

Improved Prediction of Imminent Progression to Clinically Significant Memory Decline Using Surface Multivariate Morphometry Statistics and Sparse Coding

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Abstract.

Background: Besides their other roles, brain imaging and other biomarkers of Alzheimer's disease (AD) have the potential to inform a cognitively unimpaired (CU) person's likelihood of progression to mild cognitive impairment (MCI) and benefit subject selection when evaluating promising prevention therapies. We previously described that among baseline FDG-PET and MRI measures known to be preferentially affected in the preclinical and clinical stages of AD, hippocampal volume was the best predictor of incident MCI within 2 years (79% sensitivity/78% specificity), using standard automated MRI volumetric algorithmic programs, binary logistic regression, and leave-one-out procedures.

Objective: To improve the same prediction by using different hippocampal features and machine learning methods, cross-validated via two independent and prospective cohorts (Arizona and ADNI).

Methods: Patch-based sparse coding algorithms were applied to hippocampal surface features of baseline TI-MRIs from 78 CU adults who subsequently progressed to amnesic MCI in approximately 2 years ("progressors") and 80 matched adults who remained CU for at least 4 years ("nonprogressors"). Nonprogressors and progressors were matched for age, sex, education, and apolipoprotein E4 allele dose. We did not include amyloid or tau biomarkers in defining MCI.

Results: We achieved 92% prediction accuracy in the Arizona cohort, 92% prediction accuracy in the ADNI cohort, and 90% prediction accuracy when combining the two demographically distinct cohorts, as compared to 79% (Arizona) and 72% (ADNI) prediction accuracy using hippocampal volume.

Conclusion: Surface multivariate morphometry and sparse coding, applied to individual MRIs, may accurately predict imminent progression to MCI even in the absence of other AD biomarkers.

Keywords: Alzheimer's disease, magnetic resonance imaging, mild cognitive impairment, prediction, prognosis

¹Some of the data used in preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (<http://adni.loni.usc.edu>). As such, the investigators within the ADNI contributed to the design and implementation of ADNI and/or provided data but did not participate in analysis or writing of this report. A complete listing of ADNI investigators can

be found at: http://adni.loni.usc.edu/wp-content/uploads/how_to_apply/ADNI_Acknowledgement_List.pdf

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INTRODUCTION

Even though simple blood tests [1–3] promise to become a useful and less expensive tool for assessing a person’s diagnosis and prognosis in the early clinical and preclinical stages, structural magnetic resonance imaging (MRI) remains the most common biomarker assessment tool in current clinical practice. Typically, volumetric methods have utilized mass-univariate or region of interest methods to detect cortical thickness, grey matter volume, and surface areas. Accordingly, we recently reported findings from a prospective cohort of cognitively unimpaired individuals to estimate *a priori* MRI regions of interests (preferentially affected in the preclinical and clinical stages of Alzheimer’s disease (AD)) for differences between those individuals who subsequently progressed to clinically significant memory decline in approximately 2 years and those who did not. Additionally, the same study also used Statistical Parametric Mapping (SPM) (<http://www.fil.ion.ucl.ac.uk/spm/>) to examine the ^{18}F -fluorodeoxyglucose (FDG) positron emission tomography (PET) measured cerebral metabolic rate for glucose (CMRgl) differences between progressors and nonprogressors. Based on receiver operating characteristic, binary logistic regression, and leave-one-out procedures, hippocampal volume best predicted an individual’s imminent progression to the clinically significant memory decline, with 79% sensitivity/78% specificity among the *APOE*-matched cohort [4].

Multivariate methods appear to improve detection of subtle changes in MRI-based morphological features of structures relevant to preclinical detection of AD [5–7]. Machine learning methods promise to improve the accuracy of prediction for individual patients, particularly when applied to MRI based multiple features as with multivariate morphometry statistics (MMS), in the preclinical stages of AD [8–10]. In this study, we aimed to improve prediction from prior studies by employing the hippocampal surface MMS features, which have been shown to outperform the hippocampal volume measure [6, 11], and the patch based sparse coding algorithm to predict clinically significant memory impairment within two years, even in the absence of other amyloid, tau, PET, cerebrospinal fluid (CSF), or emerging blood-based biomarkers.

METHODS

Participants

Arizona cohort

These study participants were a sub-cohort of 280 drawn from our 23-year longitudinal Arizona *APOE* cohort study [12, 13]. As previously described [4], 18 “progressor” participants developed clinically significant memory impairment (16 diagnosed with amnesic MCI (aMCI), 1 with both amnesic and visuospatial MCI, and 1 with AD) and had both MRI and FDG PET data while still cognitively unimpaired at the epoch approximately 2 years prior to progression to aMCI/AD, and 20 “nonprogressor” participants who remained cognitively unimpaired at least 4 years after their last visits, all based on clinical, informant, neuropsychological data, and a Mini-Mental State Examination (MMSE) score > 26. The progressors and nonprogressors were matched for sex, age, education, and *APOE* allele dose. Participants with one abnormal score could be deemed clinically unimpaired if all other scores within the same cognitive domain were solidly normal and there were no functional impairments. The aMCI diagnosis was determined based on published criteria [14, 15] using clinical, functional, and neuropsychological data that included a wide battery of tests with > 1 test per domain. Though we subsequently introduced amyloid PET and tau PET to this overall study, we did not have these data for this specific sub-cohort available at baseline and therefore did not have amyloid or tau biomarkers to confirm AD pathology.

ADNI cohort

The Principal Investigator of this initiative is Michael W. Weiner, MD, VA Medical Center and University of California – San Francisco. For up-to-date information, see <http://www.adni-info.org>. Study participants were drawn from ADNI data bases utilizing the same criteria to categorize and match progressors and nonprogressors described above for the Arizona cohort. From ADNI-1, ADNI-2, ADNI-Go, and ADNI-3 we found 60 participants who developed clinically significant memory impairment, i.e., aMCI, in approximately 2 years and 60 age, sex, education and *APOE*-matched nonprogressors who remained cognitively unimpaired for at least 4 years. “Baseline” scans were the MRI scans from progressors at 2 years prior to clinically significant decline and the corresponding matched nonprogressors’ MRI scans.

131 The parent study for the Arizona cohort was
 132 approved by the Mayo Clinic and Banner Health
 133 (originally Banner Good Samaritan) Institutional
 134 Review Boards, and after complete description of the
 135 study to the subjects, written informed consent was
 136 obtained.

137 *Hippocampus segmentation and surface* 138 *reconstruction*

139 All the T1-weighted MR images were automat-
 140 ically segmented by using FIRST [16], which is a
 141 model based subcortical structure registration and
 142 segmentation tool that we have used in our pre-
 143 vious hippocampal morphometry research [6, 10,
 144 11]. In comparison to FreeSurfer, FIRST is capa-
 145 ble of generating topologically sound segmentation
 146 results with classification of relatively large, scaled
 147 databases. FIRST is one part of FSL library devel-
 148 oped mainly by Analysis Group, FMRIB, Oxford,
 149 UK. With default parameters, we ran the *run_first_all*
 150 command and extracted the segmentation of left and
 151 right hippocampi. Then all the extracted images were
 152 binarized with a simple thresholding process. With
 153 the binary images, hippocampal surfaces were con-
 154 structed with a topology-preserving level set method
 155 [18] and triangular surface meshes were further
 156 acquired based on marching cubes algorithm [19]. We
 157 then refined the meshes [6] to get the smooth surfaces
 158 which are suitable for generating conformal grids.
 159 Finally, all these smoothed meshes were aligned into
 160 the MNI standard space with a 9-DOF (degree of
 161 freedom) global affine transformation (Fig. 1).

162 *Surface conformal representation*

163 On each hippocampal surface, we generated a
 164 conformal grid as a canonical space for surface regis-
 165 tration and multivariate statistical analysis [6]. Firstly,
 166 two cuts were introduced on the hippocampal surface
 167 (Fig. 2) and thus the surface could be converted into
 168 a tube-like genus zero surface. The two cuts locate at
 169 the front and back of the hippocampal surfaces, rep-
 170 resenting anterior junction with the amygdala, and
 171 its posterior limit as it turns into the white matter
 172 of the fornix. Thus, they are biologically valid and
 173 can be used as consistent landmarks across subjects.
 174 With the tube-like surface, the landmark curves can
 175 be automatically determined by locating the extreme
 176 points and searching along the first principle direc-
 177 tion of geometric moments of the surface [7, 20, 21].
 178 Finally, we calculated the holomorphic 1-form basis

of each tube-like surface and conformally mapped the
 hippocampal surface to a planar surface.

Many of the geometric features of the surface could
 be contained in the conformal parameterization. In
 this paper, we calculated the local conformal factor
 and mean curvature, which represents the intrinsic
 and extrinsic features of the surface respectively. The
 conformal factor is the area ratio of the infinitesimal
 region around the same point on the original hip-
 pocampal surface and the conformal planar surface.
 Mean curvature is an extrinsic measure of curvature
 which comes from differential geometry and can rep-
 resent the flatness of the surface around a vertex. Both
 the conformal factor and mean curvature are local fea-
 tures defined on each vertex. The conformal factor
 and mean curvature are called the *surface conformal*
representation because they can encode both intrinsic
 structure and 3D embedding information.

Hippocampal surface registrations

All the hippocampal surfaces need to be regis-
 tered to a common template surface for morphometric
 analysis. We used the aforementioned features, sur-
 face conformal factor and mean curvature, to enforce
 surface correspondence. So, with the conformal
 parameterization, we converted the 3D surface to a
 2D image registration problem. We applied the well-
 studied image fluid registration algorithm [22, 23] to
 induce a deformation flow in the parameter domain.
 To simulate fluid flow on the surfaces, we introduced
 the Navier-Sokes equation into surface space using
 a manifold version of the Laplacian and divergence
 operators [24, 25]. With an inverse consistent frame-
 work, we could optimize the surface registration by
 minimizing the sum of squared surface feature inten-
 sity differences between the deforming image and
 the template. Since both the conformal mapping and
 the inverse consistent framework generate diffeomor-
 phic mappings, the mapping between the surfaces is
 diffeomorphic.

Surface multivariate morphometry statistics

Surface MMS consists of two different features:
 multivariate tensor-based morphometry (mTBM)
 [26] and radial distance analysis [27, 28]. The mTBM
 can measure the deformation within the surface while
 the radial distance can measure hippocampal size
 according to the surface normal direction.

The mTBM statistics measure local surface defor-
 mation and have demonstrated improved signal

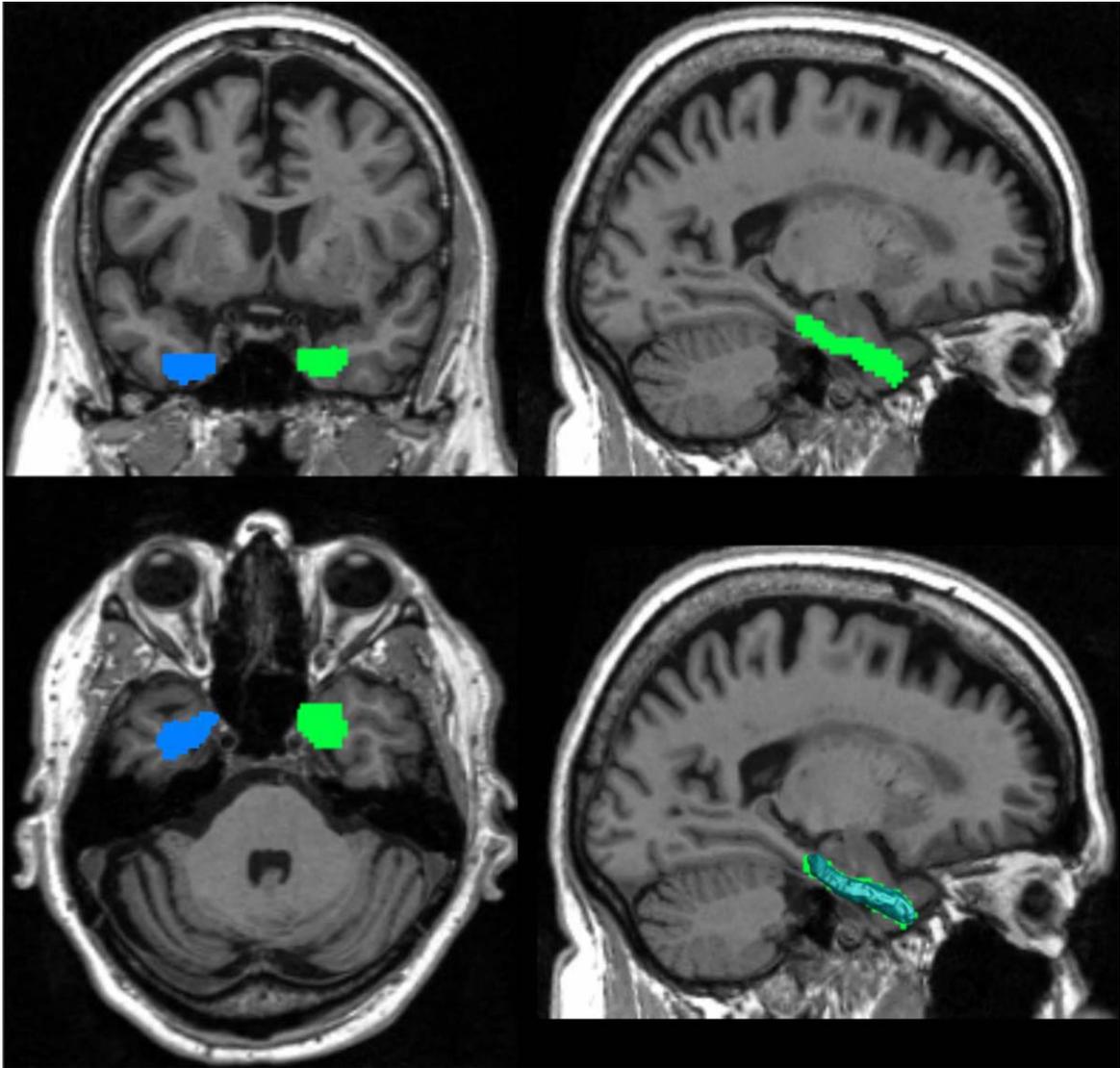


Fig. 1. Hippocampus segment The blue and green parts in these images represent the left and right hippocampus that FIRST segments of the image. The bottom right picture shows the shape of the hippocampal surface, which fits the segmented image well.

227 detection power relative to more standard tensor-
 228 based morphometry (TBM) measure computed as the
 229 determinant of Jacobian matrix [29].

230 Since the hippocampal surface is cut like a tube,
 231 the distance from each surface point to its medi-
 232 cal core is affected by its atrophy and enlargement.
 233 We named the distance as the radial distance of a
 234 hippocampus surface, which represents the morpho-
 235 metric changes along the surface normal direction.
 236 Thus, radial distance and mTBM are complementary
 237 to each other; finally, we formed the new multivariate
 238 surface morphometry statistic as a 4×1 vector,
 239 of which the mTBM was computed as a 3×1 vector

240 consisting of the “Log-Euclidean metric” [30] and
 241 the radial distance is just a scalar.

*Patch analysis-based surface
 242 correntropy-induced- sparse-coding (PASCS)*
 243

244 Recently, sparse representation and sparse coding
 245 methodology developed in the machine learning field
 246 has been shown to be efficient in learning diverse
 247 and discriminative features for optimal representa-
 248 tions [31, 32]. Our prior work adopting sparse coding
 249 for MRI data analysis in AD showed promising per-
 250 formance [33–36]. The basic idea of sparse coding is

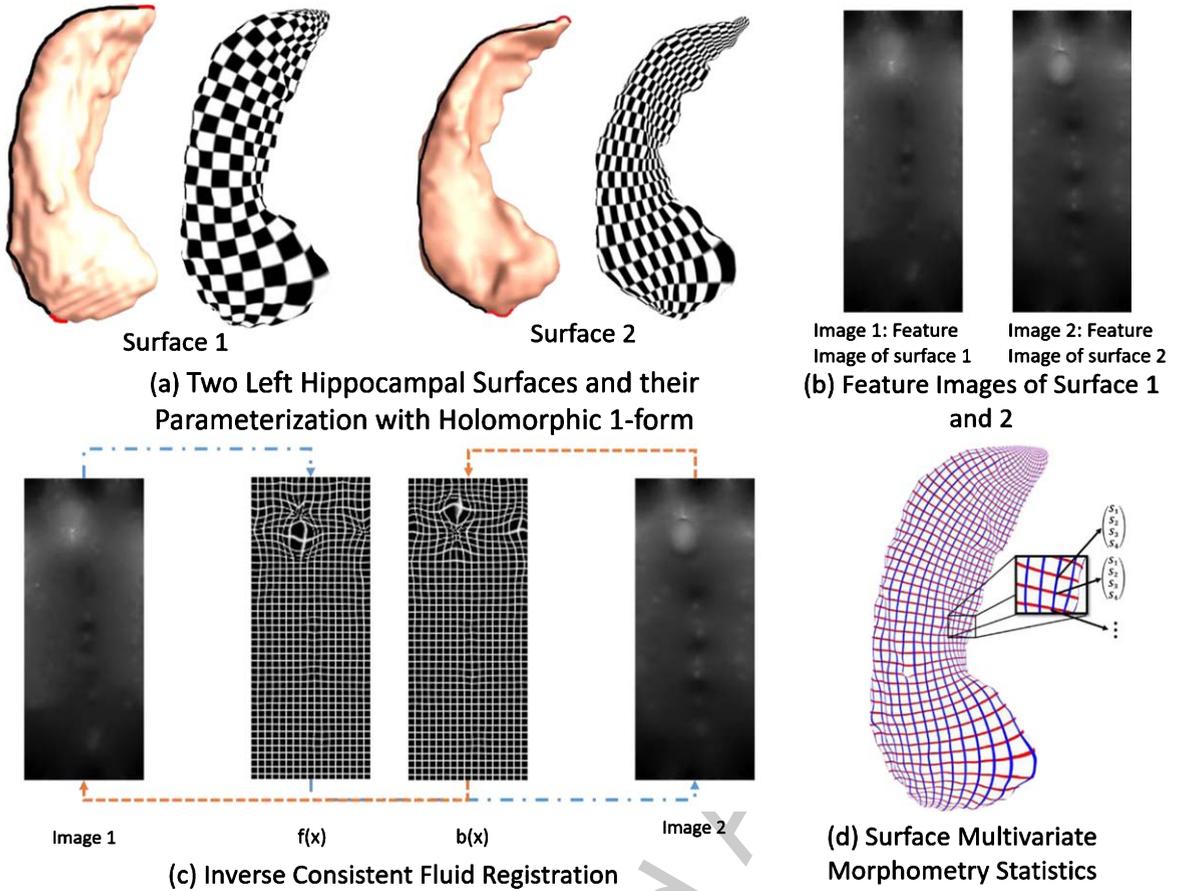


Fig. 2. Hippocampal surface morphometry pipeline (a) The hippocampus is segmented from T1-weighted images and a conformal grid is built on the surface. Here examples are shown for 2 different subjects. (b) Examples of features selected in the image for the two subjects in (a). (c) From left to right: Intensity map on the surface 1 in (a). Forward map $f(x)$ for the conformal grid fluid registration to the image 2. Backward map $b(x)$ from the image 2 to image 1. Intensity map on the surface 2. (d). Surface multivariate morphometry statistics is applied to analyze morphometric changes.

251 to generate an over-complete dictionary that allows
 252 us to represent the original high-dimensional features
 253 with a sparse coefficient matrix (sparse codes) for
 254 learning the optimal representation. The advantage
 255 of sparse coding is that it can use a small number of
 256 basis vectors to represent local features effectively
 257 and concisely and help extract the most discrimi-
 258 native features for image content analysis. Sparse
 259 coding has shown to be efficient for many medi-
 260 cal image tasks, including image classification [37],
 261 image denoising [38], image segmentation [39], and
 262 functional connectivity [40]. In our research, we use
 263 the combination of surface patch features as input
 264 and construct both dictionary and their sparse codes
 265 to reconstruct the input features. Usually, the objec-
 266 tive function aims to optimize two terms: the first
 267 term measures how well it represents the surface
 268 patches, and the second term ensures the sparsity of

the representation, with an l_1 -regularized correntropy
 loss function. In this work, stochastic coordinate cod-
 ing [42] is adopted due to its ability to dramatically
 reduce the computational cost while keeping compa-
 rable performance. We further use the learned sparse
 representation as surface features.

Patch selection with sparse coding

After registering each hippocampal surface to a
 uniformed grid, each surface contains $150 * 100$ ver-
 tices and the feature dimension of each hippocampal
 surface is 60,000, where each vertice has $1 * 4$ dimen-
 sional MMS features. We then randomly generated
 10×10 square windows on each hippocampal sur-
 face and collected 504 surface patches with different
 amounts of overlapping on each side of the hippam-
 pus. We randomly selected 1008 patches on each

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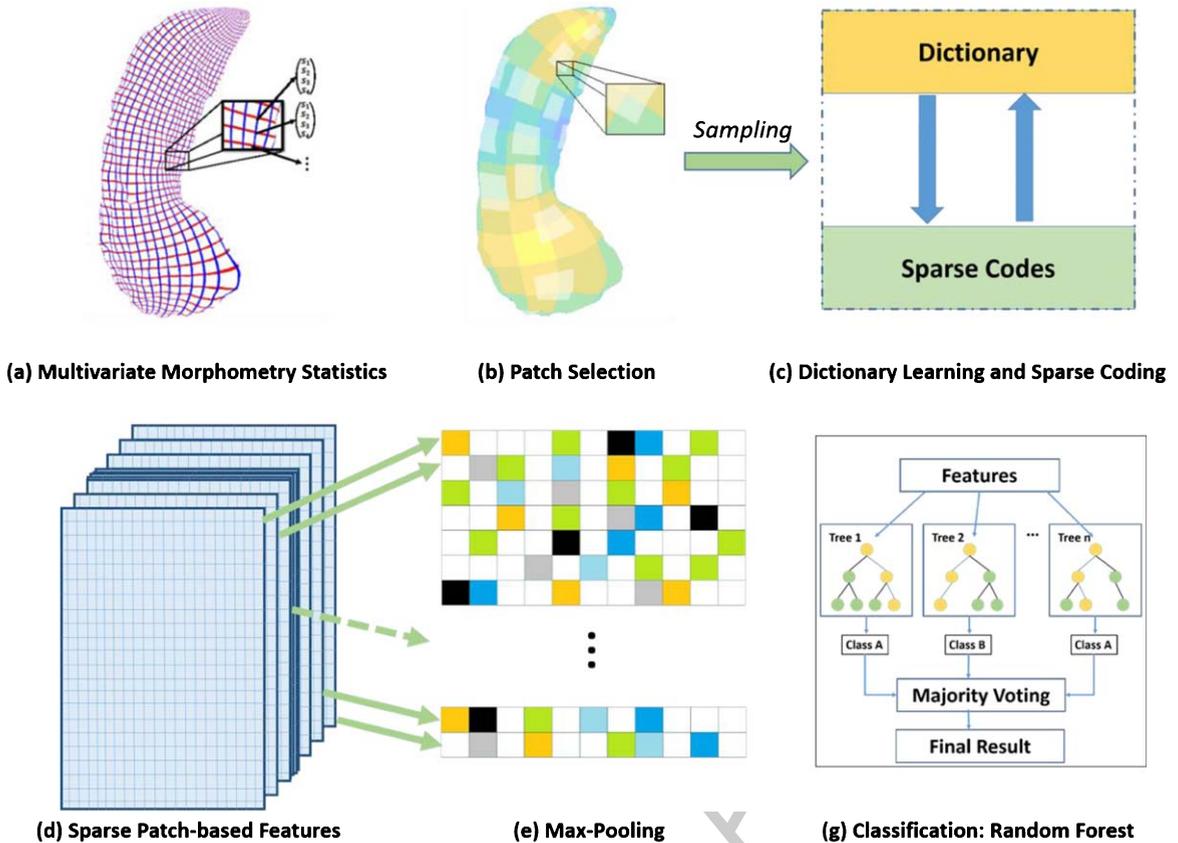


Fig. 3. Patch-based sparse coding system (a) Surface multivariate morphometry statistics. (b) Generate patches and randomly select patches on the surface. (c) Dictionary learning and sparse coding. (d) Sparse patch-based features got from (c). (e) Max-pooling to resize the features in (d). (f) Classification by using random forest classifier with the features after Max-pooling.

subject's hippocampal surfaces (1008 for both left and right). For different subjects, we used the same random seed to choose the patches. In other words, the distribution for the random-selected patches is the same on the hippocampal surfaces for all the subjects. Then we reformed these patches of features to a vector, of which the dimension is 400×1008 . The dictionary was initialized by randomly selecting patches [43], which has proved to be an efficient method in practice, and then we started learning the dictionary and sparse codes by stochastic coordinate coding [42]. The size of the batch is one and the model is trained for ten epochs. After sparse coding, we acquired 1008 samples, each of which has 1800 features on each subject. Finally, with max-pooling, we chose the maximum values for each feature over 1008 patches and obtained 1800-dimensional features for each subject.

In this study, we chose random forest algorithm [44]. Random forests are a combination of tree predictors such that each tree depends on the values

of a random vector sampled independently and with the same distribution for all trees in the forest (Fig. 3). This algorithm adapts a learning process called "feature bagging." In this process, we selected a random subset of the features for several times and then trained a decision tree for each subset. If some features are strong predictors for the response, they will be selected in many decision trees and thus make them correlated. In comparison with decision trees, random forests have the same bias but lower variance, which means it can overcome the drawback of overfitting caused by the small data set. For our sparse surface features, when the training number becomes smaller, diversification becomes more subtle, and the method can better detect these subtle differences. Finally, we employed cross-validation to evaluate the performance of the classification. For the k-fold cross-validation, we randomly shuffled the dataset and split it to k groups. For each group, we take it as the test data set and use the remaining groups to train a model. Then, the model

Table 1

Characteristics progressors and nonprogressors at the time of baseline scan

	Progressors	Nonprogressors	<i>p</i>
Sex (M/F)	7/11 (AZ) 25/35 (ADNI)	7/13 (AZ) 25/35 (ADNI)	0.80 1.00
$\epsilon 4$ Genotype (N)	13:03:02 (AZ) 2:17:41 (ADNI)	13:04:03 (AZ) 1:17:42 (ADNI)	0.89 0.99
% (HM:HT:NC)	(72:17:11) (AZ) (0:39:61) (ADNI)	(65:20:15) (AZ) (0:21:79) (ADNI)	
Age	68.75 \pm 4.65 (AZ) 76.97 \pm 6.89 (ADNI)	66.76 \pm 3.29 (AZ) 75.19 \pm 5.62 (ADNI)	0.13 0.12
Education	16.44 \pm 1.69 (AZ) 15.95 \pm 2.87 (ADNI)	15.50 \pm 3.33 (AZ) 16.12 \pm 2.74 (ADNI)	0.29 0.70

Sex and genotype *p*-values were calculated by chi-squared tests, Age and education *p*-values were calculated by *t*-tests. HM, $\epsilon 4$ homozygote; HT, $\epsilon 4$ heterozygote; NC, $\epsilon 4$ non-carrier; AZ, Arizona cohort; ADNI, Alzheimer's Disease Neuroimaging Initiative cohort.

is evaluated by the test group. In this way, we can get a predicted class label for all the samples. To indicate the number of correct class labels, we built a contingency table, of which the rows are the true classes and the columns represent assigned classes. And then, we could represent the combination of ground truth and predicted result as $\begin{Bmatrix} C_{11} & C_{12} \\ C_{21} & C_{22} \end{Bmatrix}$ and compute the following performance measures, Sensitivity = $C_{11}/(C_{11} + C_{12})$, Specificity = $C_{22}/(C_{21} + C_{22})$ and Accuracy = $(C_{11} + C_{22})/(C_{11} + C_{12} + C_{21} + C_{22})$.

Data availability

Any data not published within the article is available, and anonymized data will be shared by request from any qualified investigator.

RESULTS

Characteristics of the progressors and nonprogressors are shown in Table 1. Overall, the ADNI participants were older and had a greater percentage of males and *APOE4* non-carriers than the Arizona participants.

Prediction results are shown in Tables 2 and 3. In the Arizona cohort, the prediction result of progression to clinically significant decline using hippocampal surface MMS features was achieved with 92% accuracy and 89% sensitivity and 95% specificity. The same method with the ADNI cohort achieved 92% accuracy, 88% sensitivity, and 97%

Table 2

Experimental results: Arizona and ADNI cohorts (leave-one-out cross-validation)

Hippocampal surface	MMS	MMS left	MMS right
Accuracy	0.92 (AZ) 0.92 (ADNI)	0.74 (AZ) 0.85 (ADNI)	0.66 (AZ) 0.84 (ADNI)
Sensitivity	0.89 (AZ) 0.88 (ADNI)	0.72 (AZ) 0.84 (ADNI)	0.61 (AZ) 0.83 (ADNI)
Specificity	0.95 (AZ) 0.97 (ADNI)	0.75 (AZ) 0.87 (ADNI)	0.70 (AZ) 0.85 (ADNI)

Multivariate morphometry statistics (MMS) column indicates the classification results with MMS from both left and right hippocampal surfaces while MMS left and MMS right columns are the classification results with MMS from left and right hippocampal surfaces, respectively. AZ, Arizona Cohort; ADNI, Alzheimer's Disease Neuroimaging Initiative Cohort.

Table 3

Experimental results: combined cohorts (5-fold cross-validation)

Hippocampal surface	MMS	MMS left	MMS right
Accuracy	0.90	0.84	0.80
Sensitivity	0.90	0.82	0.79
Specificity	0.90	0.85	0.81

Multivariate morphometry statistics (MMS) column indicates the classification results with MMS from both left and right hippocampal surfaces while MMS left and MMS right columns are the classification results with MMS from left and right hippocampal surfaces, respectively.

specificity. Combining the Arizona and ADNI cohorts (78 progressors and 80 nonprogressors) achieved 90% prediction accuracy, 90% sensitivity, and 90% specificity.

A *post-hoc* analysis using random forest classification and leave-one-out cross-validation showed that AVLT long-term memory (LTM) scores predicted progression with only 74% prediction accuracy (65% sensitivity and 83% specificity) in the Arizona cohort, and 62% prediction accuracy (59% sensitivity and 65% specificity) in the ADNI cohort despite the potential bias of using that same measure (along with other criteria) when making the diagnosis of aMCI. Furthermore, as a comparison to our new methods that utilize surface multivariate morphometry, prediction of aMCI using baseline hippocampal volume, random forest classification with leave-one-out cross-validation in the same data sets yielded only 79% prediction accuracy in the Arizona cohort and 72% in the ADNI cohort (Table 4).

DISCUSSION

This study extended previous work by showing that combining hippocampal surface MMS and

Table 4

Hippocampal volume prediction using random forest classifier and leave-one-out cross-validation

Hippocampal Volume*	Accuracy	Sensitivity	Specificity
Left hippocampus	0.74 (AZ) 0.68 (ADNI)	0.65 (AZ) 0.68 (ADNI)	0.83 (AZ) 0.68 (ADNI)
Right hippocampus	0.74 (AZ) 0.65 (ADNI)	0.80 (AZ) 0.60 (ADNI)	0.67 (AZ) 0.70 (ADNI)
Left+Right hippocampus	0.79 (AZ) 0.72 (ADNI)	0.85 (AZ) 0.69 (ADNI)	0.72 (AZ) 0.73 (ADNI)

*The automated brain mapping algorithmic program FreeSurfer (<http://surfer.nmr.mgh.harvard.edu/>) was used to pre-process MRI volumetric data.

378 machine learning methods affords improved prediction of imminent clinically significant cognitive
 379 decline compared to typical automated volumetric MRI methods and standard statistics. Our methods
 380 achieved high prediction accuracy in two separate and independent data sets, each balanced for age, sex, and
 381 presence or absence of the *APOE4* allele, even in the absence of other brain imaging or fluid biomarkers
 382 of AD. Furthermore, we retained accuracy when the two data sets, which differed from each other in age,
 383 sex, and percentage *APOE4* carriers, were combined. The predictions using hippocampal surface MMS and
 384 machine learning methods were also much better than predictions using either hippocampal volume or base-
 385 line cognitive scores, even though the latter are biased due to the circularity of using the same measure
 386 when making the diagnosis of aMCI. Although lacking amyloid and tau biomarker confirmation of AD
 387 pathology in this study, the data set from Arizona is well-defined, with high confidence regarding the like-
 388 lihood of AD in those who subsequently developed aMCI. Thus far, the majority of those in the Arizona
 389 progressor group later developed definite or probable AD, with the exception of one person who developed
 390 dementia with Lewy bodies and one aMCI individual who 2 years later had slight improvement in cogni-
 391 tion. Although we do not know how many of those in the nonprogressor group will ultimately develop AD,
 392 we have high confidence that none developed MCI for 4 years following the scan. To date, 3 in the Ari-
 393 zona nonprogressor group subsequently developed MCI and none have progressed to dementia. Thus,
 394 the training and testing groups were well defined and mostly accurate, which mirrors the accuracy of our
 395 novel feature-based sparse coding methods. Instead of using the automated brain mapping algorithmic
 396 programs FreeSurfer (<http://surfer.nmr.mgh.harvard.edu/>) and Statistical Parametric Mapping ([http://](http://www.fil.ion.ucl.ac.uk/spm/)

www.fil.ion.ucl.ac.uk/spm/) as we did in our prior study with the same data set [4], in this study we
 utilized arguably more sensitive methods involving MMS to discover subregional hippocampal surface
 differences, patched-based sparse coding for feature selection, and the random forest machine learning
 classifier. We were able to replicate our improved results in a completely independent data set from
 ADNI that differed from the Arizona data set in age, sex, and percentage *APOE4* carriers.

Because the Arizona data set was identical to our prior study [4], the improved accuracy in this
 study can be explained by our use of hippocampal surface MMS combined with patch-based sparse
 coding algorithms. Similar to the methods from our most recent work [36], in this paper we propose
 a novel Patch Analysis-based Surface Correntropy-induced Sparse coding, PASCs, to help predict future
 cognitive decline. We demonstrate that PASCs is surprisingly useful for surface features classifica-
 tion and surface multivariate morphometry statistics features consisting of surface multivariate tensor-
 based morphometry and radial distance (the distance from the medial core to each surface point), and we
 also move a step forward from group difference to that of individual subject classification. Unlike other
 sparse coding work [37–40], PASCs takes advantage of surface morphometry features that practically
 encode neighboring intrinsic 3D geometry information. Meanwhile, MMS features also benefit from
 the succinct representation and strong discrimination power that sparse coding provides for effective
 AD classifications, i.e., capturing more important information so that MMS features not only have the
 significant group difference but also have an effective classification power.

In this work, we adopted FIRST for hippocampus segmentation, which, having previously explored dif-
 ferent segmented hippocampal data as input, appears to most reliably generate topologically sound seg-
 mentation results. For example, our earlier work used manually segmented hippocampi to build surface
 meshes [26, 45]. Later, we adopted FIRST for automatic hippocampus segmentation [6] and used it in
 almost all our hippocampal morphometry research. Meanwhile, we also used FreeSurfer segmented hip-
 pocampi to build hippocampal surface meshes [17]. All achieved reasonable results in group differ-
 ence studies, thus demonstrating that our pipeline is robust to segmentation methods. However, FIRST
 can always generate topologically sound segmentation results, whereas FreeSurfer does not guarantee

Table 5
Classifications for 10 different patch selections

Cohorts	AZ	ADNI	Combined
Accuracy \pm SD	0.89 \pm 0.02	0.90 \pm 0.01	0.90 \pm 0.02
Sensitivity \pm SD	0.85 \pm 0.04	0.89 \pm 0.02	0.90 \pm 0.04
Specificity \pm SD	0.93 \pm 0.06	0.91 \pm 0.02	0.90 \pm 0.04

We repeated the experiments ten times with ten different patch selections on both sides of the hippocampal surface. The left and middle columns of the table indicate the classification results for the AZ cohort and ADNI cohort respectively with leave-one-out cross-validation. The last column shows the results for the combined cohorts with 5-fold cross-validation. SD, standard deviation.

topologically correct results. Therefore, manual quality control is necessary to incorporate FreeSurfer in our pipeline. Thus far, our related prediction/classification work adopted FIRST segmented hippocampal surfaces in order to more efficiently work with relatively large-scaled datasets [10, 11]. Since the input of our MMLC is the surface features rather than the output from segmentation tools, it is reasonable for us to expect that our method is not sensitive to the hippocampus segmentation tools used.

To evaluate the influence of these random-select patches on the classification accuracy and the stability of our framework, we repeated the experiments ten times with ten different patch selection on both sides of the hippocampal surface. The mean and standard deviation of the results are shown in Table 5. The results show our method is relatively stable with different patch selection and comparable to the best accuracy results reported in Tables 2 and 3. It is worth noting that the variance results were not purely caused by the patch selection, since other components in the pipeline, such as random forest and cross-validation parts, may also perturb the final results. For example, during the training of random forest, the classifier will randomly select a subset of features to build a decision tree. Similarly, in the 5-fold cross-validation, the training data may be different. Considering the small dataset size in the current experiments, the minor variance in our results demonstrates that the influence of random patch selection is in a reasonable range and does not appreciably affect the stability of the results. In future, we will further explore the random patch selection issue with larger imaging cohorts.

Future directions will include integrating convolutional neural network (CNN) with our proposed approach. CNN is considered one of the most successful deep models for identifying, classifying, and quantifying patterns in medical images [46, 47]. Based on promising results from our most recent work [48, 49],

integrating CNN with the proposed approach could further improve the PASS results. Specifically, we applied CNN and an unsupervised learning method (multi-task stochastic coordinate coding) algorithm to the ADNI dataset to predict future cognitive clinical measures with baseline hippocampal/ventricle mTBM features and cortical thickness, achieving accurate predictions of MMSE/ADAS-Cog scales [48, 49]. However, there is a trade-off between computation efficiency and prediction performance. Training a CNN model usually requires substantial computational resources (multiple GPUs). Our PASS-MP is a generative toolbox for brain image analysis with fast running time and does not require GPU for training. It can apply to different subcortical of brain images with relatively high performance. We therefore will continue to explore the efficient CNN based sparse coding method that could both improve the prediction power and maintain a low-cost of computational resources and fast running time as PASS-MP for better help with clinical diagnosis and prognosis.

Although there are many other sensitive biomarkers to detect the pathology associated with AD, this method capitalizes on MRI scans, which is a clinical diagnostic capability that virtually all clinicians have access to. Further testing is needed to verify the results in larger data sets, but our method appears to accurately predict whether an individual will progress to the clinical stages of AD within the next 2 years. Thus, this method has the potential to be developed into a clinically useful tool. We currently have no proven medication treatments for AD; however, well-tested behavioral programs that provide lifestyle and behavioral training to adapt to memory loss associated with MCI are available [50]. These behavioral programs appear to be most effective when done prior to significant memory decline [51]. If we had an accurate and inexpensive tool to predict likelihood of clinically significant decline, we could target those individuals who would most benefit from a similar intervention that is delivered preclinically.

Limitations of this study include relatively small numbers of progressors and nonprogressors in both cohorts and thus this method will need to be replicated in other, larger data sets. Importantly, we also did not include other biomarkers such as amyloid or tau to verify that progressors had MCI due to AD or include other imaging, CSF, and emerging, less expensive and more scalable blood-based biomarkers of amyloid, tau, and neurodegeneration [1–3], and future applications of this technique should do

so to ensure accurate training sets and generalizable results. However, we were interested in seeing the “added value” of this MRI based image analysis technique as a complement to those emerging methods. We did not test brain regions other than hippocampus, but the purpose of this study was to evaluate the utility of prediction using hippocampal surface multivariate morphometry statistics combined with patch-based sparse coding algorithms. It was therefore convenient to compare these methods using the same data set that we had previously evaluated with standard automated brain mapping algorithmic programs, binary logistic regression, and leave-one-out procedures. Also, our previous study did explore other imaging-based biomarkers and found that the hippocampus was the best predictor 2 years prior to clinically significant decline (including both FDG-PET and MRI biomarkers). Finally, because of the overlapping patch selection and max-pooling scheme, we generally cannot visualize the selected features, which may decrease the interpretability of biomarkers and, in turn, translation to clinical applications. However, we can always visualize statistically significant regions using group differences [6]. In addition, our recent work [52] better addresses this problem with the adoption of group lasso screening [53] to select the most significant features. It was not adopted in our current study because of its relatively small sample size. In the future, we will incorporate this approach into our current framework to improve its interpretability.

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