Stan Code Used to Run Analyses

```
data {
	int<lower=0> N;				#Number of data points
	int<lower=1> P;				#Number of fixed effects
	int<lower=0> J;				#Number of subjects
	int<lower=1,upper=J> subj[N];		#Subject indicator
	int<lower=1> K;				#Number of regions
	int<lower=1> n_u;			#Number of subject random effects
	int<lower=1> n_corr;			#Dimension of random effects correlation matrix
	vector[K] y[N];				#Response variables
	vector[P] X[N];				#Fixed effects design matrix
	vector[n_u] Z_u[N];			#Subject random effects design matrix
}

parameters {
	matrix[K, P] beta;				#Fixed effect coefficients
	cholesky_factor_corr[n_corr] L_u;		#Cholesky factor for subject random effects
	vector<lower=0>[n_corr] sigma_u;		#Subject random effects standard deviation
	vector<lower=0,upper=1>[K] sigma_e;		#Residual standard deviation
	matrix[n_corr, J] z_u;				#Spherical subject random effects
}

transformed parameters {
	matrix[K,n_u] u[J];		#Subject random effect coefficients
	{
		matrix[n_corr,n_corr] Sigma_u;	#Subject random effects covariance matrix
		matrix[n_corr,J] u_mat;
		Sigma_u = diag_pre_multiply(sigma_u,L_u);
		u_mat = Sigma_u * z_u;
		for (i in 1:J)
			u[i] = append_col(u_mat[1:K,i],u_mat[(1+K):n_corr,i]);
	}
}

model {
	vector[K] mu[N];
	L_u ~ lkj_corr_cholesky(1.0);
	to_vector(beta) ~ normal(0,5);
	to_vector(z_u) ~ normal(0,1);
	for (i in 1:N)
		mu[i] <- beta*X[i] + u[subj[i]]*Z_u[i];
	y ~ multi_normal(mu,diag_matrix(sigma_e .* sigma_e));
}
```

Online Interactive Models

An interactive tool created with the R package Shiny[15] is hosted online at https://briangordon.shinyapps.io/apoe4/ This application provides a more in-depth depiction of the statistical models and results than is possible in the main manuscript. The online application makes it possible to see the model estimates for each modality in every single brain region. By default the credible intervals are set at 99%, but the slider allows for an adjustment and recalculation of the credible intervals on the displayed panels down to 90%. Other options include varying the minimum number of visits a displayed subject has, displaying subject level credible intervals, and displaying the subjects' raw data. Note altering the minimum number of visits only impacts the display and does not generate a recalculation of the models.

Supplemental Table 1:

Comparison of Demographics between E4 and Non-E4 groups with Longitudinal MRI

	ε4+ (ε34 or ε44)	**ε4- (ε22, ε23, or ε33)**	**Significance Test**
(N)umber of participants	150	332	
Age (sd)	65.5 (9.9)	67.2 (10.0)	$F_{1,480}$=3.02, p=0.08
Gender, N male (%)	56 (37.3%)	129 (38.9%)	X^2=0.05, p=0.8
Education (sd)	15.7 (2.5)	15.9 (2.5)	$F_{1,457}$=0.43, p=0.51
MMSE (sd)	29.1 (1.3)	29.1 (1.0)	$F_{1,480}$=0.10, p=0.75
CDR Sum of Boxes (sd)	0.02 (0.09)	0.02 (0.10)	$F_{1,480}$=0.36, p=0.55
# of scans, mean (sd)	3.0 (1.2)	3.1 (1.3)	$F_{1,480}$=0.83, p=0.36
Years of follow-up (sd)	5.4 (3.1)	5.6 (3.1)	$F_{1,480}$=0.33, p=0.56

MMSE=Mini-Mental State Examination CDR=Clinical Dementia Rating
[+]Education values were not available for 23 individuals

Does effects of APOE ε4 genotype.

Linear mixed effects models were run modelling heterozygous (ε4 and ε3) and homozygotes (ε4 ε4) as separate groups. To be as focused as possible analyses were run only for PIB measurements in the precuneus and hippocampal volume. We found that the homozygotes did accumulate Aβ faster than heterozygotes and noncarriers. Similarly, APOE ε4 homozygotes had greater rates of structural atrophy than heterozygotes and noncarriers. Due to the restricted number of homozygotes with longitudinal PIB (n=11) and MRI (n=23), the credible intervals around model estimates were quite large at the older range of our distribution.