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Predicting Alzheimer's Disease Using Combined Imaging-Whole Genome SNP Data

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Abstract

The growing public threat of Alzheimer's disease (AD) has raised the urgency to discover and validate prognostic biomarkers in order to predicting time to onset of AD. It is anticipated that both whole genome single nucleotide polymorphism (SNP) data and high dimensional whole brain imaging data offer predictive values to identify subjects at risk for progressing to AD. The aim of this paper is to test whether both whole genome SNP data and whole brain imaging data offer predictive values to identify subjects at risk for progressing to AD. In 343 subjects with mild cognitive impairment (MCI) enrolled in the Alzheimer's Disease Neuroimaging Initiative (ADNI-1), we extracted high dimensional MR imaging (volumetric data on 93 brain regions plus a surface fluid registration based hippocampal subregion and surface data), and whole genome data (504,095 SNPs from GWAS), as well as routine neurocognitive and clinical data at baseline. MCI patients were then followed over 48 months, with 150 participants progressing to AD. Combining

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information from whole brain MR imaging and whole genome data was substantially superior to the standard model for predicting time to onset of AD in a 48-month national study of subjects at risk. Our findings demonstrate the promise of combined imaging-whole genome prognostic markers in people with mild memory impairment.

Keywords

Alzheimer's disease; genetics; magnetic resonance imaging; proportional hazards models; risk

INTRODUCTION

The growing public threat of Alzheimer's disease (AD) has raised the urgency to discover and validate prognostic biomarkers that may identify subjects at greatest risk for future cognitive decline and accelerate the testing of preventive strategies [1, 2]. In this regard, studies of combinatorial biomarkers may have greater ability to capture the heterogeneity and multifactorial complexity of AD, than a traditional single biomarker study [3].

Prior studies of subjects at risk for AD have examined the utility of various individual biomarkers, such as cognitive tests, fluid markers, imaging measures, and some individual genetic markers (e.g., ApoE4) [1]. In particular, imaging markers such as hippocampal volume and shape, cortical regional volumes and thickness, and positron emission tomography (PET) (amyloid imaging, FDG) abnormalities have all been linked in one or more studies to faster progression in at risk subjects [4–16], but are not yet optimally predictive at an individual level.

More recently, genome-wide association study (GWAS) data has been used to characterize several potential genetic risk factors for AD with several cross-sectional studies also correlating these data with imaging and fluid biomarkers [17]. There are also some studies combining imaging and genetics information to predict the conversion of MCI to AD [18, 19], however, they only consider the conversion of MCI to AD as a binary response, and they do not investigate the risk of progression to AD for each specific MCI individual. To our knowledge, no prior study has leveraged both GWAS SNP data, as well as high dimensional whole brain imaging data to examine their combined value in identifying subjects at greatest risk for progressing to AD.

METHODS

Alzheimer's Disease Neuroimaging Initiative

Data used in the preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (http://www.loni.usc.edu/ADNI). The ADNI was launched in 2003 by the National Institute on Aging (NIA), the National Institute of Biomedical Imaging and Bioengineering (NIBIB), the Food and Drug Administration (FDA), private pharmaceutical companies, and non-profit organizations, as a $60 million, 5-year public private partnership. The primary goal of ADNI has been to test whether serial magnetic resonance imaging (MRI), PET, other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of mild

cognitive impairment (aMCI) and early AD. Determination of sensitive and specific markers of very early AD progression is intended to aid researchers and clinicians to develop new treatments and monitor their effectiveness, as well as lessen the time and cost of clinical trials. The Principal Investigator of this initiative is Michael W. Weiner, M.D., VA Medical Center and University of California - San Francisco. ADNI is the result of efforts of many co-investigators from a broad range of academic institutions and private corporations, and subjects have been recruited from over 50 sites across the U.S. and Canada. The initial goal of ADNI was to recruit 800 adults, ages 55 to 90, to participate in the research—approximately 200 cognitively normal older individuals to be followed for 3 years, 400 people with aMCI to be followed for 3 years, and 200 people with early AD to be followed for 2 years. For up-to-date information, see http://www.adni-info.org.

Study sample

We considered 343 subjects with mild cognitive impairment (MCI) enrolled in the Alzheimer's Disease Neuroimaging Initiative (ADNI-1). These MCI patients were then followed over 48 months, with 150 participants progressing to AD (Table 1). MCI converters did not differ from MCI noncoverters in gender, handedness, marital status, retirement percentage, and age (p-values>0.05), but as expected, differed from them in APOE4 status as well as baseline cognition ($p<0.05$) (Table 1). Mean follow up time was 75 days longer in converters ($p=0.06$). From them, we extracted high dimensional MR imaging and whole genome data, as well as routine neurocognitive and clinical data at baseline.

MRI imaging

These scans on 343 subjects were performed on a 1.5 T MRI scanners by using a sagittal MPRAGE sequence with the following parameters: repetition time (TR) = 2400 ms, inversion time (TI) = 1000 ms, flip angle = 8°, and field of view (FOV) = 24 cm with a 256 x 256 x 170 acquisition matrix in the x-, y-, and z-dimensions, which yields a voxel size of 1.25 x 1.261 x 2.

We processed the MRI data by using standard steps including anterior commissure and posterior commissure correction, skull-stripping, cerebellum removing, intensity inhomogeneity correction, segmentation, and registration [20]. After segmentation, we segmented the brain data into four different tissues: grey matter, white matter, and cerebrospinal fluid. Moreover, we automatically labeled 93 regions of interest (ROIs) on the Jacob atlas [21], and transferred the labels following the deformable registration of subject images [22]. In addition, we chose 23 ROIs, which may significantly influence MCI progression from the existing literature [10, 23, 24]. The 23 ROIs were bilateral entorhinal cortices, bilateral hippocampal formation, bilateral amygdala, bilateral caudate nuclei, bilateral putamen, bilateral posterior limb of internal capsule including cerebral peduncle, bilateral nucleus accumbens, bilateral lateral ventricles, bilateral thalamus, bilateral fornix, bilateral cingulate, and the corpus callosum.

Hippocampus image preprocessing

We adopted a surface fluid registration based hippocampal subregional analysis package [25], which uses isothermal coordinates and fluid registration to generate one-to-one

hippocampal surface registration for following surface statistics computation. This software package has been adopted by various studies [22, 26–30].

Given the 3D MRI scans, hippocampal substructures were segmented with FIRST [31] and hippocampal surfaces were automatically reconstructed with the marching cube method [32]. We applied an automatic algorithm, topology optimization, to introduce two cuts on a hippocampal surface to convert it into a genus zero surface with two open boundaries. The locations of the two cuts were at the front and back of the hippocampal surface, representing its anterior junction with the amygdala, and its posterior limit as it turns into the white matter of the fornix. Then holomorphic 1-form basis functions were computed [33]. These induced conformal grids the hippocampal surfaces, which were consistent across subjects. With this conformal grid, we computed the conformal representation of the surface [25], i.e., the conformal factor and mean curvature, which represent the intrinsic and extrinsic features of the surface, respectively. The “feature image” of a surface was computed by combining the conformal factor and mean curvature and linearly scaling the dynamic range into [0, 255]. Next, we registered the feature image of each surface in the dataset to a common template with an inverse consistent fluid registration algorithm [26]. With conformal parameterization, we essentially converted a 3D surface registration problem into a 2D image registration problem. The flow induced in the parameter domain establishes high-order correspondences between 3D surfaces. Finally, various surface statistics were computed on the registered surface, such as multivariate tensor-based morphometry statistics [33], which retain the full tensor information of the deformation Jacobian matrix, together with the radial distance [34], which retains information on the deformation along the surface normal direction.

SNP data

The subjects’ genotype variables were acquired based on the Human 610-Quad Bead-Chip (Illumina, Inc., San Diego, CA) in the ADNI database, which resulted in 620,901 SNPs. To reduce the population stratification effect, we used 749 Caucasians from all 818 subjects with complete imaging measurements at baseline. Quality control procedures included (i) call rate check per subject and per SNP marker, (ii) gender check, (iii) sibling pair identification, (iv) the Hardy-Weinberg equilibrium test, (v) marker removal by the minor allele frequency, and (vi) population stratification. The second line preprocessing steps include removal of SNPs with (a) more than 5% missing values, (b) minor allele frequency smaller than 5%, and (c) Hardy-Weinberg equilibrium p-value < 1e–6. Remaining missing genotype variables were imputed as the modal value. 747 subjects and 504,095 SNPs remained.

We included information from all the 22 chromosomes. Since each chromosome contains a number of SNPs, we used principal component analysis for each chromosome and picked the first two principal components for each chromosome. We then used the PLINK package (https://pngu.mgh.harvard.edu/~purcell/plink/data.shtml#plink) to perform quality control for the genomic data. The principal component analysis for each chromosome was conducted using ‘svd’ function in R software.

Statistical analyses

A popular model used in literature is the Cox proportional hazards model, which accounts for other covariates that are associated with the timing of the events. Covariates of interest include demographic information (8 covariates), the APOE4 genotype (3 covariates), the Alzheimer's Disease Assessment Scale-cognitive subscale (ADAS-Cog) score (1 covariate), the hippocampus surface data (7 covariates for each curve, total 14 covariates), the ROI volume data (23 covariates), the chromosomewise information (2 covariates for each chromosome, total 44 covariates), and the significant SNPs information (5 covariates). We used the R function "coxph" to implement the fitting of the Cox proportional hazards model. We fitted a Cox regression model with demographic, clinical, and cognitive (ADAS-Cog score) predictors as well as APOE, referred to as the Clinical-Cognitive model (Model 1), and obtained its estimation and testing results. This model did not include any other imaging and genetic data. We fitted a second Cox regression model with demographic, imaging, and chromosome-wise predictors, but without the ADAS-Cog score and significant SNPs information, referred to as the Imaging-Genetics model (Model 2), and obtained its estimation and testing results.

As a comparison, we also used the results obtained from GWAS to incorporate the genetic information. Specifically, we selected the top 101 significant SNPs by using a kernel machine method [35], and then calculated their top 5 PCs and used them as predictors (significant SNP information). We fitted a third Cox regression model with demographic, imaging, and significant SNP information, but without the ADAS-Cog score and chromosome-wise information, and then obtained parameter estimation and testing results. We referred this model to as the Traditional Imaging-Genetics Model (Model 3).

When we fitted Cox regression models, we treated the left and right hippocampus surface data as functional predictors. For each subject, the radial distance was obtained from baseline hippocampal surfaces data, which yields two 15,000 dimensional vectors denoting data from left hippocampus and right hippocampus, respectively. We applied functional principal component analysis (FPCA) [36, 37]. We selected 7 functional principal component (FPC) scores for each functional predictor, which explain approximately 70% of the variance. For implementation of FPCA, we use the 'svd' function in R software.

We used FPCA to extract the first 7 FPCs of each of the left and right hippocampus surface data and the first 2 FPCs of the SNP data along each chromosome, then used these as basis functions to represent the regression coefficient functions associated with the hippocampus surface and SNP on all chromosomes in the Cox regression. As an illustration, we plotted the first FPCs for both left and right hippocampi in Figure 1.

Since we do not have the validation data set, we investigated the predictive performance of the candidate models using the receiving operating characteristic (ROC) curve. In particular, we calculated the area under the curve (AUC), which is often used to measure the prediction of survival models. In particular, we first randomly picked 200 subjects for the training data and fit all the candidate models. After that, we used the remaining 143 individuals for the testing and calculated the AUC [38]. The method can be implemented by using the R function "AUC.cd". We repeated the above steps for 100 times, i.e., randomly separated the

data for 100 times and obtained 100 AUCs. The mean and standard deviations can be obtained using these 100 AUCs.

RESULTS

We compared the predictive value of standard of care (clinical demographic variables, APOE4, the ADAS-Cog score, Model 1) versus imaging-genetic markers (MRI volumes and surface data plus GWAS SNP and demographics, Model 2). We have obtained the first five principal components of the 101 top SNPs obtained from GWAS and added it into our Model 2 (call it Model 3). We have compared our Model 2 versus Model 3 as well.

ROC analysis revealed that Model 1 (combining just routine clinical demographics and cognitive data with a single genotype APOE4) had a low predictive value at 48 months (AUC 0.75) (Figure 2, Supplementary Table 1, Supplementary Figure 3). In this model, APOE4 and ADAS-Cog were the significant predictors. In contrast, Model 2 (combining full genetic SNP and high dimension imaging data with demographics but without any cognitive data) had a much higher predictive value (AUC 0.95) (Figure 2, Supplementary Table 2, Supplementary Figure 3). SNPS on chromosome 2, 10, 11, 15, 17, and 18 (Supplementary Figure 2), APOE4 status, surface morphology data of both hippocampi (especially anterior regions, Figure 1, Supplementary Figure 1) and volumes of hippocampus, amygdala, and thalamus contributed significantly. The 100-fold cross validation using a test and training data set revealed AUC of 0.95 (±0.014) for the imaging-genetic model and 0.75 (±0.024) for the clinical-cognitive model. For the Traditional Imaging-Genetics model, we can only obtain a predictive value (AUC 0.90) (Figure 2, Supplementary Table 3, Supplementary Figure 3), which indicates the advantages of using the chromosome-wise information instead of the traditional significant SNPs information. The reason may be due to the pitfalls of prediction using significant SNPs [40]. Meanwhile, we have found that combining all variables (cognitive data plus imaging-genetic data) showed high predictive accuracy (AUC 0.96) but was not different from the value provided by imaging-genetics data alone. Besides, combining the significant SNPs information with all the predictors in our Imaging Genetics Model achieved slightly higher predictive accuracy (AUC 0.97), but was not different from the value provided by Imaging-Genetic Model alone.

From the estimation results of our imaging-genetics model, we have found that divorced individuals, older people, individuals with 2nd allele of APOE4 genotype 3 may have smaller hazard function. The individuals with larger ROI volumes in hippocampal left, amygdala right, and thalamus left may have smaller hazard function, while the individuals with larger ROI volumes in hippocampal right, amygdala left, posterior limb of internal capsule, and thalamus right may have larger hazard function.

DISCUSSION

These findings are the first demonstration, to our knowledge, of the value of combined whole brain MR and whole genome SNP data in the 48-month prognosis of subjects at risk for AD. Our finding support prior MRI studies of volumetric hippocampal changes in

prodromal AD [8, 39] and extend them by finding that the possible prognostic value of combining information from high dimensional imaging and genetics may be superior to that provided by routine clinical-cognitive testing data.

Our findings also confirm the association between APOE4 status and AD, and identify additional new markers on chromosomes 2, 10, 11, 15, 17, and 18 as having significant effects on conversion. A variety of genes have been identified in prior GWAS studies as potential risk factors for AD such as clusterin (chromosome 8), complement receptor 1 (chromosome 1), phosphatidylinositol binding clathrin assembly protein (chromosome 11), sortilin-related receptor (chromosome 11), triggering receptor expressed on myeloid cells 2 (chromosome 6), and cluster of differentiation 33 (chromosome 19) as well as TOMM40 (chromosome 19) [41]. Our study did not examine any of these newer gene markers specifically but provides support to the notion that there is additional genetic heritability in late-onset AD beyond that accounted for by APOE.

There are some strengths and limitations to our analyses. ADNI is a national biomarker study that utilized rigorous standardized data collection procedures, and well established criteria to select MCI subjects. Rather than using the individual data on all SNPs, we used the more conservative statistical method of doing principal component analysis for each chromosome and picking the first two principal components for each chromosome. Our findings survived internal cross validation but need replication in an independent community based sample. We did not include measures of pathology (e.g., amyloid-β) in our models since cerebrospinal fluid and amyloid-PET were available only in a small subset of individuals in ADNI-1. However, a study of ADNI-2 subjects has shown a robust correlation between the APOE ε4 allele and cortical amyloid burden [42], suggesting that APOE ε4 may have served as a surrogate for cortical amyloid plaque load in our analysis. It is important to confirm the above findings obtained from ADNI-1 in other independent data sets [40].

Prior investigations of prediction of MCI-AD to AD have utilized feature selection to assess the most important biomarkers of prediction of conversion. Here, we have demonstrated the utility of Cox hazard models as a valuable method for identifying the “optimal combination” of early markers of conversion to AD in patients with MCI. If replicated in independent cohorts, such combinatorial markers of early AD could be useful for selecting at risk individuals for prevention trials and for discovering novel targets for discovering disease modifying therapies.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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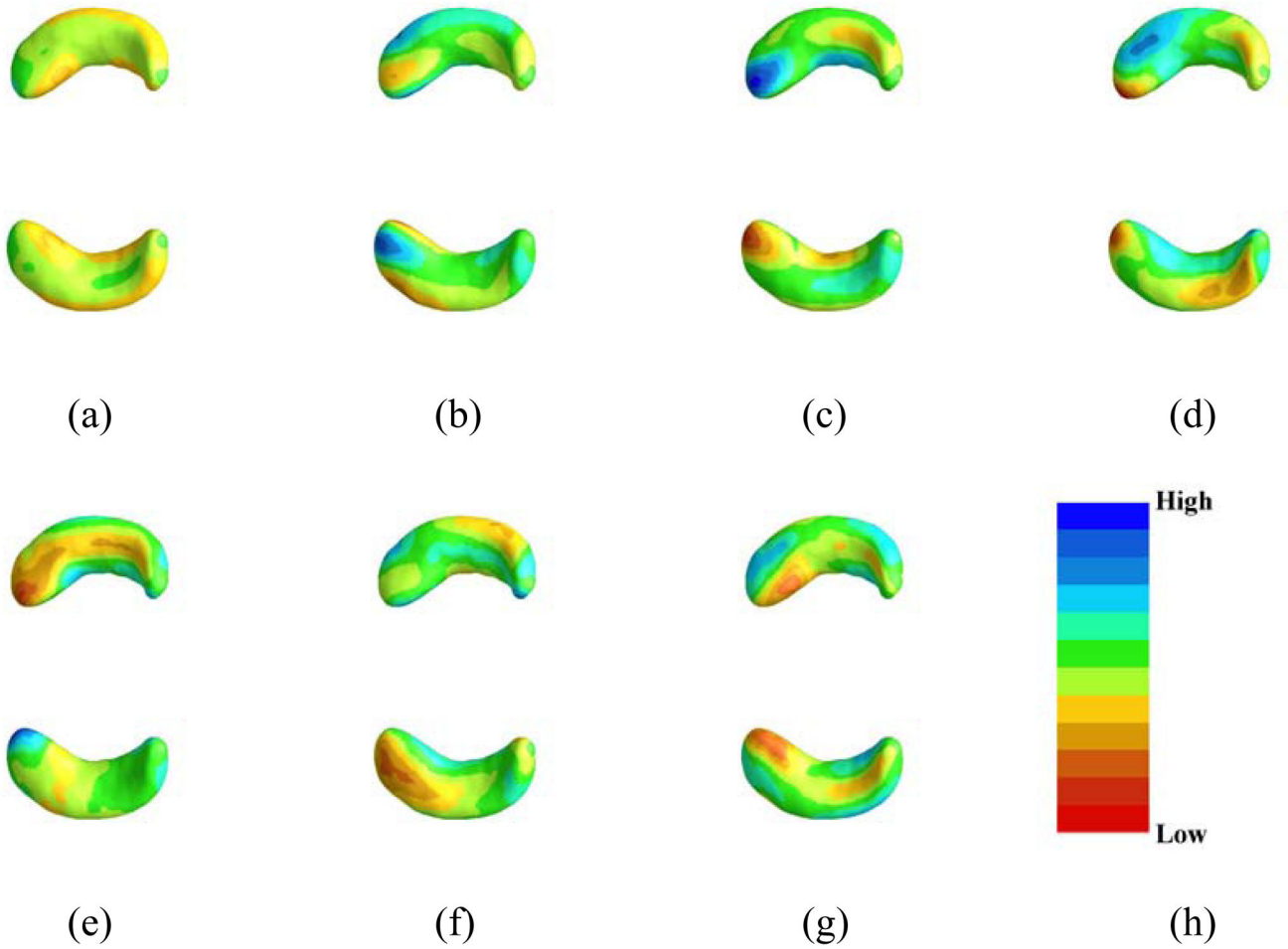

Figure 1.

Estimated coefficient functions associated with the hippocampus surface data. Panel (a)-(g) are the estimates of the first seven functional principal components corresponding to the sorted seven eigenvalues, in which (a) corresponds the largest eigenvalue and (h) is the color bar with 11 lines representing 11 equally spaced points between [−0.0462, 0.0421].

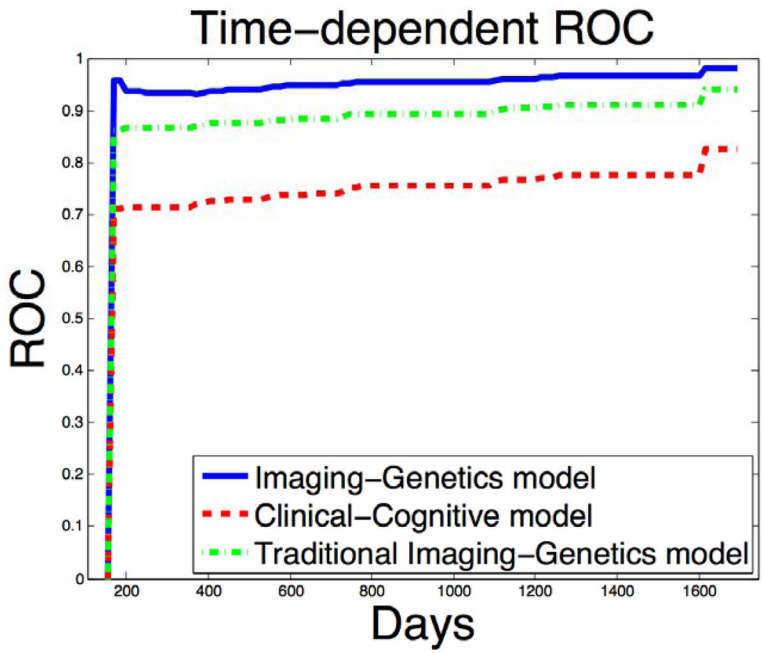

Figure 2.

The ROC curves comparison for the imaging plus genetics model versus the cognitive model plotted using one pair of training and testing data set. The blue solid line denotes the ROC curve for the image-genetics model and the red dash line denotes the ROC curve for clinical-cognitive model.

Table 1

Study sample: comparison of converters and nonconverters.

Sample Size	MCI converters n=150	MCI nonconverters n=193	Test statistics
Mean Age (in years)	74.7 (7.0)	75.1 (7.5)	T test: p=0.69
Gender (Male percentage)	60.0%	66.8%	Chi-square test: p=0.23
Handedness (Right hand percentage)	92.0%	90.7%	Chi-square test: p=0.81
Marital Status (Widowed percentage)	10.7%	11.9%	Chi-square test: p=0.95
Marital Status (Divorced percentage)	4.7%	6.2%	
Marital Status (Never Married percentage)	1.3%	1.0%	
Mean Education Length (in years)	15.6 (2.9)	15.8 (3.0)	T test: p=0.52
Retirement percentage	80.0%	79.3%	Chi-square test: p=0.98
APOE 4 carriers (%): APOE4 first allele (genotype 3 %)	78.7%	81.4%	Chi-square test: p=0.02
APOE4 first allele (genotype 4 %)	17.3%	9.3%	
APOE4 second allele (genotype 4 %)	30.0%	56.0%	Chi-square test: p<0.0001
Mean ADAS-Cog 11 Score	13.2 (4.0)	10.2 (4.3)	T test: p<0.0001
Mean Duration of Follow up (in days)	1009.9	934.4	T test: p=0.06

MCI, mild cognitive impairment; ADAS-Cog, Alzheimer's Disease Assessment Scale-cognitive subscale