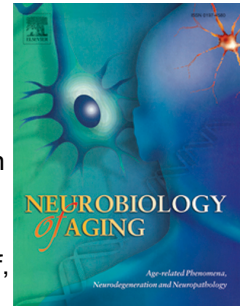


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APOE  $\epsilon$ 4 status is associated with white matter hyperintensities volume accumulation rate independent of AD diagnosis

Carole H. Sudre, M. Jorge Cardoso, Chris Frost, Josephine Barnes, Frederik Barkhof, Nick Fox, Sébastien Ourselin



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Carole H. Sudre<sup>a,b</sup>, M. Jorge Cardoso<sup>a,b</sup>, Chris Frost<sup>c</sup>, Josephine Barnes<sup>b</sup>, Frederik Barkhof<sup>a,d</sup>, Nick Fox<sup>b</sup>, Sébastien Ourselin<sup>a,b</sup>, for the Alzheimer's Disease Neuroimaging Initiative\*

a) Translational Imaging Group, Centre for Medical Image Computing, Department of Medical Physics and Biomedical Engineering, University College London 8<sup>th</sup> Floor Malet Place Engineering Building, 2 Malet Place WC1 7JE

b) Dementia Research Centre, UCL Institute of Neurology, University College London

c) London School of Hygiene and Tropical Medicine, Department of Medical Statistics, Faculty of Epidemiology and Medical Health, University College London

d) Department of Radiology & Nuclear Medicine, VU University Medical Centre, Amsterdam, NL

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Corresponding Author:

Carole H Sudre

Translational Imaging Group

8<sup>th</sup> Floor Malet Place Engineering Building, University College London

2 Malet Place

WC1E 7JE London

United Kingdom

carole.sudre.12@ucl.ac.uk

M.Jorge Cardoso: [m.jorge.cardoso@ucl.ac.uk](mailto:m.jorge.cardoso@ucl.ac.uk)

Chris Frost: [c.frost@lshtm.ac.uk](mailto:c.frost@lshtm.ac.uk)

Josephine Barnes: [j.barnes@ucl.ac.uk](mailto:j.barnes@ucl.ac.uk)

Frederik Barkhof: [f.barkhof@ucl.ac.uk](mailto:f.barkhof@ucl.ac.uk)

Sébastien Ourselin: [s.ourselin@ucl.ac.uk](mailto:s.ourselin@ucl.ac.uk)

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APOE  $\epsilon$ 4 status is associated with white matter hyperintensities volume accumulation rate independent of AD diagnosis

## Abstract

To assess the relationship between carriage of *APOE*  $\epsilon$ 4 allele and evolution of white matter hyperintensities (WMH) volume, we longitudinally studied 339 subjects from the ADNI cohort with diagnoses ranging from normal controls to probable Alzheimer's disease (AD). A purpose-built longitudinal automatic method was used to segment WMH using constraints derived from an atlas-based model selection applied to a time-averaged image. Linear mixed models were used to evaluate the differences in rate of change across diagnosis and genetic groups. After adjustment for covariates (age, sex, and total intracranial volume), homozygous *APOE*  $\epsilon$ 4 $\epsilon$ 4 subjects had a significantly higher rate of WMH accumulation (22.5 % per year 95% CI [14.4, 31.2] for a standardized population having typical values of covariates) compared with the heterozygous ( $\epsilon$ 4 $\epsilon$ 3) subjects (10.0 % per year [6.7, 13.4]) and homozygous  $\epsilon$ 3 $\epsilon$ 3 (6.6 % per year [4.1, 9.3]) subjects. Rates of accumulation increased with diagnostic severity; controls accumulated 5.8% per year 95% CI[2.2, 9.6] for the standardized population, early mild cognitive impairment (MCI) 6.6% per year [3.9, 9.4], late MCI 12.5% per year [8.2 17.0] and AD subjects 14.7% per year [6.0 24.0]. Following adjustment for *APOE* status these differences became non-statistically significant suggesting that *APOE*  $\epsilon$ 4 genotype is the major driver of accumulation of WMH volume rather than diagnosis of AD.

## Introduction

The *APOE* gene, and specifically its  $\epsilon 4$  allelic variant, has an important dose-dependent association with Alzheimer's disease (AD) risk (Verghese, Castellano, & Holtzman, 2011). *APOE*  $\epsilon 4$  is associated with increased cerebral amyloid plaque deposition and amount of white matter hyperintensities (WMH).

WMH are associated with increasing age in apparently healthy elderly subjects and inversely related to executive function and processing speed (Mortamais, Artero, & Ritchie, 2013). They are thought to be a marker of cerebral small vessel disease, and possible pathophysiological explanations for the imaging change include partial ischemia of the tissue and degradation of the blood brain barrier (Wardlaw, Valdés Hernández, & Muñoz-Maniega, 2015). In line with a possible vascular etiology, WMH are associated with cardiovascular risk factors such as hypertension (Abraham et al., 2015), diabetes (Brundel, Kappelle, & Biessels, 2014) and smoking (Power et al., 2015). However, WMH also occur with greater frequency in AD patients (Holland et al., 2008; Provenzano et al., 2013) compared with normal controls. Interestingly, from the point of view of AD, parenchymal WMH can also be related to cerebral amyloid angiopathy (CAA), where amyloid protein affects blood vessel function, potentially impairing the supply of oxygen and nutrients to the brain (Esiri et al., 2015; Greenberg, 2002; Holland et al., 2008; Zipfel, Han, Ford, & Lee, 2009). Studies that have investigated the link between WMH and *APOE* status have led to contradictory results (Benedictus et al., 2013; Brickman et al., 2014; Esiri et al.,

2015; Kim et al., 2013). Many of those studies, however, were hampered by a cross-sectional design.

We studied the association between *APOE*  $\epsilon 4$  status and WMH in a longitudinal framework, for a population with limited cardiovascular risk factors but heterogeneous in terms of AD diagnoses. We used a novel approach for automatic longitudinal WMH lesion segmentation, with the aim of providing greater precision to the assessment of WMH changes and thereby clarifying the relevance of *APOE*  $\epsilon 4$  in the accumulation of WMH.

## Methods

### Data selection

Data used were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database ([adni.loni.usc.edu](http://adni.loni.usc.edu)). The ADNI project was launched in 2003 as a public-private partnership, whose primary goal has been to test whether serial magnetic resonance imaging (MRI), positron emission tomography (PET), other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of mild cognitive impairment (MCI) and early AD. Information about the study can be found at [www.adni-info.org](http://www.adni-info.org). Data collection was approved by each centre's Institutional Review Board and participants gave written informed consent at time of enrolment.

At their initial visit, following clinical and neuropsychological assessment, each subject was given one of four diagnoses: normal control (NC), early mild cognitive

impairment (EMCI), late mild cognitive impairment (LMCI) or probable AD. To be included in the ADNI study, newly recruited participants had to score 4 or below on the modified Hachinski scale for cerebrovascular disease, thereby limiting the range of WMH at baseline. Furthermore, included MCI subjects had to present with an amnesic form of cognitive decline as opposed to a vascular form associated with executive dysfunction.

We selected subjects from the ADNI database using criteria based on available quality scans. Only subjects for whom at least four imaging time points with adequate FLAIR images were selected. In order to avoid introducing any preprocessing bias into the analysis, only subjects with T1 scans preprocessed with N3 histogram sharpening, and corrected for B1 bias field and gradient non linearity were used. Subjects were further excluded if they had poor quality imaging. Figure 1 presents the flowchart of data selection. According to the ADNI record of adverse events, none of the selected subjects suffered from stroke during the course of the study.

The genotyping for *APOE* was performed at screening visit using DNA extracted by Cogenix using a 3mL aliquot of EDTA blood while the level of CSF A $\beta$  is obtained using the xMAP Luminex platform and the Innogenetics/Fujirebio AlzBio3 immunoassay kits. Further details on the diagnostic procedure, scanning and imaging protocols as well as genotyping and A $\beta$  measurement can be found at <http://www.adni-info.org/scientists/ADNIStudyProcedures.aspx>.

## Image analysis

We developed a novel fully automatic multimodal lesion segmentation pipeline to jointly analyze all longitudinal imaging time points together. Instead of considering each time point independently and thereby increasing the variability in the longitudinal assessment, an average image was iteratively created. Alignment was achieved through matching intensities of normal tissue in the images in an iterative procedure involving steps of affine and non-rigid registration using jointly the two pulse sequences, the FLAIR sequence being affinely aligned to the T1 weighted image (Modat et al., 2010, 2014). Based on the results of an existing method (Sudre et al., 2015) applied to the average image, the WMH segmentation at each time point was generated. In brief, this method builds a Bayesian probabilistic data model based on an evolving Gaussian mixture model (GMM) which is able to account for observation outliers and incorporates anatomical priors and contextual information for the average appearance model. The model was then further used to constrain the segmentation at each time point. To do so, the model structure (number of Gaussian components) and its associated parameters and resultant segmentation were used to initialize the optimization of the data modelling in the original space of each time point and provide *a priori* information. Probabilistic lesion maps were obtained from the GMM based on the evaluation of outlierness when compared to the healthy WM and integrated to determine the final WMH volumes.

Figure 2 displays the flowchart of the longitudinal framework with its 3 main steps: average image building, probabilistic model selection and constraint over the individual time points.

The total intracranial volume (TIV), that included total brain volume, ventricles and CSF between the brain and meninges, was automatically obtained using a previously



described method (Cardoso et al., 2015). A single measure of TIV for each individual, generated from the average image, was used as a covariate in statistical analyses.

### **Statistical analysis**

In order to assess how our method compared to the first measurements obtained through the method detailed by De Carli et al. (De Carli, Maillard, & Fletcher, 2013) (UC Davis' method), made available on the ADNI database, we calculated Pearson's and Spearman's correlation coefficients. In addition, we assessed agreement between methods through construction of the geometric mean of the ratio of the volumes together with 95% reference ranges. Since differences in volumes may be related to lesion size we reported these ratios and corresponding reference ranges separately in low vs. high lesion volumes (bisected at the median of the mean of the two volumes).

All the statistical analyses were performed using Stata 12 v1. Due to the skewness of the WMH volumes they were log-transformed prior to analysis. Cross-sectional analysis of the baseline log-transformed WMH volumes was performed using linear regression models including age, TIV and sex as covariates in all models. Four models were fitted: these included diagnosis status (Model ASTD), genetic status (Model ASTG), genetic and diagnosis status (Model ASTGD), and genetic status and CSF A $\beta$ 42 concentration (Model ASTGA $\beta$ ) as predictor variables. F-tests were used to assess differences between groups after adjustment for covariates. Fitted group specific means, standardized to a 50/50 mixture of males and females at age 72.2 years with a TIV of 1552 mL (with 95% confidence intervals), were also computed

and back-transformed. These age and TIV values were chosen as they were the mean values across all subjects.

Longitudinal changes in WMH volume were assessed using linear mixed models, with random intercepts and slopes, for the repeated measures. Linear mixed models, provided that they are properly specified, appropriately allow for the non-independence of repeated measures from the same subject (Verbeke & Molenberghs, 2000). The dependent variable in all models was the log-transformed volume of WMH with time from initial measurement treated as both a fixed and random effect (thereby allowing slopes to differ between subjects). Other fixed effects were group terms (diagnosis and/or *APOE* status) and group-time interaction terms (thereby allowing mean rates of change to differ between groups) and age, TIV, and sex and their interactions with time. One model (Model ASTG) investigated differences in slope between the *APOE* groups, a second (Model ASTD) differences between the diagnostic groups and a third (Model ASTGD) differences according to both of these factors simultaneously. A fourth model (Model ASTGA $\beta$ ) investigated *APOE* status and CSF A $\beta$ 42 concentration as predictors of rates of WMH volume progression. Wald tests were used to compare rates of change between groups after adjustment for covariates. Fitted group specific mean rates of change (and 95% confidence intervals), standardized to a 50/50 mixture of males and females aged 72.2 with a TIV of 1552mL, were computed and back-transformed from each model.

Both cross-sectional and longitudinal analyses were also performed adding systolic blood pressure and diabetes status as additional covariates, treating these in the same way as age, sex and TIV in all models. However, since hypertension and

diabetes are associated with WMH volumes, and are likely on the causal pathway between *APOE* status and WMH levels, these results are presented in supplementary analyses. Finally, in order to understand whether length of follow-up influenced rate of WMH accumulation we added this variable as an additional covariate in all longitudinal models.

## Results

### Demographic results

The inclusion criteria led to the selection of 339 subjects that collectively had 1620 scans. The number of acquired time points per subject varied from 4 to 7 (mean 5.15 SD 1.82) and the total length of time from baseline assessment varied from 11 to 52 months (mean 24, SD 9.3). Table 1 shows the demographics of the study population by genetic status and diagnostic group. As expected, the AD subjects had lower CSF A $\beta$  42 concentrations than control subjects, with the MCI subjects having intermediate values (AD < LMCI < EMCI < NC). CSF A $\beta$  42 concentrations were lower in subjects with an *APOE*  $\epsilon$ 4 allele (44 < 42 < 43 < 33). Although age was comparable across *APOE* status, EMCI and LMCI were on average younger than NC and AD. Volumes using our method and the method from UC Davis at first available measurement were strongly associated (Pearson correlation = 0.9, Spearman = 0.95). Absolute volume differences were apparent between methods with our method typically producing smaller values than UC Davis' method. For low lesion volumes, the geometric mean of the ratio was 0.4 with a 95% reference range of 0.1 to 1.2. Analogous results for high volumes (greater than the median) were 0.6 with a 95% reference range of 0.3 to 1.1.

### Cross-sectional associations of WMH

The baseline data are summarized in Table 2. There was evidence ( $p = 0.016$ , Model ASTD) that the volume of WMH differed between the diagnosis severity groups, the difference being driven mostly by the low volumes observed in NC compared with the three other groups. Although the mean WMH volume in the AD group was slightly lower than that in the EMCI and LMCI groups, these differences were not statistically significant and the 95% confidence interval for the AD group mean was wide, reflecting the fact that this group contains the fewest subjects. Similar results were seen when the differences between the diagnostic groups were adjusted for *APOE* status ( $p$ -value from joint test of differences = 0.033, Model ASTGD).

Considering the  $A\beta_{42}$  level as a continuous marker also provided evidence of an association ( $p < 0.0005$ ) with WMH volume when adjusting for *APOE* (Model ASTGA $\beta$ ).

Across *APOE* status, an increase in WMH volume with the number of  $\epsilon 4$  alleles was observed, although this was not statistically significant when *APOE* was considered with or without adjustment for diagnostic group or  $A\beta$ . In all these models, the associations with age and TIV were significant ( $p < 0.001$ ) and the gender difference was significant for Model ASTG ( $p = 0.013$ ) such that females tended to have more WMH. There was no evidence that diabetes was related to WMH volume, but there was evidence of an association for systolic blood pressure with each 10 mmHg increase associated with a 12% (95% CI (4.8, 21.1) increase in volume. The inclusion of these factors as covariates however did not materially alter the pattern of results (see Supplemental Material).

### Models of longitudinal WMH volume change.

Table 3 summarizes the results for the longitudinal assessment of the WMH rate of change. Evolution rates are presented as standardized mean values of percentage change in volume per year, with the standardized population being a 50:50 mix of males and females having the mean value of age and TIV across all participants..

There was strong evidence ( $p=0.0002$ ) that mean rates of change differed between the *APOE* groups with the largest mean rate in the *APOE*  $\epsilon_4\epsilon_4$  group and the lowest in the *APOE*  $\epsilon_4\epsilon_2$  group. The standardized mean rate in the *APOE*  $\epsilon_4\epsilon_4$  group (22.5%/year CI [14.4, 31.2]) was significantly higher than in each of the other groups (10.0%/year [6.7, 13.4] in the  $\epsilon_4\epsilon_3$  group and 6.6%/year [4.1, 9.3] in the  $\epsilon_3\epsilon_3$  group, 2.8%/year [-2.6, 8.5] in the  $\epsilon_3\epsilon_2$  group and -3.2%/year [-14.8, 9.9] in the  $\epsilon_4\epsilon_2$  group). The rates in the  $\epsilon_4\epsilon_3$  and  $\epsilon_3\epsilon_3$  groups did not differ significantly from each other. The progression in  $\epsilon_4\epsilon_2$  group appeared lower than for the  $\epsilon_4\epsilon_3$  group, although this was not formally statistically significant ( $p=0.055$ ). Due to the very small sample size, the CI for the  $\epsilon_4\epsilon_2$  group was very large. Adjustment for either diagnostic group (Model ASTGD) or  $A\beta$  status (Model ASTGA $\beta$ ) slightly attenuated the differences between the groups without altering the overall pattern. In the latter model the dependency of the rate of change on the CSF  $A\beta$  level was just formally statistically significant ( $p < 0.041$  for interaction with time).

Rates of change also appeared to increase with diagnosis severity (AD > LMCI > EMCI > NC) ( $p=0.03$ , Model ASTD) ranging from a mean rate of 5.6%/year in the NC

to 14.8%/year for the AD. This effect was no longer significant when adjusting additionally for *APOE* status ( $p=0.18$ ). There was no evidence that diabetes or systolic blood pressure was related to rate of change and the inclusion of these factors as covariates did not materially alter the pattern of results (see Supplemental Material).

There was no evidence that the length of follow-up influenced rate of WMH accumulation ( $p\text{-value} > 0.5$ , all tests).

Figure 3 presents the evolution in WMH for two LMCI subjects with the same WMH load at baseline, one with  $\epsilon_{33}$  and the other with  $\epsilon_{44}$ . Images are shown at baseline and after 2 years.

## Discussion

This longitudinal study shows a strong association between the *APOE* status and the rate of WMH volume accumulation. We observed an increased rate of change in the homozygous  $\epsilon 4\epsilon 4$  compared to the  $\epsilon 3\epsilon 3$  and  $\epsilon 3\epsilon 4$  carriers in a cohort with relatively low vascular risk factors and WMH burden at baseline. This study included healthy control subjects, people with mild cognitive impairment and individuals with an AD diagnosis. These findings were observed independently of diagnosis, and when adjusted for CSF  $A\beta 42$  levels, although the latter adjustment did modify the effect size.

In the ADNI study, exclusion criteria were designed to limit the amount of vascular disease using a threshold of 4 on the Hachinski score. Therefore, results obtained from this sample may not necessarily generalize to the population at large. For instance, the change of 22 % per year observed for the *APOE*  $\epsilon 4\epsilon 4$  group might be less likely to occur at higher initial lesion loads (with a larger denominator). The bias towards a vascular-risk free population may further explain why no statistically significant differences at baseline were observed in our sample with respect to *APOE* status. Compared with the general population, this cohort appears enriched in subjects carrying *APOE*  $\epsilon 4$  alleles mostly in the MCI group, which may have helped in extracting relevant patterns and allowed the distinction between heterozygous  $\epsilon 4\epsilon 3$  and homozygous  $\epsilon 4\epsilon 4$ . Additionally, the differences observed in terms of study length for the LMCI and AD groups may have led to an underestimation of the observed pattern differences. In the case of the AD population an additional

selection bias might be added since subjects accumulating higher loads of WMH and AD pathology may drop out more quickly than those with few WMH; in ADs four time points may be more difficult to achieve. Despite these potential limitations, a tendency for increased WMH volume and rates of change with diagnostic severity was still observed.

Ensuring the appropriate modelling of biological processes is not trivial. A variety of different ways of modelling change in WMH are used in the literature making comparisons difficult across studies. Most studies calculate absolute changes on an untransformed scale. However, since there is evidence that WMH changes are positively related to baseline WMH volume load in both normal and dementia populations (Sachdev, Wen, Chen, & Brodaty, 2007; Schmidt, Enzinger, Ropele, Schmidt, & Fazekas, 2003) we chose to analyze changes on a log scale since they implicitly allow the magnitude of absolute change to be related to baseline level.

Our finding that different patterns of WMH evolution were related to *APOE* status is consistent with previously reported results (Godin et al., 2009) in normal aging, with a much higher rate of increase in subjects homozygous for *APOE*  $\epsilon 4$  compared with heterozygous subjects or non-carriers. The observation of no statistically significant difference in rate of change between heterozygous 43 and homozygous 33 may be taken as a possible explanation for disagreements regarding the link of *APOE*  $\epsilon 4$  and WMH evolution since in some studies the population was simply dichotomized into carriers and non-carriers (Lo & Jagust, 2012). The different strengths observed with the covariates for the 43 and 33 carriers may reflect potential differences in the pathological process between these two groups.



The association between amyloid pathology, *APOE* and WMH probably reflects the link between  $A\beta$ , *APOE*  $\epsilon 4$  and cerebral amyloid angiopathy (CAA)(Haglund & Englund, 2002; Verghese et al., 2011). Since a similar tendency was observed after adjustment for diagnostic group or  $A\beta$  level, the additional effects of *APOE* on the vasculature, independently of amyloid, are likely to account for the much faster increase in WMH for subjects homozygous  $\epsilon 4$  subjects; though amyloid has an independent effect in itself, as indicated by the significant interaction term.

Though the synergetic circle linking WMH,  $A\beta$  and amyloid deposition is widely documented (Donahue & Johanson, 2008; Gupta, Iadecola, & York, 2015; Verghese et al., 2011; Zlokovic, 2011), other explanations for the relationships between *APOE* status and WMH have been suggested. The *APOE*  $\epsilon 4$  allele has been linked with the permeability of the blood brain barrier (BBB) and with a decrease in the tight junctions of the blood vessels' endothelium (Nishitsuji, Hosono, Nakamura, Bu, & Michikawa, 2011). An increased permeability could in turn lead to neuroinflammatory processes, which may contribute to the development of WMH. The dose-dependent association with the number of  $\epsilon 4$  alleles could be linked to the hypothesis of the potential protective effect of allele  $\epsilon 3$  on the BBB with respect to neuroinflammation (Bell et al., 2012). Furthermore, *APOE*  $\epsilon 4$  has been associated with a decrease in glucose uptake, thus leading to deprived regions more vulnerable to ischemia (Alata, Ye, St-Amour, Vandal, & Calon, 2014). *APOE*  $\epsilon 4$  homozygotes have also been associated with a reduction in capillary surface (Salloway et al., 2002) in AD; this reduction would directly affect the blood supply in white matter thereby promoting the development of WMH lesions. The association of *APOE*  $\epsilon 4$  with

microbleeds (Yates et al., 2014) could be related to the exacerbated deleterious effects of vascular risk factors on WM in *APOE*  $\epsilon 4$  carriers (De Leeuw et al., 2004; Wang et al., 2015). The possible joint effects and interaction of vascular risk factors such as hypertension and *APOE*  $\epsilon 4$  on the blood vessels is therefore in need of further investigation with respect to the development of WMH.

So far, cross-sectional studies have reported contradictory findings regarding the relationship between *APOE*  $\epsilon 4$  and WMH. This is further illustrated here by the absence of evidence of a difference across genetic status at baseline while significantly different rates of change were observed. This finding strongly supports the need to better understand the time course and developmental pattern of pathological processes. Cross-sectional studies need to consider age imbalances between groups since it is well understood that increasing age has a strong association with WMH accrual (van Dijk et al., 2008). In our study, we chose to adjust for age as is done in most WMH accrual studies (Godin et al., 2009). This age adjustment explains why the AD group have larger WMH volumes than the somewhat younger late MCI group before (table 1), but not after age adjustment (table 2). Limitations of cross-sectional studies may be partially overcome by the application of longitudinal models.

One of the main strengths of this study is the use of a novel longitudinal method of WMH assessment developed for this purpose. The average image on which a generative model is built enables the reduction of measurement noise and accounts for the within-subject correlation. Accounting for such correlation instead of simply applying cross-sectional methods to serial scans for quantitative assessment has

been shown to reduce the measurement variability (Reuter, Schmansky, Rosas, & Fischl, 2012). Furthermore, the creation of an average image in a mid-space overcomes the problem of a bias towards a specific time-point (Fox, Ridgway, & Schott, 2011; Reuter & Fischl, 2011). Lastly, the use of the generative model to constrain the segmentation at each time point allows subtle changes to be measured while maintaining robustness.

This study has a number of limitations. Due to the complexity of the possible biophysiological interactions between amyloid compounds and apolipoprotein, any statistical conclusions should be treated cautiously. As such, CSF level of A $\beta$ -42 used as a surrogate disease marker for AD pathology (Andreasen et al., 1999) is also known to be related to WMH (Stenset et al., 2006). Use of CSF A $\beta$ -40 measures, more associated to vascular deposition, may be informative of the pathological process. Further work is thus needed to help disentangle WMH progression and CSF A $\beta$ -42 level changes in the pathogenesis of Alzheimer's disease. Moreover, only global WMH loads were considered here, but regional assessment of the lesion growth and differences in pattern across regions could improve our understanding of the complex relationship between *APOE*, AD and vascular pathology. Allele  $\epsilon$ 2 carriers were included in this study and results suggested a protective effect of allele  $\epsilon$ 2 but the very low prevalence of this allele makes investigation difficult. Although a similar link between the allele  $\epsilon$ 2 and WMH has been reported (Gesierich et al., 2015), the very limited number of subjects means our results should be considered very cautiously. In particular, given the 95% CI found for the 42 group (only 6 subjects), the mean negative accrual of WMH cannot be interpreted as significantly different from 0. This is mostly representative of the difficulty to represent relative changes

for very small measured volumes. Caution in the interpretation is also warranted here with respect to the  $\epsilon 4$  carriers since only 24 homozygous  $\epsilon 4$  participants were included in the study.

In conclusion, this study shows the impact of *APOE*  $\epsilon 4$  on the rate of WMH accrual over and above diagnosis of AD. Carriage of a single  $\epsilon 4$  allele with a complementary allele  $\epsilon 3$  gave a non-significant additional increase of 3% per year, whereas homozygous carriers had a significant additional increase of 16% per year compared with  $\epsilon 3$  homozygotes. *APOE*  $\epsilon 4$ , especially when in the homozygous form, is an important independent factor in the progression of WMH.

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Figure 1. Flowchart of the subject selection. Red boxes reflect the number of discarded subjects.

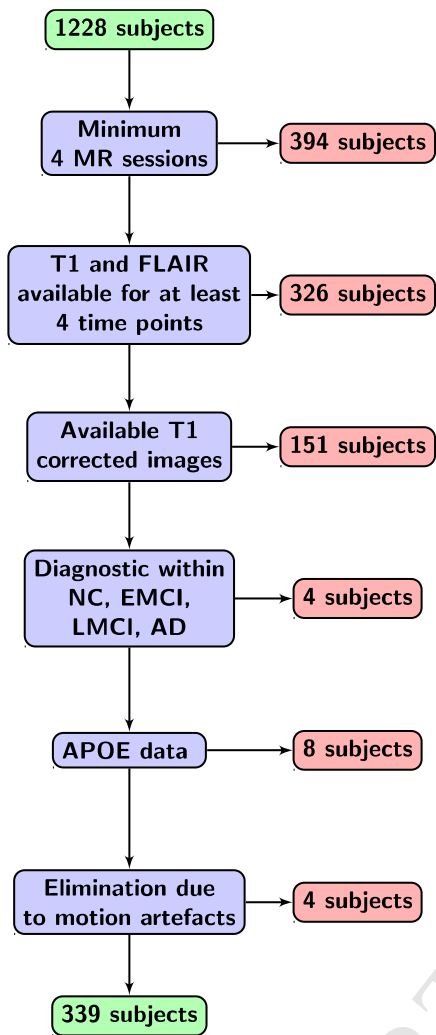


Figure 2. Flowchart of the longitudinal framework and its three main components.

The red filled boxes refer to the space of the average image while the blue boxes correspond to the set of individual time points images and the green boxes to performed actions

Table 1: Demographics findings across *APOE* and diagnostic

Criterion	Diagnostic	<i>APOE</i> status					Global
		32	33	42	43	44	
Number Total (Female)	NC	11 (6)	56 (29)	0 (0)	18 (9)	3 (3)	88 (47)
	EMCI	14 (11)	76 (39)	3 (2)	52 (31)	4 (4)	149 (87)
	LMCI	8 (3)	27 (15)	2 (0)	24 (7)	11 (6)	72 (31)
	AD	0 (0)	9 (6)	1 (1)	14 (9)	6 (5)	30 (21)
	Global	33 (20)	168 (89)	6 (3)	108 (56)	24 (18)	339 (186)
Age years mean (SD)	NC	73.3 (6.2)	74.2 (5.8)	/	73.0 (8.0)	78.1 (9.7)	74.0 (6.4)
	EMCI	68.7 (6.6)	71.6 (7.2)	75.3 (5.7)	69.7 (7.2)	68.4 (5.1)	70.7 (7.1)
	LMCI	78.4 (9.5)	71.4 (7.5)	64.3 (2)	71.4 (8.1)	70.6 (7.2)	71.9 (8.1)
	AD	/	78.8 (6.0)	71.1 (0)	74.6 (7.3)	70.1 (7.2)	74.8 (7.3)
	Global	72.6 (8.0)	72.8 (7.0)	71.0 (6.5)	71.3 (7.7)	71.1 (7.3)	72.2 (7.3)
TIV mL mean (SD)	NC	1497 (133)	1530 (169)	/	1543 (152)	1680 (46)	1534 (160)
	EMCI	1604 (167)	1564 (123)	1537 (81)	1565 (165)	1720 (45)	1572 (143)
	LMCI	1579 (148)	1553 (158)	1435 (92)	1516 (201)	1492 (127)	1531 (167)
	AD	/	1568 (178)	1510 (0)	1557 (174)	1537 (131)	1555 (159)
	Global	1562 (155)	1551 (148)	1498 (83)	1549 (171)	1565 (141)	1552 (155)
Study duration months mean (SD)	NC	25.8 (3.5)	23.1 (7.4)	/	21.9 (4.9)	25.3 (0.6)	23.3 (6.5)
	EMCI	25.1 (11.7)	26.1 (10.4)	28.3 (16.6)	27.4 (12.1)	30.8 (12.2)	26.6 (11.2)
	LMCI	22.8 (5.8)	23.9 (5.6)	25.5 (0.7)	23.4 (8.1)	19.1 (6)	22.9 (6.6)
	AD	/	14.6 (4.1)	12.0 (0)	15.8 (5.9)	20.5 (6.2)	16.2 (5.7)
	Global	24.8 (8.2)	24.1 (8.9)	24.7 (12.3)	24.1 (10.4)	22.2 (7.9)	24.0 (9.3)
$A\beta$ ng/L mean (SD;N)	NC	220 (53;10)	201 (43;53)	/	173 (42;15)	111 (42;3)	194 (48;81)
	EMCI	216 (42;10)	198 (47;73)	115 (0;1)	170 (48;50)	121 (14;3)	187 (50;137)
	LMCI	193 (43;8)	196 (45;26)	129 (51;2)	138 (33;23)	114 (31;11)	162 (51;70)
	AD	/	156 (52;9)	/	143 (41;14)	102 (10;6)	139 (45;29)
	Global	211 (46;28)	196 (46;161)	125 (37;3)	160 (45;102)	111 (26;23)	179 (52;317)
WMH mL median [IQR]	NC	0.98 [0.72 1.85]	0.99 [0.54 2.51]	/	1.38 [0.84 3.92]	2.07 [1.84 12.65]	1.10 [0.65 2.75]
	EMCI	0.77 [0.33 2.42]	1.23 [0.65 4.79]	0.40 [0.30 12.68]	1.69 [0.36 4.23]	0.9 [0.51 10.3]	1.23 [0.50 4.27]
	LMCI	5.55 [3.26 11.75]	1.70 [0.83 3.95]	1.62 [0.47 2.76]	0.97 [0.50 4.32]	2.18 [1.04 6.22]	1.78 [0.73 5.49]
	AD	/	5.56 [1.88 6.30]	1.05 [1.05 1.05]	3.05 [1.33 5.32]	0.61 [0.30 3.05]	2.66 [1.06 5.56]
	Global	1.25 [0.71 3.95]	1.32 [0.67 4.21]	0.76 [0.40 2.76]	1.63 [0.50 4.26]	1.71 [0.75 4.15]	1.36 [0.61 4.25]

Acronyms expansion: TIV - Total Intracranial Volume ; NC - NC Control ; EMCI - Early Mild Cognitive Impairment ; LMCI - Late Mild Cognitive Impairment ; AD - Alzheimer's Disease ;  $A\beta$  -  $A\beta$  CSF level; WMH - White Matter Hyperintensities ; IQR - InterQuartile Range; SD - standard deviation; N - Number .

Table 2 Baseline models: effects of covariates on differences in WMH volumes across diagnostic groups and *APOE* genotypes when adjusting for age, sex and TIV. Results are presented back-transformed to their original scale.

Values are for a standardized 50/50 mixture of males and females at age 72.2 years with a TIV of 1552 mL

	Number (A $\beta$ )	Diagnosis								
		32 33 (28)	33 168 (161)	APOE 42 6 (3)	43 108 (102)	44 24 (23)	NC 88(81)	EMCI 149 (137)	LMCI 72 (70)	AD 30 (29)
ASTG	Volume (mL)	1.54	1.44	1.42	1.69	2.12				
	CI	[1.06 2.23]	[1.22 1.70]	[0.59 3.40]	[1.37 2.07]	[1.36 3.29]				
	Overall p-value			0.5069						NA
	Pairwise			/						
ASTD	Volume (mL)						1.15	1.67	1.92	1.71
	CI						[0.92 1.44]	[1.40 2.00]	[1.49 2.46]	[1.15 2.52]
	Overall p-value			NA				0.0157		
	Pairwise							NC vs EMCI *	NC vs LMCI **	
ASTGD	Volume (mL)	1.57	1.49	1.28	1.64	1.98	1.17	1.70	1.88	1.64
	CI	[1.07 2.30]	[1.23 1.80]	[0.54 3.04]	[1.32 2.03]	[1.27 3.08]	[0.86 1.59]	[1.31 2.21]	[1.39 2.52]	[1.07 2.52]
	Overall p-value			0.7786					0.0331	
	Pairwise			/				NC vs EMCI *	NC vs LMCI **	
ASTGA $\beta$	Volume (mL)	2.09	1.58	1.08	1.50	1.49				
	CI	[1.38 3.15]	[1.33 1.89]	[0.31 3.73]	[1.21 1.87]	[0.91 2.41]				
	Overall p-value			0.6996						NA
	Pairwise			/						

Model covariates: ASTD - Age Sex TIV Diagnosis ; ASTG - Age Sex TIV Genetic status ; ASTGD - Age Sex TIV Diagnosis Genetic status ; ASTGA $\beta$  - Age Sex TIV Genetic status A $\beta$  level

Other acronyms: TIV - Total Intracranial Volume ; NA - Not applicable ; NC - Normal Control ; EMCI - Early Mild cognitive Impairment; LMCI - Late Mild Cognitive Impairment; AD - Alzheimer's Disease ; CI - Confidence Interval  
p-values: \* p<0.05 ; \*\* p<0.01



Table 3 Longitudinal models: effect of baseline predictors on differences in WMH volume change when adjusting for age, sex and TIV. Standardized percentage changes are presented along with the confidence intervals. Values are standardized to a 50/50 mixture of males and females of age 72.2 years with a TIV of 1552 mL

	Number (A $\beta$ )	APOE					Diagnosis			
		32 33 (28)	33 168 (161)	42 6 (3)	43 108 (102)	44 24 (23)	NC 88(81)	EMCI 149 (137)	LMCI 72 (70)	AD 30 (29)
ASTG	% change/year	2.80	6.64	-3.21	9.98	22.54				
	CI	[-2.58 8.47]	[4.09 9.26]	[-14.76 9.91]	[6.66 13.40]	[14.43 31.22]				
	Overall p-value			0.0002						NA
	Pairwise	32 vs 43 * ; 32 vs 44 ***; 33 vs 44 ***; 42 vs 44 **; 43 vs 44 **								
ASTD	% change/year						5.81	6.57	12.54	14.65
	CI						[2.15 9.59]	[3.86 9.36]	[8.24 17.02]	[5.97 24.03]
	Overall p-value			NA					0.0303	
	Pairwise	EMCI vs LMCI *; NC vs LMCI *								
ASTGD	% change/year	3.88	7.96	-3.21	10.76	21.69	5.25	5.92	10.80	9.76
	CI	[-1.91 10.01]	[4.65 11.36]	[-14.82 9.98]	[7.00 14.65]	[13.63 30.31]	[0.56 10.16]	[1.99 10.00]	[5.96 15.87]	[1.09 19.17]
	Overall p-value			0.0016					0.1811	
	Pairwise	32 vs 43 *; 32 vs 44 ***; 33 vs 44 ***; 42 vs 43 *; 42 vs 44 ***; 43 vs 44 *								
ASTGA $\beta$	% change/year	6.10	7.21	-10.59	9.16	20.22				
	CI	[0.24 12.32]	[4.54 9.95]	[-24.53 5.92]	[5.79 12.63]	[11.79 29.28]				
	Overall p-value			0.0061						NA
	Pairwise	32 vs 44 *; 33 vs 44 **; 42 vs 43 *; 42 vs 44 **; 43 vs 44 *								

Model covariates: ASTD - Age Sex TIV Diagnosis ; ASTG - Age Sex TIV Genetic status ; ASTDG - Age Sex TIV Diagnosis Genetic status ; ASTGA $\beta$  - Age Sex TIV Genetic status A $\beta$  level

Other acronyms: TIV - Total Intracranial Volume ; NA - Not applicable ; NC - Normal Control ; EMCI - Early Mild cognitive Impairment; LMCI - Late Mild Cognitive Impairment; AD - Alzheimer's Disease ; CI - Confidence Interval

p-values: \* p<0.05 ; \*\* p<0.01; \*\*\* p<0.001

Figure 3 Longitudinal segmentation for two LMCI subjects with *APOE* status 33 (first row) and 44 (second row) with same lesion load at baseline. For each subject the FLAIR image and the corresponding lesion segmentation (red filled) are presented for the baseline (left) and after two years (right). Note the faster rate of accumulation for the homozygous *APOE*  $\epsilon$ 4 subject (right).

Criterion	Diagnosis	APOE status					Global
		32	33	42	43	44	
Number Total (Female)	NC	11 (6)	56 (29)	0 (0)	18 (9)	3 (3)	88 (47)
	EMCI	14 (11)	76 (39)	3 (2)	52 (31)	4 (4)	149 (87)
	LMCI	8 (3)	27 (15)	2 (0)	24 (7)	11 (6)	72 (31)
	AD	0 (0)	9 (6)	1 (1)	14 (9)	6 (5)	30 (21)
	Global	33 (20)	168 (89)	6 (3)	108 (56)	24 (18)	339 (186)
Age years mean (SD)	NC	73.3 (6.2)	74.2 (5.8)	/	73 (8)	78.1 (9.7)	74 (6.4)
	EMCI	68.7 (6.6)	71.6 (7.2)	75.3 (5.7)	69.7 (7.2)	68.4 (5.1)	70.7 (7.1)
	LMCI	78.4 (9.5)	71.4 (7.5)	64.3 (2)	71.4 (8.1)	70.6 (7.2)	71.9 (8.1)
	AD	/	78.8 (6)	71.1 (0)	74.6 (7.3)	70.1 (7.2)	74.8 (7.3)
	Global	72.6 (8)	72.8 (7)	71 (6.5)	71.3 (7.7)	71.1 (7.3)	72.2 (7.3)
TIV mL mean (SD)	NC	1497 (133)	1530 (169)	/	1543 (152)	1680 (46)	1534 (160)
	EMCI	1604 (167)	1564 (123)	1537 (81)	1565 (165)	1720 (45)	1572 (143)
	LMCI	1579 (148)	1553 (158)	1435 (92)	1516 (201)	1492 (127)	1531 (167)
	AD	/	1568 (178)	1510 (0)	1557 (174)	1537 (131)	1555 (159)
	Global	1562 (155)	1551 (148)	1498 (83)	1549 (171)	1565 (141)	1552 (155)
Study duration months mean (SD)	NC	25.8 (3.5)	23.1 (7.4)	/	21.9 (4.9)	25.3 (0.6)	23.3 (6.5)
	EMCI	25.1 (11.7)	26.1 (10.4)	28.3 (16.6)	27.4 (12.1)	30.8 (12.2)	26.6 (11.2)
	LMCI	22.8 (5.8)	23.9 (5.6)	25.5 (0.7)	23.4 (8.1)	19.1 (6)	22.9 (6.6)
	AD	/	14.6 (4.1)	12 (0)	15.8 (5.9)	20.5 (6.2)	16.2 (5.7)
	Global	24.8 (8.2)	24.1 (8.9)	24.7 (12.3)	24.1 (10.4)	22.2 (7.9)	24 (9.3)
A $\beta$ ng/mL mean [SD;N]	NC	220 [53; 10]	201 [43; 53]	/	173 [42; 15]	111 [42; 3]	194 [48; 81]
	EMCI	216 [42; 10]	198 [47; 73]	115 [0; 1]	170 [48; 50]	121 [14; 3]	187 [50; 137]
	LMCI	193 [43; 8]	196 [45; 26]	129 [51; 2]	138 [33; 23]	114 [31; 11]	162 [51; 70]
	AD	/	156 [52; 9]	/	143 [41; 14]	102 [10; 6]	139 [45; 29]
	Global	211 [46; 28]	196 [46; 161]	125 [37; 3]	160 [45; 102]	111 [26; 23]	179 [52; 317]
WMH mL median [IQR]	NC	0.98 [0.72 1.85]	0.99 [0.54 2.51]	/	1.38 [0.84 3.92]	2.07 [1.84 12.65]	1.1 [0.65 2.75]
	EMCI	0.77 [0.33 2.42]	1.23 [0.65 4.79]	0.4 [0.3 12.68]	1.69 [0.36 4.23]	0.9 [0.51 10.30]	1.23 [0.50 4.27]
	LMCI	5.55 [3.26 11.75]	1.7 [0.83 3.95]	1.62 [0.47 2.76]	0.97 [0.50 4.32]	2.18 [1.04 6.22]	1.78 [0.73 5.49]
	AD	/	5.56 [1.88 6.30]	1.05 [1.05 1.05]	3.05 [1.33 5.32]	0.61 [0.30 3.05]	2.66 [1.06 5.56]
	Global	1.25 [0.71 3.95]	1.32 [0.67 4.21]	0.76 [0.4 2.76]	1.63 [0.50 4.26]	1.71 [0.75 4.15]	1.36 [0.61 4.25]

Acronyms expansion: TIV – Total Intracranial Volume; NC – Normal Controls; EMCI – Early Mild Cognitive Impairment; LMCI – Late Mild Cognitive Impairment; AD – Alzheimer’s Disease; A $\beta$  - A $\beta$  CSF level; WMH – White Matter Hyperintensity; IQR – InterQuartile Range; SD – Standard Deviation; N - Number

	Number (A $\beta$ )	APOE					Diagnosis			
		32	33	42	43	44	Normal	EMCI	LMCI	AD
		33 (28)	168 (161)	6 (3)	108 (102)	24 (23)	88 (81)	149 (137)	72 (70)	30 (29)
<b>ASTG</b>	Mean	1.54	1.44	1.42	1.69	2.12				
	CI	[1.06 2.23]	[1.22 1.70]	[0.59 3.40]	[1.37 2.07]	[1.36 3.29]				
	Overall p-value			0.5069					NA	
	Pairwise			/						
<b>ASTD</b>	Mean						1.15	1.67	1.92	1.71
	CI						[0.92 1.44]	[1.4 2]	[1.49 2.46]	[1.15 2.52]
	Overall p-value			NA				0.0157		
	Pairwise								EMCI vs Normal *; LMCI vs Normal **	
<b>ASTGD</b>	Mean	1.57	1.49	1.28	1.64	1.98	1.17	1.7	1.88	1.64
	CI	[1.07 2.3]	[1.23 1.80]	[0.54 3.04]	[1.32 2.03]	[1.27 3.08]	[0.86 1.59]	[1.31 2.21]	[1.39 2.52]	[1.07 2.52]
	Overall p-value			0.7786					0.0331	
	Pairwise			/					EMCI vs Normal *; LMCI vs Normal **	
<b>ASTGA<math>\beta</math></b>	Mean	2.09	1.58	1.08	1.50	1.49				
	CI	[1.38 3.15]	[1.33 1.89]	[0.31 3.73]	[1.21 1.87]	[0.91 2.41]				
	Overall p-value			0.6996					NA	
	Pairwise			/						

Model covariates: ASTD – Age Sex TIV Diagnosis; ASTG – Age Sex TIV Genetic status; ASTGD – Age Sex TIV Diagnosis Genetic status; ASTGA $\beta$  - Age Sex TIV Genetic status A $\beta$  level

Other acronyms: TIV – Total Intracranial Volume; NA – Not applicable; NC – Normal Control; EMCI – Early Mild Cognitive Impairment; LMCI – Late Mild Cognitive Impairment; AD – Alzheimer's Disease; CI – Confidence Interval

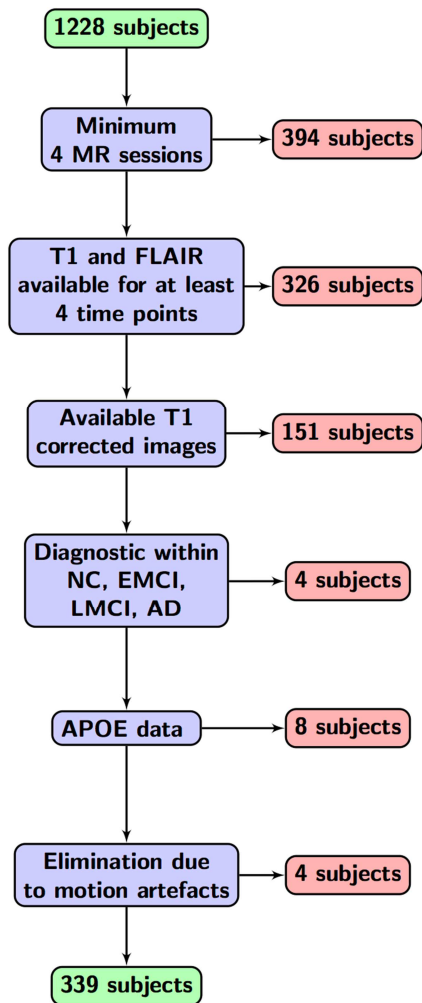
p-values: \* p<0.05; \*\* p<0.01

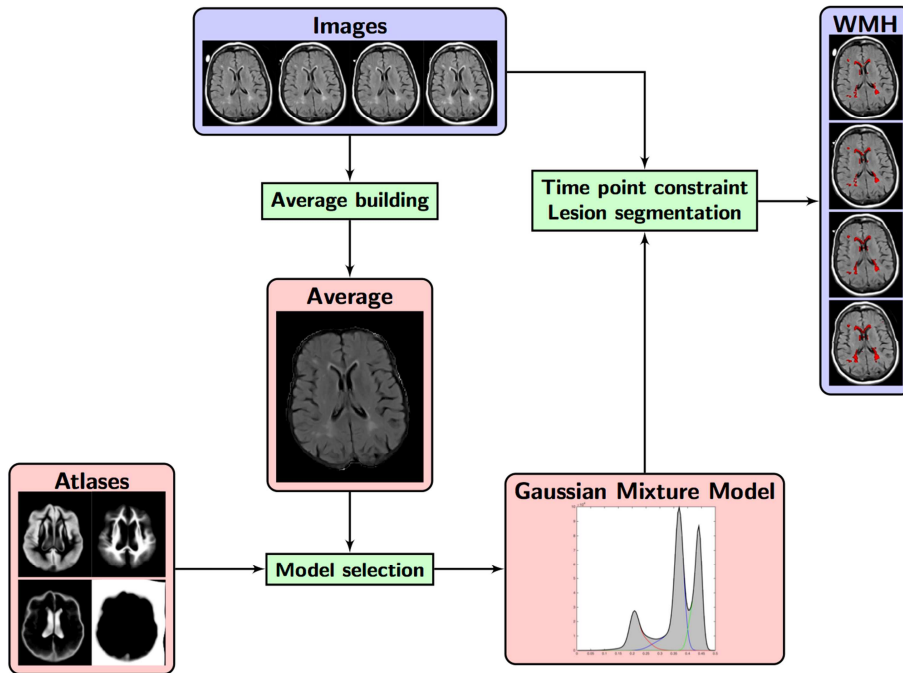
		APOE					Diagnosis			
		32	33	42	43	44	Normal	EMCI	LMCI	AD
<b>Number (A<math>\beta</math>)</b>		33 (28)	168 (161)	6 (3)	108 (102)	24 (23)	88 (81)	149 (137)	72 (70)	30 (29)
<b>ASTG</b>	% change/year	2.80	6.64	-3.21	9.98	22.54				
	CI	[-2.58 8.47]	[4.09 9.26]	[-14.76 9.91]	[6.66 13.40]	[14.43 31.22]				NA
	Overall p-value	0.0002								
	Pairwise	32 vs 43 *; 32 vs 44 ***; 33 vs 44 ***; 42 vs 44 **; 43 vs 44 **								
<b>ASTD</b>	% change/year						5.81	6.57	12.54	14.65
	CI						[2.15 9.59]	[3.86 9.36]	[8.24 17.02]	[5.97 24.03]
	Overall p-value	NA								
	Pairwise	EMCI vs LMCI *; Normal vs LMCI *								
<b>ASTGD</b>	% change/year	3.88	7.96	-3.21	10.76	21.69	5.25	5.92	10.80	9.76
	CI	[-1.91 10.01]	[4.65 11.36]	[-14.82 9.98]	[7.00 14.65]	[13.63 30.31]	[0.56 10.16]	[1.99 10.00]	[5.96 15.87]	[1.09 19.17]
	Overall p-value	0.0016								
	Pairwise	32 vs 43 *; 32 vs 44 ***; 33 vs 44 **; 42 vs 43 *; 42 vs 44 **; 43 vs 44 *								
<b>ASTGA<math>\beta</math></b>	% change/year	6.10	7.21	-10.59	9.16	20.22				
	CI	[0.24 12.32]	[4.54 9.95]	[-24.53 5.92]	[5.79 12.63]	[11.79 29.28]				NA
	Overall p-value	0.0061								
	Pairwise	32 vs 44 *; 33 vs 44 **; 42 vs 43 *; 42 vs 44 **; 43 vs 44 *								

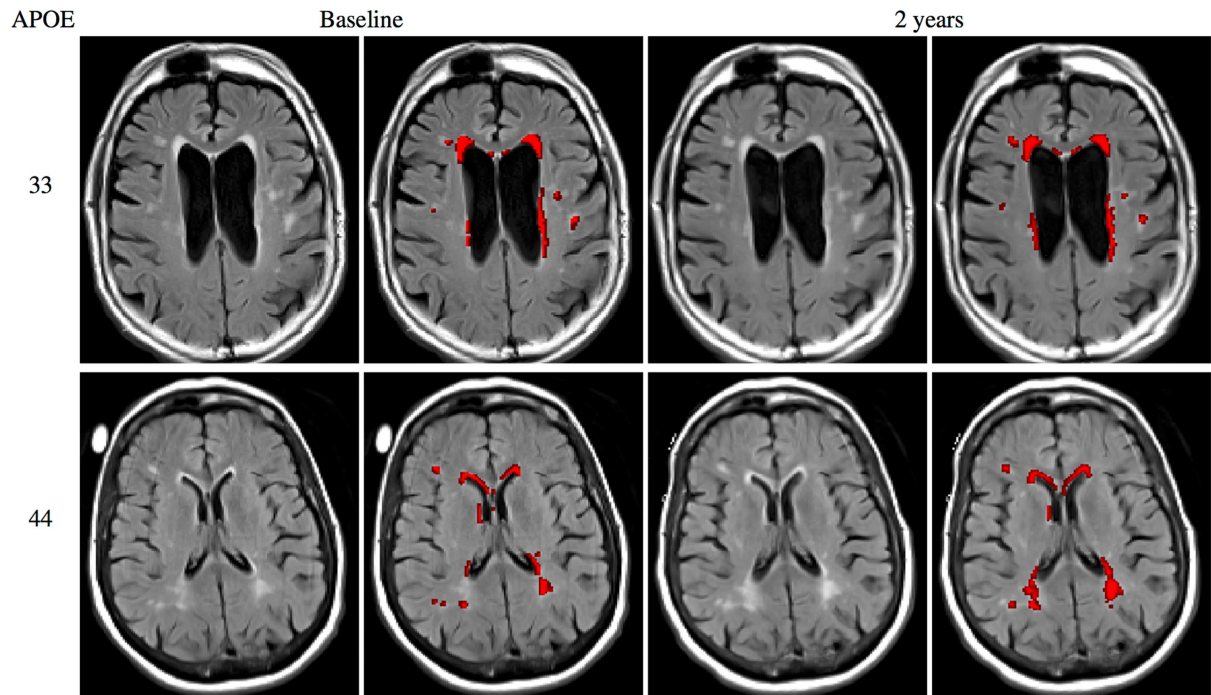
Model covariates: ASTD – Age Sex TIV Diagnosis; ASTG – Age Sex TIV Genetic status; ASTGD – Age Sex TIV Diagnosis Genetic status; ASTGA $\beta$  - Age Sex TIV Genetic status A $\beta$  level

Other acronyms: TIV – Total Intracranial Volume; NA – Not applicable; NC – Normal Control; EMCI – Early Mild Cognitive Impairment; LMCI – Late Mild Cognitive Impairment; AD – Alzheimer's Disease; CI – Confidence Interval

p-values: \* p<0.05; \*\* p<0.01; \*\*\* p<0.001









## Highlights NBA

- Longitudinal automated lesion segmentation applied to ADNI cohort
- Stronger rate of increase of WMH in homozygous APOE  $\epsilon 4\epsilon 4$  than other groups
- APOE  $\epsilon 4$  effect on white matter lesion independent of diagnosis

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