure. At this processing stage, ROI masks overlap due to the 6mm sampling grid.

Crosshair MNI position: 0, -18, -10. Z-direction step size is 2mm.

Spatial distribution of ROI masks (each corresponding to the center of mass of an F statistic cluster) identified by 3D ANOVA with a left MTL anchor ROI. 22 anchor ROIs in left hemisphere (*not shown*; see Supplemental Figure 2) comprised the first ("anchor") element in 50 ROI pairs of interest. The spatial distribution of the sum of the ROI masks corresponding to these 50 ROIs is shown.

In this figure, a value greater than one means that this position comprised an ROI pair of interest with more than one anchor MTL ROI.

ANOVA (with correction for multiple hypothesis testing) is used to determine which of the ROI pairs of interest show significant change as an effect of clinical group.

Sagittal plane step size is 2mm. Cross-hair MNI coordinate (0, -18, 0).

Spatial distribution of ROI masks (each corresponding to the center of mass of an F statistic cluster) identified by 3D ANOVA with a left MTL anchor ROI. 38 anchor ROIs in right hemisphere (*not shown*; see Supplemental Figure 2) comprised the first ("anchor") element in 82 ROI pairs of interest. The spatial distribution of the sum of the ROI masks corresponding to these 82 ROIs is shown.

In this figure, a value greater than one means that this position comprised an ROI pair of interest with more than one anchor MTL ROI.

ANOVA (with correction for multiple hypothesis testing) is used to determine which of the ROI pairs of interest show significant change as an effect of clinical group.

Sagittal plane step size is 2mm. Cross-hair MNI coordinate (0, -18, 0).

Representative progression of cortical thinning and subcortical structure volume changes with clinical group. *(a-g)*: Representative left and right hemisphere CN, MCI and D diagnosis group average and standard error of FreeSurfer 6.0 estimates of labelled regional cortical layer thickness where one or both hemispheres were significant in a one-way, three-factor (CN, MCI, D), ANOVA, FDR-corrected (q=0.1, 68 tests). *(h-i)*: Representative left and right hemisphere CN, MCI and D clinical group average and standard error of FreeSurfer 6.0 estimates of labelled subcortical structure volume where one or both hemispheres were significant in a one-way, three-factor (CN, MCI, D), ANOVA, FDR-corrected (q=0.1, 16 tests).

Position of ROI pair of interest non-anchor elements in 10 ROI pairs of interest that were significant in the left hemisphere MCI–CN contrast. The anchor ROIs were in left MTL. Shown are ROI masks consisting of a 6-mm radius volume centered at the ROI seed.

Direction of ROI pair functional change is color-coded for hyperconnected (hyperC) (*red*), hypoconnected (hypoC) (*blue*), and hyperconnected and hypoconnected (*green*).

Position of ROI pair of interest non-anchor elements in 13 ROI pairs of interest that were significant in the right hemisphere MCI–CN contrast. The anchor ROIs were in right MTL. Shown are ROI masks consisting of a 6-mm radius volume centered at the ROI seed.

Direction of ROI pair functional change is color-coded for hyperconnected (hyperC) (*red*), hypoconnected (hypoC) (*blue*), and hyperconnected and hypoconnected (*green*).

Position of ROI pair of interest non-anchor elements in 21 ROI pairs of interest that were significant in the left hemisphere AD–CN contrast. The anchor ROIs were in left MTL. Shown are ROI masks consisting of a 6-mm radius volume centered at the ROI seed.

Direction of ROI pair functional change is color-coded for hyperconnected (hyperC) (*red*), hypoconnected (hypoC) (*blue*), and hyperconnected and hypoconnected (*green*).

Position of ROI pair of interest non-anchor elements in 6 ROI pairs of interest that were significant in the right hemisphere AD–CN contrast. The anchor ROIs were in right MTL. Shown are ROI masks consisting of a 6-mm radius volume centered at the ROI seed.

Direction of ROI pair functional change is color-coded for hyperconnected (hyperC) (*red*), hypoconnected (hypoC) (*blue*), and hyperconnected and hypoconnected (*green*).