Regional Brain Hypometabolism Is Unrelated to Regional Amyloid Plaque Burden

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Abstract

In its original form, the amyloid cascade hypothesis of Alzheimer's disease holds that fibrillar deposits of amyloid are an early, driving force in pathological events leading ultimately to neuronal death. Early clinicopathologic investigations highlighted a number of inconsistencies leading to an updated hypothesis in which amyloid plaques give way to amyloid oligomers as the driving force in pathogenesis. Rather than focusing on the inconsistencies, amyloid imaging studies have tended to highlight the overlap between regions that show early amyloid plaque signal on positron emission tomography and that also happen to be affected early in Alzheimer's disease. Recent imaging studies investigating the regional dependency between metabolism and amyloid plaque deposition have arrived at conflicting results, with some showing regional associations and other not.

We extracted multimodal neuroimaging data from the Alzheimer's disease neuroimaging database for 227 healthy controls and 434 subjects with mild cognitive impairment. We analyzed regional patterns of amyloid deposition, regional glucose metabolism and regional atrophy using florbetapir (^{18}F) positron emission tomography, ^{18}F-fuordeoxyglucose positron emission tomography and T1 weighted magnetic resonance imaging, respectively. Specifically, we derived gray matter density and standardized uptake value ratios for both positron emission tomography tracers in 404 functionally defined regions of interest.

We examined the relation between regional glucose metabolism and amyloid plaques using linear models. For each region of interest, correcting for regional gray matter density, age, education and disease status, we tested the association of regional glucose metabolism with (i) cortex-wide florbetapir uptake, (ii) regional (i.e., in the same region of interest) florbetapir uptake and (iii) regional florbetapir uptake while correcting in addition for cortex-wide florbetapir uptake. P-values for each setting were Bonferroni corrected for 404 tests.

Regions showing significant hypometabolism with increasing cortex-wide amyloid burden were classic Alzheimer's disease-related regions: the medial and lateral parietal cortices. The associations between regional amyloid burden and regional metabolism were more heterogeneous: there were significant hypometabolic effects in posterior cingulate, precuneus, and parietal regions but also significant positive associations in bilateral hippocampus and entorhinal cortex. However, after correcting for global amyloid burden, very few of the negative associations remained and the number of positive associations increased.

Given the wide-spread distribution of amyloid plaques, if the canonical cascade hypothesis were true, we would expect wide-spread, cortical hypometabolism. Instead, cortical hypometabolism appears to be linked to global amyloid burden. Thus we conclude that regional fibrillar amyloid deposition has little to no association with regional hypometabolism.

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Abbreviations: Aβ = amyloid-β; ADNI = Alzheimer's disease neuroimaging initiative; DF = degrees of freedom; DMN = default mode network; FDG = ^{18}F-fuordeoxyglucose; FWHM = full-width half maximum; ICV = intracranial volume; IPC = inferolateral parietal cortex; MCI = mild cognitive impairment; MMSE = mini mental state examination; MNI = Montreal neurological institute; PCC = posterior cingulate cortex; ROI = region of interest; SD = standard deviation; SUVR = standard uptake value ratio

Introduction

The amyloid cascade hypothesis of Alzheimer's disease, in its original, unmodified form, posits that the protein amyloid-β is the starting point for a series of pathogenic changes that lead from neuronal dysfunction and synapse loss to cell death (Hardy and Allsop, 1991; Hardy and Higgins, 1992). Particular weight is given, in the unmodified version of the hypothesis, to the large fibrillar aggregates of amyloid-β known as amyloid plaques. The link between amyloid-β, in some form, and Alzheimer's disease is unassailable. Disease-causing mutations in the three genes that lead to autosomal dominant Alzheimer's disease have been shown to promote the formation of the putatively neurotoxic form of amyloid-β, a peptide of 42 amino acids (Suzuki *et al.*, 1994; Scheuner *et al.*, 1996; Gomez-Isla *et al.*, 1999).

While amyloid-β is, irrefutably, an initiating factor in Alzheimer's disease pathogenesis, the remainder of the amyloid cascade hypothesis is much less firmly established. Amyloid plaques are, along with tau-based neurofibrillary tangles, one of the pathologic hallmarks of Alzheimer's disease (Braak and Braak, 1991). They are large, abundant, and easily seen with basic microscopy stains and, as such, were initially assumed to have a key role in the pathogenic cascade (Hardy and Higgins, 1992). From the earliest days of clinicopathologic investigations, however, a number of glaring inconsistencies arose. Chief among these is the oft-replicated finding that there is little association between where amyloid plaques are found at autopsy and which brain regions were dysfunctional in the patient's clinical course (Price *et al.*, 1991; Arriagada *et al.*, 1992; Giannakopoulos *et al.*, 1997; Hardy and Selkoe, 2002). This discordance is most obvious in the entorhinal cortex and hippocampus. These medial temporal lobe structures, crucial to episodic memory function, are the first to fail clinically and the first to develop neurofibrillary tangle pathology. Amyloid plaque deposition, however, does not occur in these regions until relatively late in the course (Price *et al.*, 1991; Arriagada *et al.*, 1992; Giannakopoulos *et al.*, 1997). Conversely, other regions, like the medial prefrontal cortex, typically show abundant amyloid plaque pathology at autopsy despite being relatively

functionally spared clinically (Price *et al.*, 1991; Arriagada *et al.*, 1992; Giannakopoulos *et al.*, 1997). As the field wrestled with these inconsistencies, evidence began to accrue suggesting that Aβ was still the key driver but that its pathogenic properties were related to smaller soluble aggregates of the peptide referred to as oligomers (Lambert *et al.*, 1998; Hartley *et al.*, 1999). These findings have allowed for an updated, reconciled version of the amyloid cascade hypothesis in which amyloid plaques give way to amyloid oligomers as the driving force in pathogenesis (Hardy and Selkoe, 2002).

The advent of amyloid PET imaging should have reinforced this update to the hypothesis. The correlation between plaque quantity and distribution as measured with PET and plaque quantity and distribution at autopsy is extraordinarily high (Ikonomovic *et al.*, 2008; Hatsuta *et al.*, 2015). Unsurprisingly, therefore, imaging studies of Alzheimer's began to show many of the same patterns that the neuropathology literature had been documenting for the last several decades. After age 70, roughly 25% of healthy older controls without cognitive complaints or deficits on testing harbor a large burden of amyloid plaques on PET imaging (Rowe *et al.*, 2010; Chetelat *et al.*, 2013; Jack *et al.*, 2014). The medial prefrontal cortex is among the first regions to show high signal on amyloid PET scans in healthy older controls despite remaining clinically unaffected even late into the course of Alzheimer's disease (Jack *et al.*, 2008). Conversely, even late into the course of Alzheimer's disease cognitive symptoms, the medial temporal lobes tend to show little to no increased signal on amyloid PET (Jack *et al.*, 2008). Despite its role in re-introducing these decades-old arguments against the primacy of plaques in Alzheimer's disease pathogenesis, amyloid PET imaging has, oddly, seemed to have the opposite effect on the field. Rather than focusing on the inconsistencies, studies have tended to highlight the overlap between regions that show early amyloid plaque signal on PET and that happen to be affected early in Alzheimer's disease (Buckner *et al.*, 2005; Sperling *et al.*, 2009; Koch *et al.*, 2014). The PCC and the IPC are most commonly cited in this regard. The PCC and IPC form the posterior aspect of the brain's DMN, a set of functionally connected regions—that

also includes the medial prefrontal cortex and medial temporal lobe structures—that relates to memory function and appears to be targeted early by Alzheimer's disease pathology (Raichle *et al.*, 2001; Greicius *et al.*, 2003; Greicius *et al.*, 2004; Shirer *et al.*, 2012). One highly cited early study in this vein pointed out the qualitative similarity between a resting-state fMRI map of the DMN, a map of glucose hypometabolism in Alzheimer's disease patients, and a map of amyloid deposition in Alzheimer's disease patients (Buckner *et al.*, 2005). This led to the oversimplified interpretation that amyloid plaque deposition occurs in the DMN and results in the dysfunction of this network. No attention was given to the findings, evident from the images, that Alzheimer's disease patients typically have normal metabolism in the medial prefrontal cortex despite having abundant amyloid deposition. Similarly, while the medial temporal lobe is a key component of the DMN and its metabolism is already reduced in the earliest clinical stages of Alzheimer's disease, the amyloid map in this study (as in most subsequent amyloid PET studies) shows no uptake in the hippocampus (Buckner *et al.*, 2005; Kemppainen *et al.*, 2006; Edison *et al.*, 2007; Jack *et al.*, 2008), though with rare exceptions (Frisoni *et al.*, 2009; Sepulcre *et al.*, 2013).

A few multimodal imaging studies using FDG PET and amyloid PET approached the question of whether local amyloid plaque deposition is correlated with local levels of glucose metabolism. These studies produced conflicting results with some showing an association between local amyloid plaque deposition and glucose hypometabolism in some brain regions (Engler *et al.*, 2006; Edison *et al.*, 2007; Cohen *et al.*, 2009; Lowe *et al.*, 2014) and others showing the absence of any correlation (Li *et al.*, 2008; Rabinovici *et al.*, 2010; Furst *et al.*, 2012). Further work showed that the dependency may be more complex and relationship between plaques and metabolism may change depending on disease stages (Cohen *et al.*, 2009) or brain regions (La Joie *et al.*, 2012). Discrepancies in the findings may originate from the different subject populations that were studied. For instance, Lowe *et al.* (2014) studied only healthy controls, while Furst *et al.* (2012) focused on AD subjects. A second source for the

discrepancies may be the limited sample sizes of most studies: with the exception of Lowe *et al.* (2014), previous studies comprised fewer than 100 subjects and the specific regional analysis within a single disease group did typically not exceed two dozen subjects (Engler *et al.*, 2006; Edison *et al.*, 2007; Li *et al.*, 2008; Cohen *et al.*, 2009; La Joie *et al.*, 2012). Moreover, many studies relied on a plain correlation analysis between the regional tracer intensities without correcting for cofounders such as age, sex, education and extent of amyloid pathology.

Here we investigated the relationship between regional amyloid plaque deposition and regional glucose hypometabolism, using a large dataset comprising hundreds of subjects (healthy controls and patients with MCI) obtained from the ADNI (Alzheimer's disease neuroimaging initiative) database who were imaged with both amyloid PET (^{18}F-florbetapir PET) and FDG PET.

Materials and Methods

Subjects

Data used in the preparation of this article were obtained from the ADNI database (http://adni.loni.usc.edu). The ADNI was launched in 2003 as a public-private partnership, led by Principal Investigator Michael W. Weiner, MD. The primary goal of ADNI has been to test whether serial MRI, PET, other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of MCI and early Alzheimer's disease. For up-to-date information, see www.adni-info.org.

We extracted T1 weighted structural scans, as well as florbetapir and FDG PET scans for $n = 661$ subjects from the ADNI database. The subjects were either healthy older controls ($n = 227$) or patients with MCI ($n = 434$), covering both, early and late MCI. The FDG PET scan and the structural T1 weighted scan were acquired at most 60 days before or after the subjects' first florbetapir PET scan. The closest diagnosis within 90 days of the florbetapir PET scan served as the current diagnosis. Further, CSF Aβ values obtained within 90 days of amyloid imaging were available for 544 subjects. Subject IDs and image IDs for all three modalities and subject specific information are available in Supplementary Table S1. For additional information on ADNI protocols see http://adni.loni.usc.edu/methods/documents/ and for PET analysis in particular see (Jagust *et al.*, 2010; Jagust *et al.*, 2012) and http://adni.loni.usc.edu/methods/pet-analysis/.

Regions of Interest

Anatomically defined brain regions often comprise multiple, functionally independent regions and have proven inferior to functionally-defined regions in classification of cognitive states (Shirer *et al.*, 2012) and in temporal and spatial clustering of brain regions (Craddock *et al.*, 2012). Thus, for this analysis, we used a cortex-wide parcellation based on functional connectivity during rest rather than a structure-based parcellation such as the AAL (automated

anatomical labeling) atlas (Tzourio-Mazoyer *et al.*, 2002). More precisely, the regions of interest are based on a set of 90 functional ROIs derived from resting state fMRI covering 14 major networks (Shirer *et al.*, 2012). In order to further subdivide these ROIs and extend the atlas to whole-brain coverage, we first divided the brain into 91 regions: 90 from the Shirer atlas and the rest of the gray matter voxels were treated as a single region. We then divided each region into round(nN/p) parcels using Ward clustering (Michel *et al.*, 2012), where n is the number of gray matter voxels in the given region, p is the total number of gray matter voxels in the brain, and N is the user-defined number of parcels, set to 500 in accordance to the literature (Van Essen and Ugurbil, 2012). To constrain the parcels to be spatially-contiguous, only Pearson's correlations between fMRI time courses of spatially-adjacent voxels were considered during Ward clustering. The resting-state fMRI data used to estimate the Pearson's correlations between voxels were obtained from a publicly available source comprising 21 subjects and 7 min scan time with a TR of 2000 ms (Landman *et al.*, 2011).

This original set of 499 functionally defined ROIs was modified to fit the specifics of this analysis. First, we applied a strict gray matter mask (mean gray matter of 0.4 or more in the study sample) to the ROIs in order to reduce the influence of white matter on the average PET intensities in the ROIs, which is a challenge when working with florbetapir PET. Second, we excluded cerebellar ROIs (n = 59) and ROIs smaller than six voxels (2mm isotropic; n = 36). This resulted in a final set of 404 ROIs in MNI space covering the cortical gray matter (Figure 1a). Further ROIs were a joint pons-vermis ROI (for FDG PET normalization), a whole cerebellum ROI (for florbetapir PET normalization) and a whole cortex gray matter ROI. All ROIs are available as part of the Supplemental Online Material.

Image Processing

The structural T1 images were segmented into gray matter, white matter, and cerebrospinal fluid using the *New Segment* algorithm in SPM8 (Ashburner and Friston, 2005). The DARTEL

algorithm in SPM8 was used to normalize the images to MNI 152 space (Ashburner, 2007). In order to accelerate processing, a randomly selected subset of 100 images was used to create the DARTEL template. The resulting warping for each subject's T1 image was applied to the gray matter segmented images; images were modulated following the spatial normalization. Further, images were smoothed using an 8mm FWHM Gaussian kernel. Finally, average gray matter density was computed for each of the 404 functional ROIs and the whole cortex gray matter. The resulting values were divided by the subjects' ICV for normalization.

The PET images, which were acquired from the ADNI database, were smoothed to 8mm resolution and the florbetapir and FDG PET images were coregistered for each subject. Due to technical challenges in normalizing florbetapir PET images to MNI space (Saint-Aubert *et al.*, 2014), we analyzed all PET data in subject space: SPM's MNI PET template was spatially normalized to each subject's FDG PET image using the *Normalise* algorithm in SPM8 (Ashburner *et al.*, 1997). The resulting warping was applied to all ROIs. Next, we extracted the average FDG and florbetapir tracer uptake for each of the functional 404 ROIs and the whole cortex gray matter ROI. We computed the SUVR by dividing the FDG and florbetapir intensities to the mean signal in the joint pons-vermis ROI and the whole cerebellum ROI, respectively.

Association Between Diagnosis and Imaging Modalities

For each of the three modalities and for each of the 404 functional ROIs we estimated a linear regression model with the signal intensity being the dependent variable and diagnosis, age, sex, education, ICV and APOE-ε4 status as the independent predictors. P-values for the diagnosis coefficient were Bonferroni corrected for each modality, i.e., assuming 404 tests within each modality. In order to rule out that changes observed in FDG PET and florbetapir PET were solely due to gray matter loss, in a second analysis, we added regional gray matter volume as a covariate to the linear model. Further, to assess the cortex-wide effect, we conducted this

analysis with average biomarker intensity in the whole cortex gray matter ROI for each modality.

Association Between Global Amyloid Burden and Regional Glucose Metabolism

Increased global presence of amyloid plaques in the brain and decline of Aβ levels in the CSF are signs of disease progression from healthy aging towards MCI and AD. With the next model, collapsing across diagnosis, we tested the association of global amyloid burden and local glucose metabolism. Global amyloid burden was defined as the mean florbetapir SUVR in the whole cortex gray matter ROI. For each of the 404 functional ROIs we estimated a linear model with the FDG PET SUVR as the dependent variable and diagnosis, age, sex, education, regional gray matter and global amyloid as independent predictors. The P-values for the association of global amyloid with regional FDG uptake were Bonferroni corrected for 404 tests. We repeated this analysis with a subset of subjects (n = 544) for which CSF Aβ was available close to the amyloid imaging. We used the continuous CSF Aβ value as replacement for cortex-wide florbetapir SUVR. Due to the strong association between APOE-ε4 carrier status and changes in Aβ in the CSF and in the cortex, we did not correct for APOE-ε4 carrier status in the linear model.

Association Between Regional Amyloid Burden and Regional Glucose Metabolism

The effect of regional amyloid on regional glucose metabolism was tested with the same linear regression setup as for global amyloid but instead using the florbetapir SUVR of the same ROI. As before, we are not correcting the model for APOE-ε4 carrier status. The P-values for this regional amyloid burden coefficient were Bonferroni corrected for 404 tests. Technically, we are assessing the significance of the semi-partial correlation between regional FDG SUVR and regional florbetapir SUVR.

Analyzing these data ROI by ROI is technically valid and in fact often done in related work (Cohen *et al.*, 2009; La Joie *et al.*, 2012; Lowe *et al.*, 2014). However, this local approach treats ROIs independently from each other and disregards the high correlations between local levels of amyloid and global level of amyloid burden. Thus, in order to test for the local specificity of the association we conducted two additional computations: a) estimating the linear regression as above, but correcting in addition for global amyloid burden by adding the cortex-wide florbetapir SUVR as an additional predictor (and, alternatively, CSF Aβ or the indicator variable for CSF Aβ ≤ 192 pg/ml) and b) conducting a permutation test examining the association strength to non-local amyloid burden (see details below).

Permutation Test

We define *local* linear regression as the linear regression models used above where we test for the regional association between glucose metabolism in ROI *i* and the regional amyloid plaque deposition in the same ROI *i*. Conversely, we define *non-local* linear regression as models where we test for the association between glucose metabolism in ROI *i* and the amyloid plaque deposition in a different ROI $j \neq i$. In this permutation test we compared the association strength (t-score) of the local linear regression with the association strength from all non-local linear regressions. In particular, we computed how many non-local models showed a stronger association between glucose metabolism and amyloid plaques than the local model. In this one-sided permutation test the direction of the effect (sign of the t-value) in the local model determined whether stronger meant "more positive" or "more negative". In order to minimize possible confounding effects of neighboring regions (i.e., regions adjacent to the local ROI), all ROIs adjacent to the examined ROI were excluded from the permutation test. That is, if the examined ROI had five neighbors, we were comparing it to the association strength in the 398 (= 403-5) remaining ROIs. In addition, the number of regions imposed a lower bound on the P-value, i.e., P-values could not get lower than 1/404 (≈0.0025). Given this limitation, P-values

were not corrected for multiple testing. Small P-values indicate local specificity of the association since only few non-local ROIs show an equal or stronger association. Of note, at $P = 0.05$ there may still be as many as 19 non-local regions that show a stronger association.

Amyloid Positive Scans

In order to define a cutoff for amyloid positive scans, we used cortex-wide florbetapir SUVR values from a reference subgroup of all 661 subjects: 99 control subjects with a normal CSF Aβ level (> 192 pg/ml) (Shaw *et al.*, 2009). We computed mean and standard deviation of the global florbetapir SUVR in these subjects and used these values to compute a Z-score for global amyloid burden in all subjects. We considered a Z-score of 1.65 or more to be an indication of a positive amyloid scan. This cutoff corresponds to a P-value of 0.05 in a one-sided test. In our study sample, this Z-score translates into a cortex-wide florbetapir SUVR threshold of 1.263.

Rabinovici *et al.* (2010) reported a disappearance of regional associations once the study group was restricted to subjects with the same diagnosis. Thus, we repeated the test for association between regional florbetapir SUVR and regional FDG SUVR in the subset of subjects ($n = 267$) with amyloid positive scans.

Sliding Window Analysis

To further investigate the effect of subject groupings on the significant regional associations, we conducted a sliding window approach. For this analysis all subjects were ranked according to their global amyloid burden from least burden to most burden. We used a window size of 100 subjects, which was shifted by 10 subjects; resulting in 58 groupings with 100 subjects each and increasing average global amyloid burden. For each window we conducted the regional association analysis, as we did for the entire sample set, and counted the number of negatively associated ROIs.

Results

From the ADNI database we extracted imaging data for 661 subjects (controls: 227; MCI: 434). The dataset contained more males (53.9%) and the average age at imaging was 73.4 years (SD: 7.59). Compared to the control subjects, MCI subjects were significantly younger, had a significantly lower MMSE and were more likely to be carriers of an APOE-ε4 allele (Table 1).

MCI subjects Show Regional and Global Changes in all Three Imaging Modalities

First, we examined the association between disease status (control versus MCI) and cortex-wide changes in imaging modalities. After adjusting for age, sex, ICV, education, and APOE-ε4 carrier status, compared to control subjects, MCI subjects showed a significant cortex-wide increase in amyloid (T = 4.91; DF = 652; P = 1.15e−6), while glucose metabolism (T = −3.69; DF = 652; P = 0.00024) and gray matter density (T = −2.11; DF = 652; P = 0.035) were significantly decreased (Figure S1).

Using linear regression analysis, we examined the association between clinical diagnosis and regional imaging modality intensities for all 404 ROIs (Figure 1a). Compared to controls, MCIs showed significantly ($P_{bonf} < 0.05$) reduced gray matter density in 4 ROIs (bilateral hippocampus and right inferior temporal gyrus; Figure 1b) and significantly reduced glucose metabolism in 29 ROIs (Figure 1c). We refer to these ROIs as diagnosis associated ROIs (ROI_{DX}). The ROI_{DX} cover the bilateral hippocampus, the PCC/precuneus, right angular gyrus, and paracingulate gyrus. When correcting the linear model in addition for regional gray matter density, 25 ROI_{DX} remained significant and 3 additional ROIs showed significantly reduced glucose metabolism in MCIs compared to controls. Notably, two ROIs showed significant reductions in both gray matter density and glucose metabolism: left and right hippocampus.

Further, compared to controls, MCIs showed significantly increased amyloid plaque deposition in 234 ROIs (57.9% of all tested ROIs) distributed across the entire cortex (Figure 1d). Remarkably, no ROI showed significant changes in all three modalities. When correcting

the linear model in addition by regional gray matter density, 229 of the 234 ROIs remained significant and 8 additional ROIs were significant. Detailed results for all ROIs and the three modalities are summarized in Figure S2.

Changes in Regional Glucose Metabolism are Associated with Global Amyloid Pathology

A total of 26 ROIs (6.4%) showed a significant decrease of glucose metabolism with increasing global amyloid burden (Figure 2a). We refer to these ROIs as global amyloid ROIs ($ROI_{amyloid}$). These ROIs cover the PCC/precuneus, both lateral occipital cortices, bilateral inferior temporal gyri, and parts of the bilateral hippocampi. Using CSF Aβ levels instead of global amyloid burden resulted in qualitatively the same results (46 ROIs; 25 shared with global amyloid and 21 new ROIs extending the previous regions; Figure 2b). We refer to these ROIs as $CSF_{A\beta}$ ROIs (ROI_{CSF}). As expected, CSF Aβ levels were highly correlated with global amyloid burden ($r = -0.64$; $P < 5.6e{-}64$; Figure S3).

Regional Hypometabolism is Associated with Global Amyloid Burden Rather Than Regional Amyloid Burden

The main focus of this study was to investigate the association between the presence of local amyloid plaques and local glucose hypometabolism. Of particular interest were ROIs that are linked to Alzheimer's disease pathology (ROI_{DX}, $ROI_{amyloid}$, and ROI_{CSF}) along with ROIs belonging to the default mode network (DMN; Figure S4), which is known to be primarily affected in Alzheimer's disease (Greicius *et al.*, 2004; Seeley *et al.*, 2009). Using linear regression, we found a significant association between the two PET modalities in 141 ROIs. Half of these were negative relationships ($n = 71$; the higher the amyloid PET SUVR the lower the glucose metabolism) and the other half were positive ($n = 70$; the higher the amyloid PET SUVR the higher the glucose metabolism; Figure 3a). Negative associations were mainly found

in the PCC/precuneus and the bilateral occipital gyri, while positive association were located in the bilateral hippocampi, entorhinal cortices, the thalamus, paracingulate gyrus and the supplementary motor cortex. The negatively associated ROIs largely overlap with ROI_{DX} (10 of 29), $ROI_{amyloid}$ (20 of 26) and ROI_{CSF} (27 of 46) (Table 2).

Regional florbetapir SUVR was highly correlated with cortex-wide florbetapir SUVR: 349 ROIs (86.4%) showed a Pearson's r ≥ 0.7 ($P < 8.14e{-}99$; Figure S5). After adding global florbetapir SUVR as an additional covariate to the linear model, 185 ROIs showed a significant association between the regional florbetapir SUVR and regional glucose metabolism. The number of ROIs with a negative dependency was markedly reduced (from 71 to 39; Table 2). In particular, the negative associations in the PCC/precuneus as well as the lateral occipital gyri largely disappeared, while the regions with positive associations in the entorhinal cortices and the hippocampi increased (Figure 3b). This effect also translated to fewer negative dependencies in Alzheimer's disease linked ROIs and the DMN (three ROIs instead of eight; Table 2). Repeating the analysis using CSF Aβ and dichotomized CSF Aβ (≤ 192 pg/ml) instead of global amyloid burden in order to correct for global amyloid pathology led to qualitatively unchanged results and confirmed markedly fewer negative dependencies in the whole brain and Alzheimer's disease linked regions (Table 2).

Next, we used a spatial permutation test for assessing the local specificity of the association between amyloid plaque deposition and glucose metabolism. All of the 70 positively associated ROIs remained spatially specific, while only 42 of the 71 negatively associated ROIs maintained spatial specificity (Table 2). As with global amyloid correction, the negative association in the ROIs in the PCC/precuneus and the bilateral lateral occipital cortices mostly disappeared (Figure 3c).

No Regional Associations in Subjects with a Positive Amyloid Scan

Further, when we restricted the analysis to subjects showing a positive amyloid scan (n = 267; see methods) only one ROI of all 404 showed a negative association between amyloid plaque deposition and metabolism (Table 2).

The sliding window analysis resulted in 58 groupings with 100 subjects each and increasing average global amyloid burden. With increasing global amyloid burden the number of ROIs with negative association between regional amyloid plaque deposition and metabolism decreases (Figure 4).

Discussion

Our analysis confirmed previously reported differences in imaging biomarkers between healthy controls and MCI subjects. The availability of both PET modalities in all subjects allowed us to analyze the regional association of amyloid plaque burden and glucose metabolism. At first glance, our analysis appeared to largely confirm the qualitative similarity between a map of glucose hypometabolism in Alzheimer's disease patients and a map of amyloid deposition in Alzheimer's disease patients. However, only a minority of ROIs followed the prediction of the amyloid hypothesis in its original form, where increase in amyloid plaques are linked to reductions in glucose metabolism. If the unmodified amyloid hypothesis held true, given the widespread increase of amyloid plaques in MCI subjects, there should have been a widespread decrease in glucose metabolism. Further, glucose metabolism in one of the prime regions of amyloid deposition, the prefrontal cortex, showed no significant association with regional levels of amyloid. The hippocampus, on the other hand, showed hypometabolism without significant enrichment of amyloid plaques. If these data support a regional association between amyloid plaque burden and metabolism, it is for the somewhat heretical inversion of the amyloid hypothesis. That is, regional amyloid plaque deposition is protective, possibly by pulling the more toxic amyloid oligomers out of circulation and binding them up in inert plaques, or via other mechanisms (Cuajungco *et al.*, 2000; Lee *et al.*, 2004; Wolfe and Cyr, 2011). A similar pattern has been observed in APP/PS1 mouse models: older transgenic mice showed increased FDG uptake in the hippocampus and other cortical regions when compared to age-matched controls. Follow-up experiments showed that these glucose uptake increases were located in the proximity of plaques rather than in amyloid-free tissue (Poisnel *et al.*, 2012). However, given the resolution of PET and the applied smoothing, we cannot rule out that positive association in ventral areas and subcortical areas are the result of co-registration artifacts. Our additional analyses, which were aimed at elucidating the local specificity of the association, suggest that

the pattern of hypometabolism is mainly dependent on the cortex-wide increase in amyloid burden and not due to regional deposits of fibrillar amyloid plaques.

The question of whether local deposits of fibrillar amyloid have a bearing on local glucose metabolism has been met with conflicting results. Until now, few studies have directly compared the regional association between these two modalities side-by-side in the same subjects, with some work reporting a regional association of amyloid plaques and hypometabolism (Engler *et al.*, 2006; Edison *et al.*, 2007; Cohen *et al.*, 2009; Lowe *et al.*, 2014) and other work reporting no significant association (Li *et al.*, 2008; Rabinovici *et al.*, 2010; Furst *et al.*, 2012). These discrepancies may, in part, originate from the fact that most studies examined a low number of subjects and had thus reduced power to detect an association. An additional key factor is the subject group studied. Rabinovici *et al.* (2010) noted that the initially significant regional association disappeared once healthy subjects were removed from the analysis, which further highlights the necessity to control for global amyloid levels in the regional analysis. In addition, most previous studies focused the regional analysis on a small set of brain regions such as the precuneus that are typically affected in Alzheimer's disease. Given the high correlation of local amyloid burden with global amyloid burden, picking a select set of ROIs runs the risk of accentuating the spurious effect of local amyloid on local metabolism when it is in fact linked to disease progression (as indicated by global amyloid burden). Further, our sliding window analysis showed that a pre-selection of amyloid positive subjects reduced the likelihood of observing negative associations between the two modalities. In fact, the negative associations were most pronounced in subject groups that were mainly amyloid negative, i.e., at the beginning of the disease spectrum, and therefore in line with the findings by Lowe *et al.* (2014) who studied older cognitively normal subjects exhibiting a wide range of global amyloid burden. Further, the lack of significant ROIs in subjects with substantial amyloid tracer retention can be regarded as further evidence for neurodegeneration being independent from Aβ pathology in advanced stages of the disease (Hyman, 2011).

Clearly, amyloid imaging is a valuable clinical tool. Like levels of amyloid-β in the CSF, a longstanding biomarker for Alzheimer's disease, global amyloid plaque burden is a useful marker for disease onset and progression (Okello *et al.*, 2009; Villemagne *et al.*, 2011; Jack *et al.*, 2014). Like many others, our study showed that subjects with a positive amyloid scan were more likely to show dysfunction (hypometabolism here) in Alzheimer's disease-related regions (Greicius *et al.*, 2004; Sorg *et al.*, 2007; Seeley *et al.*, 2009). However, according to our results there appears to be no added clinical or research value in studying the regional distribution of amyloid plaques. This confirms early clinicopathologic investigations (Price *et al.*, 1991; Arriagada *et al.*, 1992; Giannakopoulos *et al.*, 1997) and recent imaging studies (Rabinovici *et al.*, 2008; Lehmann *et al.*, 2013; Laforce *et al.*, 2014), all of which found no link between the regional pattern of amyloid plaques and the dysfunctional brain regions in the patient's clinical course. Tau imaging (Villemagne and Okamura, 2014) may be more suitable to provide clinically relevant regional information. One criticism our interpretation is likely to encounter is that there may be a time lag between regional amyloid plaque deposition and a given region later becoming dysfunctional (Forster *et al.*, 2012). This would probably hold up for regions like the PCC but would not explain regions like the medial prefrontal cortex (early plaques like the PCC but much later metabolism changes) or the hippocampus (early hypometabolism, late plaques).

In conclusion, given the wide-spread distribution of amyloid plaques, if the canonical cascade hypothesis were true, we would expect wide-spread, cortical hypometabolism and cortex-wide negative associations between amyloid plaques and metabolism. Instead, cortical hypometabolism appears to be mainly linked to global amyloid burden. Global amyloid plaque burden is an important biomarker of Alzheimer's disease risk. Regional amyloid plaque deposition, however, has little to no association with regional hypometabolism.

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Supplementary material

Supplementary material is available.

Figures

Figure 1: Regions of interest and effects of diagnosis on imaging modalities. The 404 ROIs used in the analysis (a). ROIs with reduced GM in MCIs are shown in cyan (b); ROIs with hypometabolism in MCI are shown in blue (c); ROIs with increased amyloid plaque deposition in MCI are shown in red and yellow (d). All slices are in neurological convention (left side of the image corresponds to the left side of the brain).

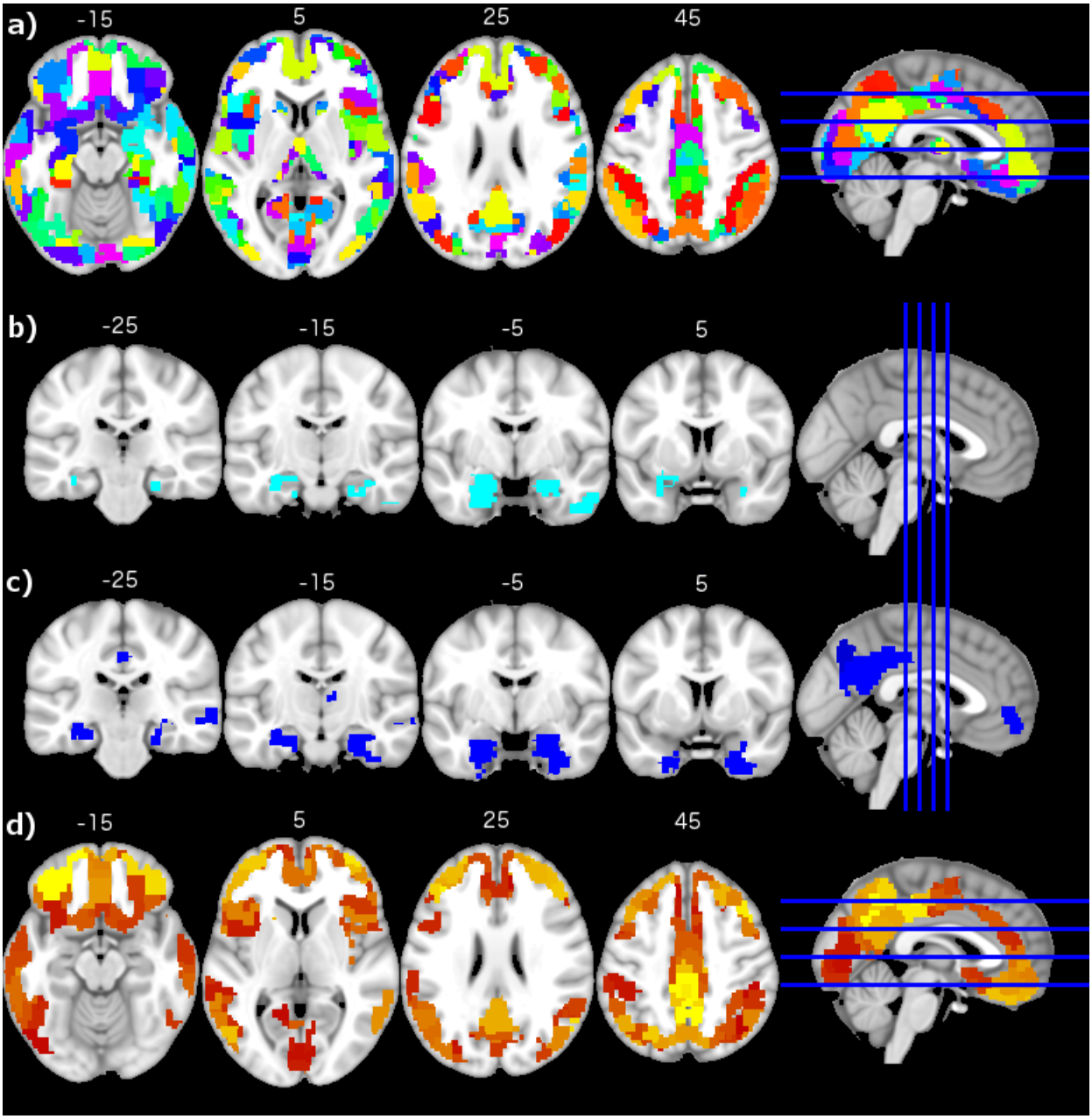

Figure 2: Regional hypometabolism in dependence of biomarkers for disease progression.

ROIs showing significant reduction in glucose metabolism with increases in cortex-wide amyloid burden (a) or with decreases in CSF Aβ (b).

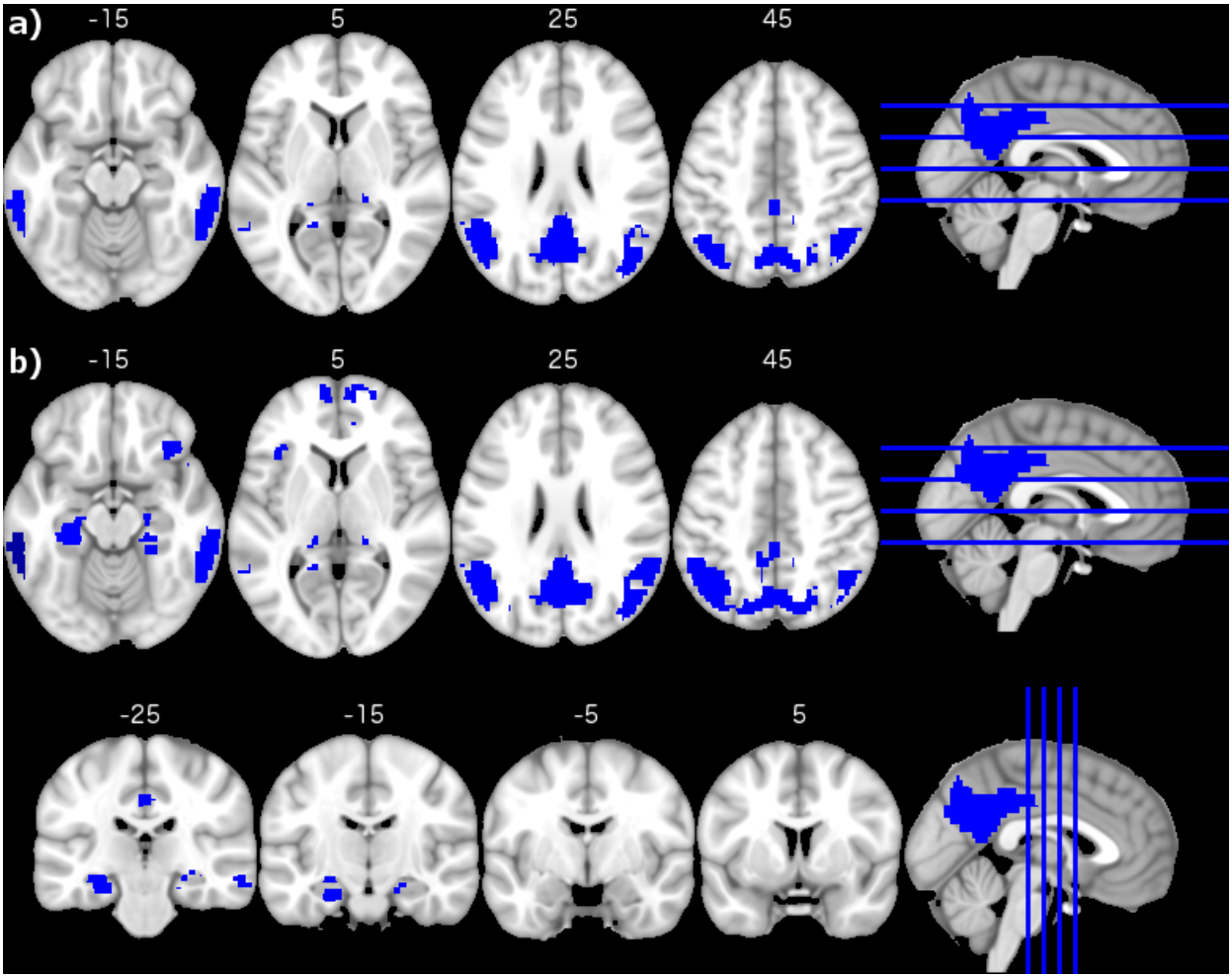

Figure 3: Regional metabolism in dependence of regional amyloid plaque deposition. ROIs with significant positive association are shown in yellow (increased metabolism with increased amyloid plaque deposition) and ROIs with significant negative association are shown in blue (decreased metabolism with increased amyloid plaque deposition). The figure displays axial and coronal slices for three sets of results: ROIs that exhibit a significant association between regional amyloid burden and glucose metabolism after correcting for DX, sex, age, education and regional gray matter (a); the same as before but additionally corrected for global amyloid burden (b); results from (a) that survived the permutation test for local specificity (c).

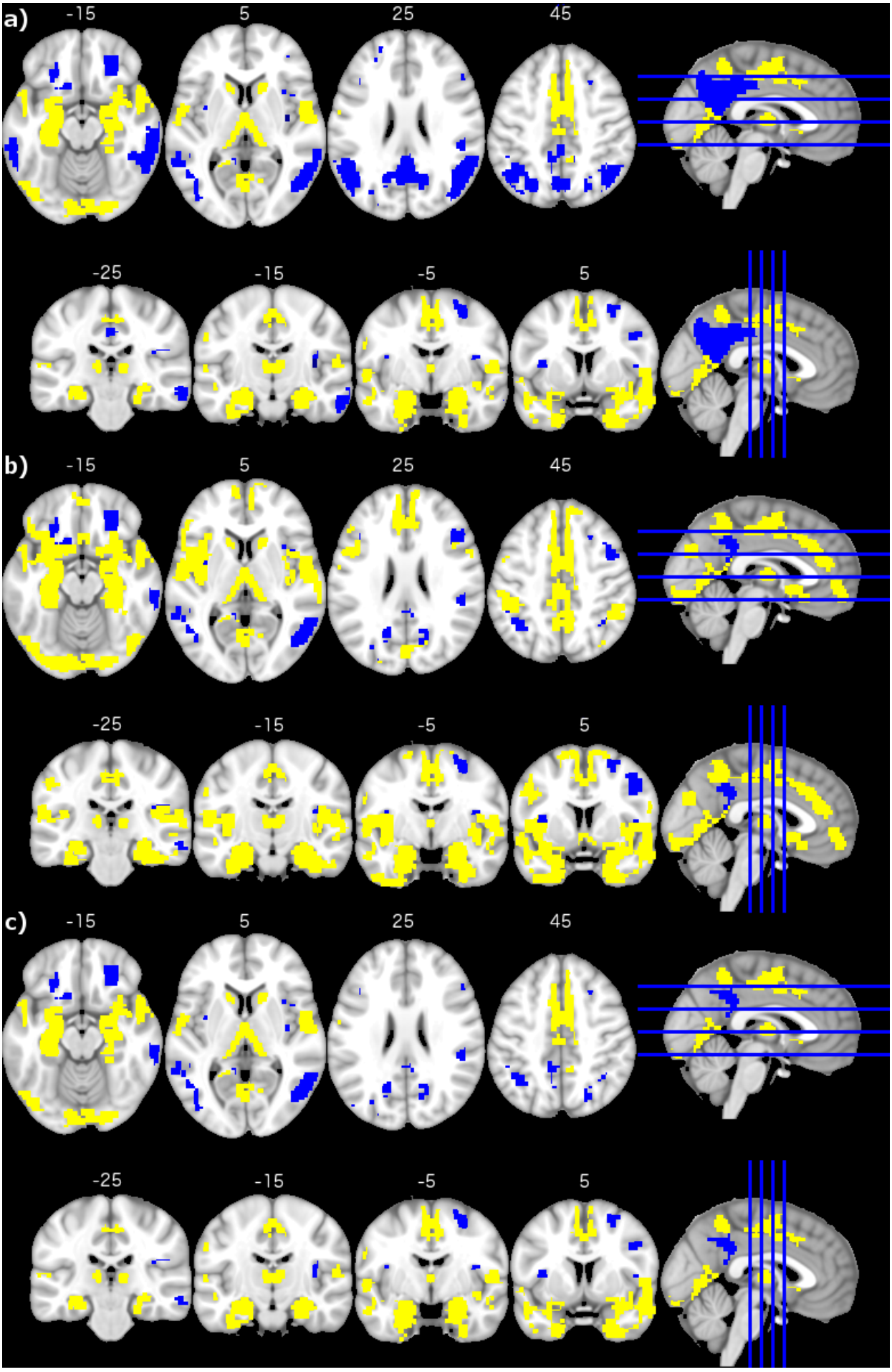
a)
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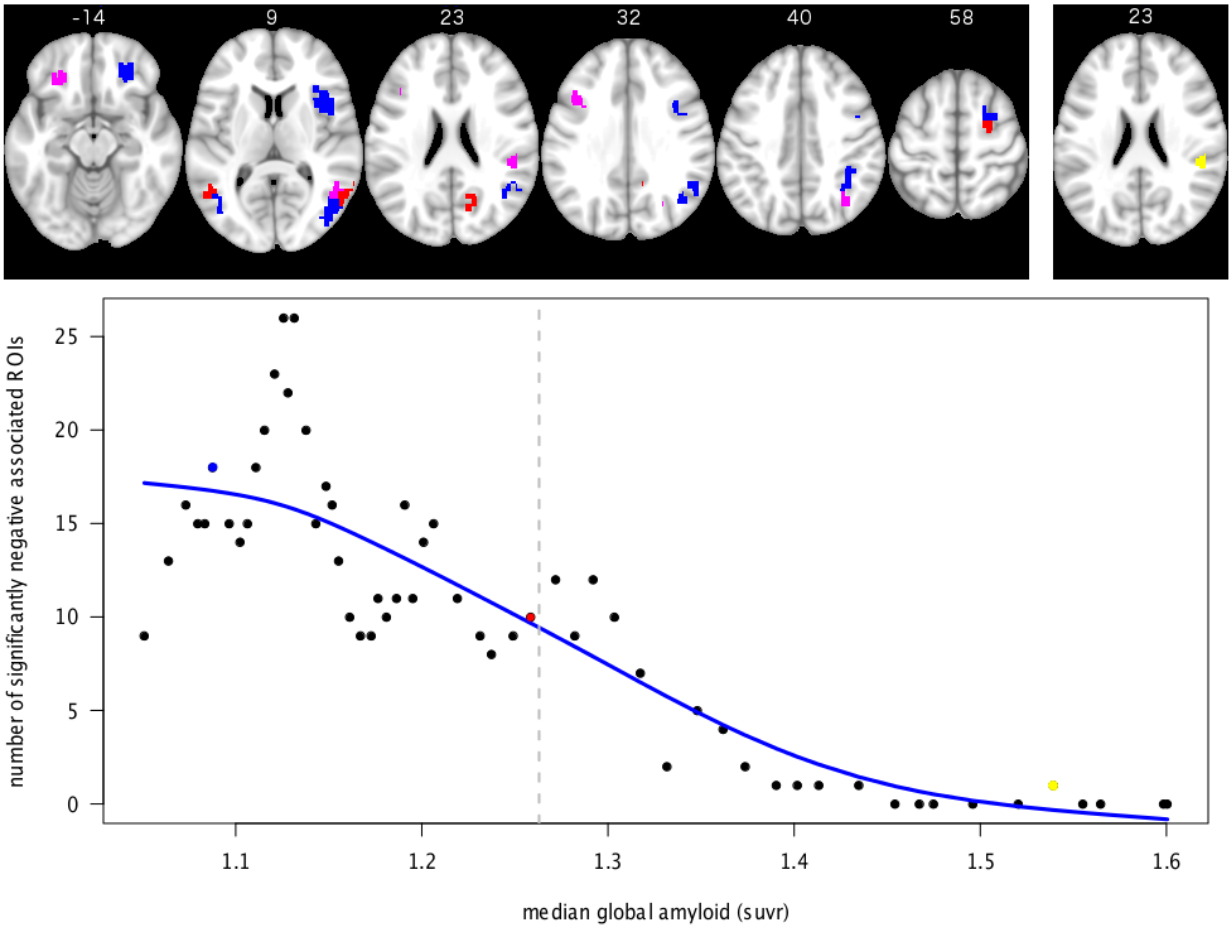
Figure 4: Number of significant negative associations in relation to global amyloid level. The lower panel shows the median of the global amyloid level for all 58 groupings of 100 subjects and the resulting number of ROIs with significant negative association between regional amyloid deposition and regional metabolism. A fitted spline with 4 degrees of freedom is shown in blue. The gray vertical line depicts the threshold for amyloid positive scans. The axial slices on top show the pattern of negative associated ROIs for three groupings: low global amyloid (blue), half amyloid positive and half amyloid negative (red) and high global amyloid (yellow). The groupings are highlighted in the graph below with the same color code. Overlaps between red and blue are shown in violet.



Tables

Table 1: Subject demographics.

	Sex (males)	Age	Education	MMSE	Apoe4+ (%)
Controls (N=227)	111	75.3 (6.68)	16.3 (2.6)	29.1 (1.2)	61 (26.9)
MCI (N=434)	245	72.5 (7.97)	16.1 (2.7)	28.1 (1.7)	200 (46.1)
P-value	0.077 [a)]	2.3×10^{-6} [b)]	0.25 [b)]	$<2.2 \times 10^{-16}$ [b)]	2.3×10^{-6} [a)]

a) P-values based on Fisher's exact test

b) P-values based on two-sided t-test.

Table 2: Number of ROIs with significant positive (+) or negative (−) association between regional florbetapir SUVR and regional FDG SUVR. The columns correspond to different sets of ROIs being considered: all 404 ROIs (whole cortex), ROIs showing hypometabolism in MCIs (ROI_{DX}), ROIs showing hypometabolism with increases in global amyloid burden ($ROI_{amyloid}$) or decreases in CSF Abeta (ROI_{CSF}), and ROIs belonging to the DMN (ROI_{DMN}). The rows correspond to different analysis setups: "Local" refers to the regional analysis of association between amyloid and metabolism; "Local+global", "Local+CSF", and "Local+CSF_{192}" are in addition corrected for global amyloid burden, CSF Aβ levels, and an indicator for CSF Aβ ≤ 192 pg/ml, respectively; Permutation indicates ROIs from the "Local" analysis that survive the permutation test; Amyloid+ is the Local restricted to all subjects with an amyloid positive scan.

	Whole cortex $n = 404$		ROI_{DX} $n = 29$		$ROI_{amyloid}$ $n = 26$		ROI_{CSF} $n = 46$		ROI_{DMN} $n = 34$	
	+	−	+	−	+	−	+	−	+	−
Local	70	71	11	10	2	20	6	27	4	8
Local+global	146	39	14	3	2	2	8	6	15	3
Local+CSF	97	31	12	2	2	4	6	6	7	3
Local+CSF_{192}	103	29	12	2	2	4	6	7	7	3
Permutation	70	42	11	3	2	3	6	8	4	3
Amyloid+	71	1	11	0	2	0	6	0	6	0

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