# A signature of cognitive deficits and brain atrophy that is highly predictive of progression to Alzheimer's dementia

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**Abstract** Only a fraction of patients with mild cognitive impairment (MCI) progress to Alzheimer's dementia. We explore here whether a high-risk MCI subgroup can be identified using a signature mixing cognitive assessments and structural neuroimaging. The signature was extracted using machine learning tools in the ADNI1 sample, and replicated known archetypes: cognitive deficits across multiple domains, with atrophy in temporal, parietal and occipital regions. We validated the signature on two MCI cohorts. In ADNI1, the signature predicted progression to dementia over three years with 80.4% positive predictive value, adjusted for a "typical" MCI baseline rate of 33% (95.6% specificity, 55.1% sensitivity). These results were replicated in ADNI2, with 87.8% adjusted positive predictive value (96.7% specificity, 47.3% sensitivity). This signature uses non-invasive and widely available markers and may prove useful for enrolling participants at high risk of decline in clinical trials or early intervention.

## Introduction

Alzheimer's disease (AD) is an age-related neurodegenerative disorder and a leading cause of dementia worldwide. AD is marked by the abnormal accumulation of amyloid $\beta$ (A$\beta$) and hyper-phosphorylated tau proteins in the brain, which leads to widespread neuronal damage. These neurobiological events may develop years, or even decades, before the emergence of mild cognitive impairment (MCI), considered a prodromal stage of AD. MCI is a clinical condition not specific of AD; many patients will remain cognitively stable over time or even revert to normal cognition.

A diagnosis of MCI is still a risk factor for AD dementia, with up to 36% of patients developing dementia within two years (***Ward et al., 2013***). Given the long preclinical and prodromal phases in AD, there is interest in developing treatments that could prevent further decline, which requires biomarkers predictive of progression to dementia from preclinical stages. Identifying MCI patients who will progress to AD dementia with enough specificity has been a challenge for clinical trials, where the inclusion criteria for MCI subjects have had low to moderate positive predictive value (***Visser et al., 2005***). This lack of prognostic power could be due to underlying heterogeneity among individuals. ***Dong et al.*** (***2017***) for example showed four distinct patterns of brain atrophy, two of which were associated with higher-than-expected rates of progression to dementia. Yet, one subtype was much more at risk than the other. The implications for prognosis are profound: only a subset of individuals will have clinical trajectories that can be predicted very reliably. In this work, we propose to apply machine learning tools to identify subgroups at very high risk of progression to AD dementia, using commonly available measures, i.e. structural magnetic resonance imaging (MRI) and cognitive tests.

There is a growing field of research dedicated to developing machine learning algorithms to automatically detect progression to AD dementia in patients with MCI. Cognitive tests measuring episodic memory and language have been identified as features with high predictive accuracy (***Belleville et al., 2017***), with specificity and sensitivity values of at least 70%. It has been suggested that the combination of several cognitive domains, notably memory, language, and executive function tests, yields the best performance and balance between specificity and sensitivity (***Belleville et al., 2017***). With structural MRI, it is well established that significant tissue loss occurs in the medial temporal lobes in AD patients (***Jack et al., 1997***). Medial temporal lobe atrophy may be an early marker of AD as it can be seen also in MCI patients relative to cognitively normal individuals (***McDonald et al., 2009***). As the disease progresses and clinical symptoms become more severe, atrophy spreads to the parietal and frontal lobes, while leaving the sensorimotor and visual cortices relatively intact (***McDonald et al., 2009***). Grey matter volumes (GMV) of regions of interest, typically defined by an atlas, have been used as features for the classification of progressor MCI (pMCI) and stable MCI (sMCI) (***Misra et al., 2009***; ***Davatzikos et al., 2011***). Cortical thickness of brain regions have similarly been used as features to classify sMCI and pMCI (***Eskildsen et al., 2013***; ***Querbes et al., 2009***; ***Wee et al., 2013***). Models using structural features alone have achieved variable performance, ranging from 38-84% specificity and 63-95% sensitivity. Models that have combined structural MRI markers with cognitive measurements have outperformed models with either structural MRI or cognition alone at predicting progression to AD dementia (***Devanand et al., 2007***; ***Korolev et al., 2017***; ***Moradi et al., 2015***). For models combining structural MRI and cognition, in terms of accuracy, the best has been reported at 79% (76% specificity, 83% sensitivity) (***Korolev et al., 2017***). Overall, the state-of-the-art, which used A$\beta$ positron emission tomography (PET) scans, has so far achieved 82% accuracy (87% specificity, 71% sensitivity) (***Mathotaarachchi et al., 2017***). Note that accuracy is defined as the proportion of subjects that were correctly identified, either as positives or negatives. Positive predictive value, on the other hand, is defined as the proportion of true positives out of all subjects that were classified as positive. A model could have high accuracy yet moderate positive predictive value if the number of true positives is low relative to the number of true negatives. In the case of predicting incipient AD, relatively few MCI subjects progress to dementia (up to 36% within two years (***Ward et al., 2013***)). Despite promising accuracy, the positive predictive values of models predicting AD progression remain moderate, ranging from 50 to 75% across the literature (***Dansereau et al., 2017***). This implies that up to half of subjects who were identified as progressors by published algorithms did not in fact progress to dementia. Furthermore, predictive power decreases as the time to conversion increases (***Eskildsen et al., 2013***), so there is even more room for improvement for long-term prognosis (beyond 2 years).

AD dementia prognosis may be difficult due to the inherent heterogeneity present across the population. While brain amyloidosis is a defining feature of AD, it is clearly insufficient at causing clinical impairment since 10-44% of cognitively normal subjects aged 50 to 90 years are amyloid-

positive, based on a meta-analysis of 55 studies with PET and cerebrospinal fluid (***Jansen et al., 2015***). Furthermore, a meta-analysis of 29 cohorts revealed that, on average, 88% of clinically diagnosed AD patients have amyloid-negative PET scans (***Ossenkoppele et al., 2015***). Similar prevalence rates have been corroborated by post-mortem neuropathological assessments (***Beach et al., 2012***; ***Bennett et al., 2006***), revealing that clinical diagnoses often do not match with pathology. ***Beach et al.*** (***2012***) also found that guidelines for a neuropathological diagnosis of AD were too restrictive, rendering 33% of cases unclassifiable. It is apparent that we need to better characterize heterogeneity within populations if we are to reach the precision levels required for individualized medicine.

To address some of this heterogeneity, several studies have explored subtypes of atrophy in AD, where homogeneous subgroups of AD patients show different patterns of gray matter loss relative to healthy controls. For example, a number of works have reproduced a subtype characterized by primarily medial temporal lobe atrophy, a second subtype characterized by parietal, occipital, and lateral temporal lobe atrophy, and a third subtype with diffuse atrophy (***Noh et al., 2014***; ***Hwang et al., 2016***; ***Park et al., 2017***; ***Varol et al., 2017***). The subgroup with parietal, occipital, and lateral temporal lobe atrophy tended to be younger and had the worst cognition (***Noh et al., 2014***; ***Park et al., 2017***), while the medial temporal lobe atrophy subtype contained a greater proportion of carriers of the APOE4 allele (***Varol et al., 2017***), a genetic risk factor for sporadic late-onset AD, and the diffuse atrophy subtype had the least A$\beta$ and tau burden (***Varol et al., 2017***). Heterogeneity is also present in the symptomatic expression of MCI patients. Often, MCI patients are categorized as amnestic MCI, subjects who have memory impairment, non-amnestic MCI, those who have impairments in non-memory domains, and multi-domain MCI, subjects with concurrent impairments in multiple kinds of cognition (***Petersen, 2003***). This would result in a patient being labeled as one of four MCI subtypes: 1) amnestic single domain MCI, 2) non-amnestic single domain MCI, 3) amnestic multidomain MCI, 4) non-amnestic multidomain MCI (***Petersen et al., 2014***). Amnestic MCI subjects are more likely to be diagnosed with dementia than non-amnestic MCI (***Aggarwal et al., 2005***; ***Busse et al., 2006***), but the group at highest risk of conversion is multi-domain MCI (***Tabert et al., 2006***). ***Mitchell et al.*** (***2009***) reported 59% of multi-domain MCI subjects progressed after two years of follow-up, while only 18% of amnestic single domain MCI progressed, and 70% of non-amnestic single domain MCI actually improved, which illustrates how outcomes can vary substantially between subgroups. Certain subtypes of brain patterns may predispose individuals to worse cognitive trajectories. Subjects with widespread brain atrophy, and especially those who also express greater loss in the temporal lobes, have worse cognitive decline compared to other subjects with more localized atrophy (***Dong et al., 2017***).

While brain structure and cognition appear to offer complementary information for prognosis of dementia, the complementarity of those modalities to identify high-risk subtypes is unclear. It is possible that a predictive signature based on atrophy may identify a subgroup of subjects that is separate from those labeled by a signature based on cognition, for example. Then despite the many works that describe subtypes of brain atrophy in AD populations (***Noh et al., 2014***; ***Hwang et al., 2016***; ***Park et al., 2017***; ***Varol et al., 2017***; ***Zhang et al., 2016***; ***Dong et al., 2016***), little has been done to leverage the heterogeneity to predict incipient dementia from a subgroup of MCI patients with high positive predictive value. We have previously shown that the combined expression of certain subtypes of cortical thinning patterns, grey matter volumes, and resting-state network functional connectivity was highly predictive of future AD progression in a subgroup of MCI subjects with 90% positive predictive value (***Dansereau et al., 2017***). While the results from ***Dansereau et al.*** (***2017***) are promising, the sample size was small, as resting-state functional MRI data is not available for the majority of ADNI participants. Large scale validation of a highly predictive signature could still be done using more widely available markers, such as cognitive assessments and structural MRI, but such validation has not been done yet to the best of our knowledge.

The main aim of this work was to develop a multimodal signature that is highly predictive of progression to AD dementia in a subgroup of MCI patients, based on cognition and subtypes of grey matter atrophy. We also aimed to evaluate the complementarity of features derived from cognition

and atrophy patterns. Although this has been extensively studied for prognosis of dementia in a general MCI population, the complementarity of these measures is not documented in the specific context of a high risk signature. We applied a cluster analysis on structural magnetic resonance images to identify subtypes of brain atrophy in a sample containing both patients with AD dementia and cognitively normal (CN) individuals. We then used a two-step machine learning algorithm (***Dansereau et al., 2017***) to train a model to identify three signatures that were highly predictive of AD dementia: 1) an anatomical signature, 2) a cognitive signature, 3) a multimodal anatomical and cognitive signature. After identifying MCI patients carrying these signatures, we examined cognitive decline, A$\beta$ and tau burden, and progression to dementia in these individuals to explore whether a highly predictive signature represented a prodromal stage of AD. We analysed whether these three signatures identified separate subgroups of subjects and how they performed against each other in terms of positive predictive value, specificity, and sensitivity at identifying progressors.

## Results

### Brain atrophy subtypes

We extracted spatial patterns of brain atrophy and cognitive measures that were used for our predictive models. For the structural MRI measures, we took the baseline T1-weighted MRI scans of patients suffering from AD dementia (N = 205) and cognitively normal (CN) individuals (N = 172) from ADNI1 and applied a voxel-based morphometry (VBM) analysis to generate maps of local grey matter volume. To measure the spatial similarity of brain atrophy between subjects, we generated spatial Pearson's correlation coefficients between all pairs of individual maps of grey matter volume. A clustering analysis on these correlation coefficients revealed the presence of 7 subgroups of subjects with homogeneous grey matter topography (Figure 1). A subtype template was generated for each subgroup by averaging the maps of individuals within that subgroup (Figure 1b). We then generated a measure of similarity between each individual map and each subtype template, using spatial correlation coefficients, referred to as weights (Figure 1a). These weights were used as features for the predictive models involving VBM in the rest of this work. As in our previous works (***Orban et al., 2017***; ***Dansereau et al., 2017***), we chose to use weights, which can be interpreted as continuous measures for subtype affinity, over discrete subtype membership because the latter is less informative as most individuals express similarity to multiple subtypes (***Zhang et al., 2016***). Note that although we chose to present our findings with 7 subtypes, we examined how the number of subtypes may impact our subsequent predictions. There was no significant difference in model performance when we changed the number of subtypes (see Table 2 in supplementary material).

### Prediction of AD dementia vs cognitively normal individuals

We used a linear support vector machine (SVM) to develop three different models to classify AD vs CN in ADNI1 based on the following features: 1) VBM-only subtypes, 2) cognitive features from neuropsychological assessments across multiple domains (COG only), 3) a combination of of VBM subtypes and cognitive features (VCOG). In all three models, age, sex, mean grey matter volume (GMV) and total intracranial volume (TIV) were also included as features. The model trained using the VCOG features achieved 94.5% positive predictive value (95.6% specificity, 93.9% sensitivity) when classifying AD vs CN in ADNI1. Such high performance was expected given the marked cognitive deficits associated with clinical dementia. COG features only actually reached excellent performance as well (97.6% positive predictive value, 98.0% specificity, 96.4% sensitivity), while using VBM features only yielded markedly lower performances (86.4% positive predictive value, 89.3% specificity, 79.6% sensitivity). Note that the performance metrics in ADNI1 were estimated through cross-validation, and represent an average performance for several models trained on different subsets of ADNI1. We then trained a model on all of ADNI1, and estimated its performance on an independent dataset, ADNI2. Using VCOG predictors, the ADNI1 model reached 92.0% positive predictive value (96.3% specificity, 92.0% sensitivity), when applied on ADNI2 AD vs CN

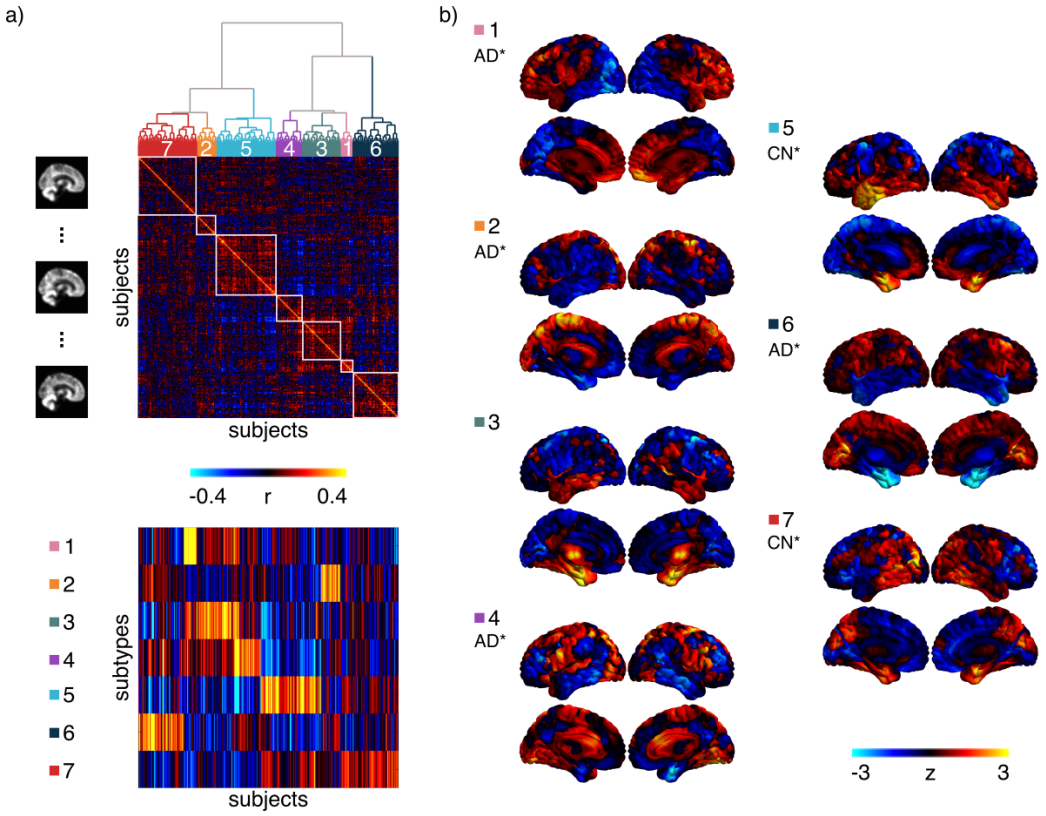


**Figure 1.** Subtyping procedure and resulting subtypes. a) A hierarchical clustering procedure identified 7 subtypes, or subgroups, of individuals with similar patterns of grey matter topography within the ADNI1 cohort of CN and AD subjects (top). A measure of spatial similarity, called subtype weight, between a single individual's grey matter volume map and the average of a given subtype was calculated for all individuals and all subtypes (bottom). b) Maps of the 7 subtypes showing the distribution of grey matter across all voxels relative to the average. CN* and AD* denote significant associations between the subtype weights and diagnoses of cognitively normal (CN) or Alzheimer's dementia (AD) respectively.

data. Again the performance was comparable with COG predictors only (92.2% positive predictive value, 96.3% specificity, 94.3% sensitivity), and lower performance with VBM features only (57.3% positive predictive value, 79.8% specificity, 56.7% sensitivity). Note that positive predictive value is dependent on the proportion of patients and controls for a given sensitivity and specificity. Since the ADNI2 sample had a substantially smaller proportion of AD subjects compared to ADNI1, the resulting positive predictive value was reduced. When we adjusted the baseline rate of AD subjects in ADNI2 to the same rate in ADNI1, the positive predictive values were 95.2%, 95.3%, and 70.2% for the VCOG, COG, and VBM models respectively.

## Identification of easy AD cases for prediction

We tested the stability of the SVM prediction with VCOG features, using random subsamples of ADNI1. We calculated hit probabilities, representing the frequency at which a given subject would be correctly identified as AD, across all subsamples that did not include that subject as part of the training of the model. When implementing this procedure on all of ADNI1, we found that 88% of subjects had a 100% hit probability, which we defined as easy cases for prediction. A logistic regression was then trained to predict the easy AD cases. The logistic regression was regularized, which means here that it selected a subset of features to perform the prediction. We called the combination of these features a highly predictive signature (HPS) of AD. The VCOG HPS model achieved 99.2% positive predictive value (99.5% specificity, 77.6% sensitivity) in classifying easy AD subjects in ADNI1. These performance scores were estimated by cross-validation of the entire two-stage process (training of SVM, estimation of hit probability, identification of HPS). However, the hyperparameters of the two-stage model were optimized on classifying pMCI vs sMCI in ADNI1, as described below. We next trained a single model on all of ADNI1, which we applied on a independent sample (ADNI2). The ADNI1 AD VCOG HPS model reached 98.6% positive predictive value (99.5% specificity, 79.5% sensitivity) on ADNI2. As was previously observed with the conventional SVM analysis, the VCOG HPS model had similar performance to the COG HPS model (ADNI1: 100% positive predictive value, 100% specificity, 87.3% sensitivity; ADNI2: 98.7% positive predictive value, 99.5% specificity, 88.6% sensitivity), and outperformed the VBM HPS model (ADNI1: 92.3% positive predictive value, 96.1% specificity, 54.6% sensitivity; ADNI2: 65.2% positive predictive value, 91.5% specificity, 33.3% sensitivity), see Figure 2a. When adjusted to the same baseline rate of AD subjects as ADNI1, the positive predictive values in ADNI2 were 99.2%, 99.3%, and 76.7% for the VCOG, COG, and VBM HPS models respectively.

The HPS models consistently outperformed the base SVM classifiers with respect to specificity ($p < 0.001$) in the classifications of AD vs CN and pMCI vs sMCI in both ADNI1 and ADNI2, regardless of the features that the models contained. The HPS also had greater positive predictive value ($p < 0.05$) adjusted for a typical prevalence of 33.6% pMCI in a given sample of MCI subjects (***Mitchell and Shiri-Feshki, 2009***). However, these increases in specificity and positive predictive value for the HPS model came at a significant cost of reduced sensitivity compared to the base classifier, across all models in both ADNI1 and ADNI2 ($p < 0.05$) (Figure 2). Note that this shift towards lower sensitivity and higher specificity and positive predictive value could be achieved by adjusting the threshold of the SVM analysis (see ROC analysis, Figure 3 in supplementary material), and is not unique to the two-stage procedure we implemented.

## High confidence prediction of progression to AD dementia

We next assessed whether the HPS AD model trained on ADNI1 could be used to predict pMCI from sMCI (within three years of follow-up). We applied the AD HPS model trained on ADNI1 on 235 subjects within the ADNI1 MCI sample. We stratified the MCI patients into three categories: negative individuals were classified as controls by the baseline SVM model, HPS+ individuals were identified as patients by the AD HPS model, and non-HPS+ individuals were identified as patients by the baseline SVM model, but not by the AD HPS model. When using the full VCOG features, 87 MCI patients were selected as HPS+ in ADNI1, out of which 81 (93.1% positive predictive value) were

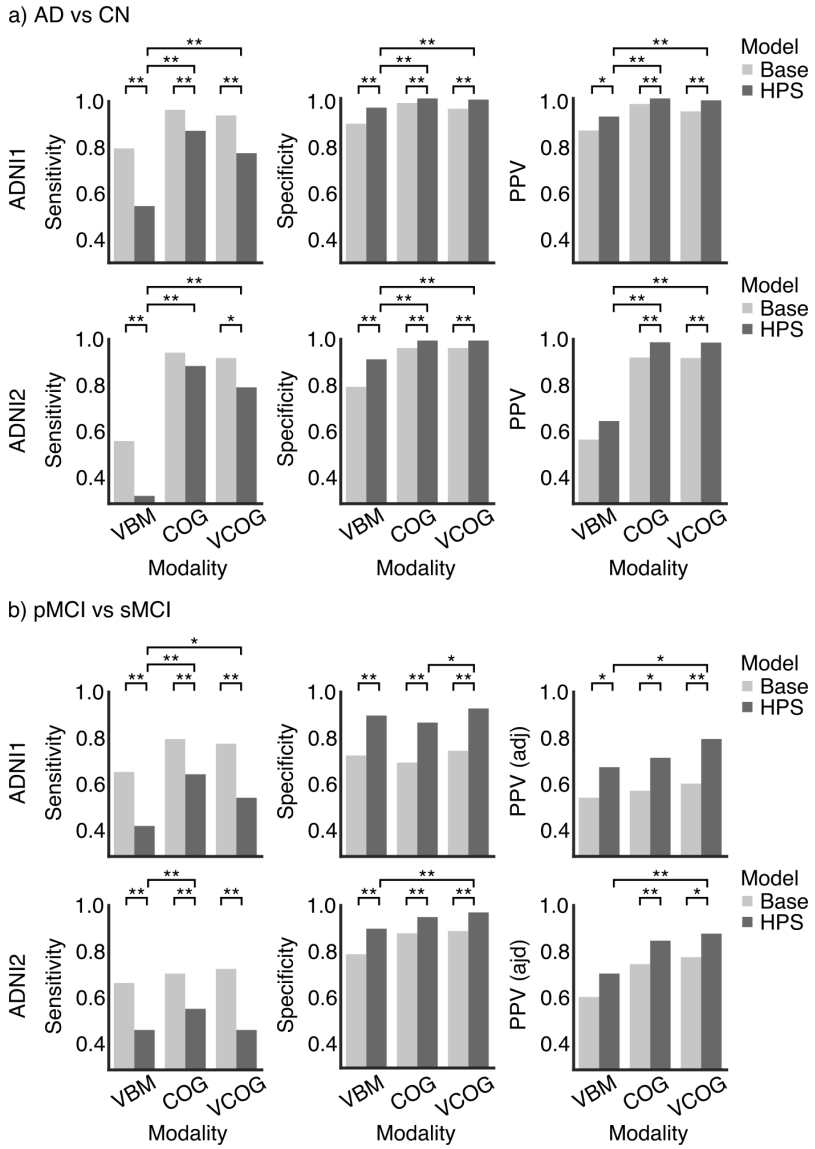


**Figure 2.** Specificity, sensitivity, and positive predictive value (PPV) for the base SVM and highly predictive signature (HPS) classifiers in the classifications of a) patients with AD dementia (AD) and cognitively normal individuals (CN) and b) patients with mild cognitive impairment who progress to AD (pMCI) and stable MCI (sMCI) in ADNI1 and ADNI2. VBM represents the model trained with VBM subtypes, COG represents the model trained with baseline cognitive scores, and VCOG represents the model trained with both VBM subtypes and cognition. Significant differences are denoted by $*$ for $p < 0.05$ and $**$ for $p < 0.001$). Positive predictive value was adjusted (PPV (adj)) for a prevalence of 33.6% pMCI in a sample of MCI subjects for both ADNI1 and ADNI2 MCI cohorts.

pMCI within 36 months follow-up. This represented a large, significant increase over the baseline rate of progressors in the entire ADNI1 MCI sample (37.4%) ($p < 0.001$). This was also a significant increase over the SVM's predictions, where 83.9% of subjects that it had labeled as hits were true progressors ($p < 0.001$). When adjusted to a 33.6% baseline rate of progressors, more typical of MCI populations, the positive predictive value of HPS+ for prognosis of dementia was 80.4% (93.2% specificity, 55.1% sensitivity).

We replicated these analyses in the MCI sample from ADNI2. Using VCOG features, 32 subjects were identified as HPS+, 26 of which progressed to AD dementia within 36 months follow-up (81.2% positive predictive value, specificity of 96.7%, sensitivity of 47.3%, 87.8% positive predictive value adjusted to a 33.6% baseline rate). This represented a significantly higher prevalence than the 30.6% baseline rate in the entire ADNI2 MCI cohort ($p < 0.001$). This was also a significant increase over the SVM's predictions, where 67.8% of subjects it had labeled as hits were true progressors ($p < 0.001$). As expected, the HPS+ model had lower sensitivity and higher specificity/positive predictive value than the baseline model, both in ADNI1 and ADNI2, and for all three feature sets (VBM, COG and VCOG), see Figure 2b. The VCOG features also lead to higher positive predictive value than VBM and COG features taken independently, both in ADNI1 and ADNI2. That increase was large and significant between VCOG and VBM (up to 17%) and marginal and non-significant between VCOG and COG (up to 8%), see Figure 2b.

## Characteristics of MCI subjects with a highly predictive VCOG signature of AD

HPS+ MCI subjects with the VCOG signature were more likely to be progressors (Figure 3a) compared to non-HPS+ subjects and negative subjects (ADNI1: $p < 0.001$; ADNI2: $p < 0.001$). HPS+ MCI subjects were also more likely to be APOE4 carriers (Figure 3b) (ADNI1: $p < 0.005$; ADNI2: $p < 0.05$). There was no difference in sex across the HPS groupings in the MCI subjects of either the ADNI1 or ADNI2 cohorts (Figure 3c). This was consistent with the whole sample, where there were equal proportions of progressors across both sexes in each dataset (ADNI1: $\chi^2 = 0.015, p = 0.90$; ADNI2: $\chi^2 = 0.0002, p = 0.99$). The HPS+ class was also significantly enriched for A$\beta$-positive subjects in ADNI1 ($p < 0.05$). However, this result was not replicated in the ADNI2 MCI subjects (Figure 3d). Similarly with tau, we found a significant increase in tau-positive subjects in the HPS+ group of ADNI1 ($p < 0.05$), but not in ADNI2 (Figure 3e). We found a significant age difference across the HPS classes in ADNI2 ($F = 5.68, p < 0.005$), where the HPS+ subjects were older than the Negative subjects by a mean of 4.4 years. However, age did not differ across the HPS classes in ADNI1 (Figure 3f). Finally, HPS+ subjects had significantly steeper cognitive declines compared to the Non-HPS+ and Negative groups (Figure 3g): there were significant interactions between the HPS groupings and time in ADNI1: (HPS+ $\beta = -0.147, t = -7.56, p < 0.001$, Non-HPS+ $\beta = -0.055, t = -2.46, p < 0.05$) and ADNI2 (HPS+ $\beta = -0.194, t = -8.69, p < 0.001$, Non-HPS+ $\beta = -0.072, t = -3.31, p = 0.001$). The HPS+ in ADNI1 and ADNI2 respectively gained 1.8 and 2.3 more points each year on the ADAS13 compared to the Non-HPS+ and Negative groups. Note that higher scores on the Alzheimer's Disease Assessment Scale - Cognitive subscale (13 items) (ADAS13) represent worse cognitive function.

## COG, VBM and VCOG signatures

The COG signature was mainly driven by scores from the ADAS13, which measures overall cognition, ADNI-MEM, a composite score that measures memory (***Crane et al., 2012***), and ADNI-EF, a composite score that measures executive function (***Gibbons et al., 2012***) (coefficients were 5.49, -4.80 and -2.50 respectively). In this model, sex, age, mean GMV, and TIV contributed very little, relative to the cognitive features (Figure 4b). Note that these coefficients should be interpreted as pseudo z-scores as the features had been normalized to zero mean and unit variance.

Almost all grey matter subtypes contributed to the VBM signature. Mean GMV, subtype 1 and subtype 6 had the highest weights in the model (coefficients were -5.07, 4.87, and 3.98 respectively) (Figure 4c). Subtype 1 was characterized by reduced relative GMV in the occipital, parietal and posterior temporal lobes. Subtype 6 was characterized by reduced relative GMV in the temporal

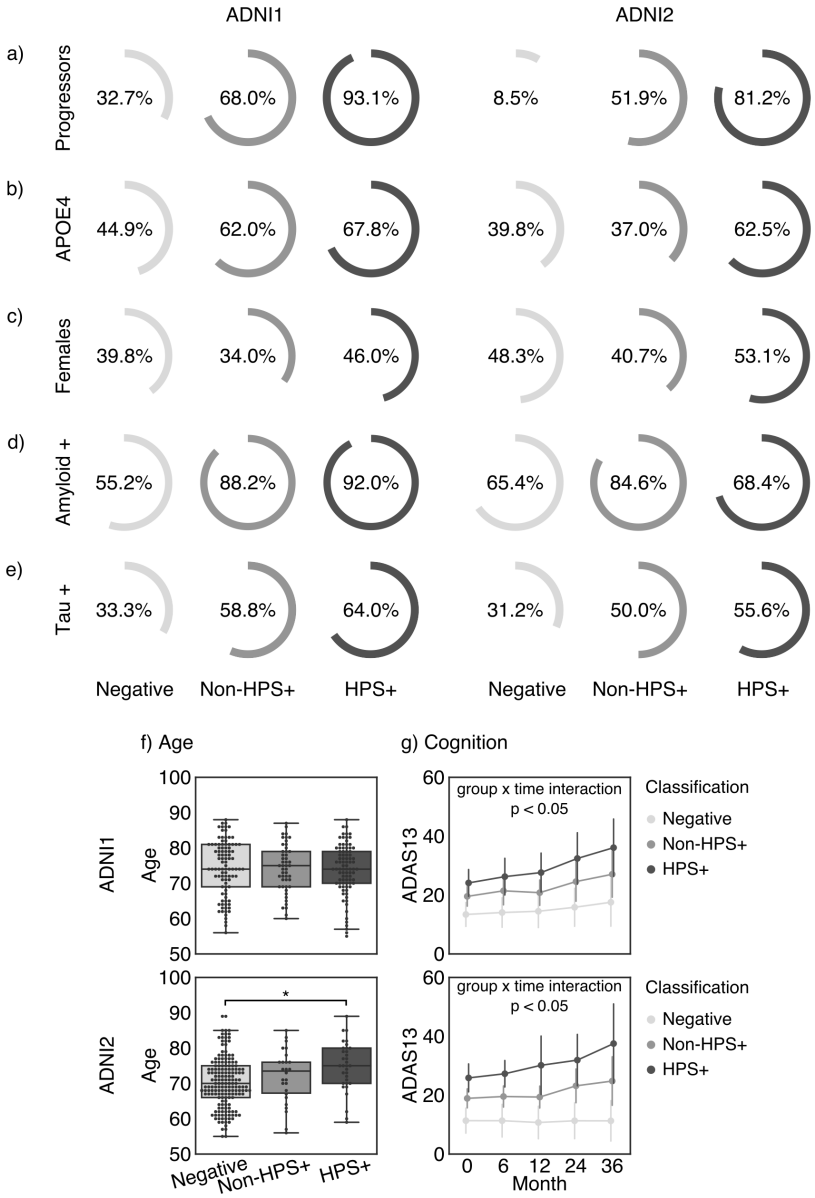


**Figure 3.** Characteristics of MCI subjects with the VCOG signature in ADNI1 and ADNI2. We show the percentage of MCI subjects who a) progressed to dementia, were b) APOE4 carriers, c) female, d) positive for A$\beta$ measured by a cut-off of 192 pg/mL in the CSF (***Shaw et al., 2009***), and e) positive for tau measured by a cut-off of 93 pg/mL in the CSF (***Shaw et al., 2009***) in each classification (HPS+, Non-HPS+, and Negative). f) Age and g) cognitive trajectories, measured by the Alzheimer's Disease Assessment Scale - Cognitive subscale with 13 items (ADAS13), across the three classes. Significant differences are denoted by $*$ for family-wise error rate-corrected $p < 0.05$.

lobes, notably the medial temporal regions. We had anticipated the larger contribution of these two subtypes as they have been described in previous AD subtyping work (***Noh et al., 2014***; ***Hwang et al., 2016***; ***Park et al., 2017***; ***Varol et al., 2017***). Diagnosis (CN, sMCI, pMCI, AD) accounted for a substantial amount of variance in these subtype weights (subtype 1: $F = 8.51, p < 0.001$; subtype 2: $F = 34.27, p < 0.001$). Post-hoc t-tests showed AD subjects had significantly higher weights compared to CN (Figure 1e), making these subtypes associated with a diagnosis of AD (subtype 1: $t = 2.88, p < 0.05$; subtype 6: $t = 7.68, p < 0.001$).

The ADAS13, memory (ADNI-MEM) and executive function (ADNI-EF) scores contributed the most to the VCOG HPS signature (coefficients were 6.27, -7.43 and -3.95 respectively, Figure 4a). Of the VBM features, subtypes 2, 3 and 7 contributed the most to the signature (coefficients were 1.36, -2.12 and -2.83 respectively). Subtypes 1 and 6, which had the highest positive weights in the VBM model, were given marginal weights in the VCOG model, which is potentially indicative of redundancy with COG features. Subtype 2, which was associated with AD, was characterized by greater relative GMV in medial parts of the parietal and occipital lobes and the cingulate cortex, but less GMV everywhere else. Subtype 3 was characterized by greater relative GMV in the temporal lobes, insula and striatum. Subtype 7, which was associated with healthy controls, was characterized by greater relative GMV in the parietal, occipital and temporal lobes. Note that the weights for subtypes 3 and 7 were negative in the model, which means that predicted AD and pMCI cases had brain atrophy patterns that were spatially dissimilar to those subtypes.

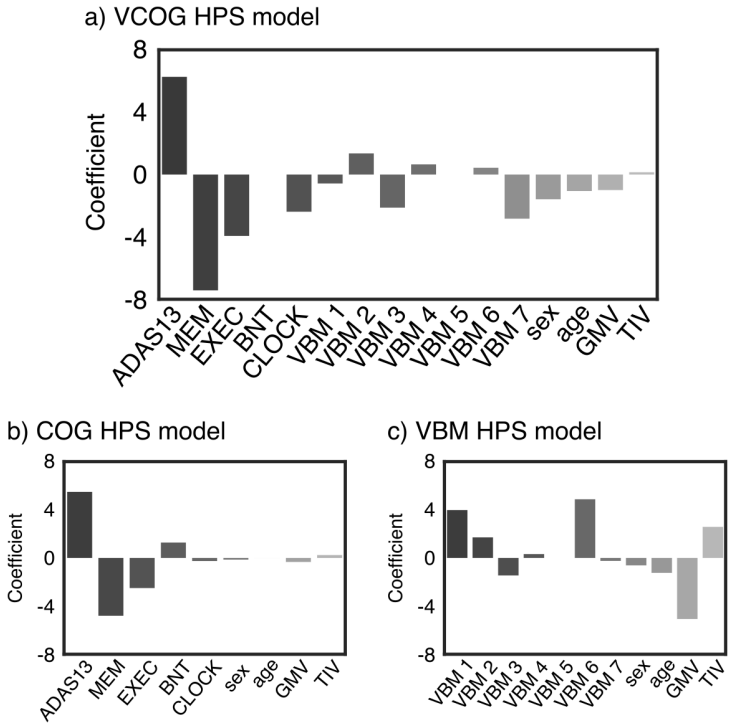


**Figure 4.** Coefficients of the high confidence prediction a) VCOG model, b) COG model, and c) VBM model. ADAS13 = Alzheimer's Disease Assessment Scale - Cognitive, MEM = ADNI-MEM score; EXEC = ADNI-EF score, BNT = Boston Naming Test, CLOCK = clock drawing test, VBM 1-7 = VBM subtype weights, GMV = mean grey matter volume, TIV = total intracranial volume.

## Discussion

We developed a highly precise and specific MRI and cognitive-based model to predict AD dementia. Our two-stage predictive model reached 93.2% specificity and 93.1% positive predictive value

(80.4% when adjusted for 33.6% prevalence of progressors) in ADNI1 when classifying progressor vs stable MCI patients (within 3 years follow-up). We replicated these results in ADNI2 where the model reached 96.7% specificity and 81.2% positive predictive value (87.8% adjusted positive predictive value). With respect to specificity and positive predictive value, these results are a substantial improvement over previous works combining structural MRI and cognition on the same prediction task, that have reported up to 76% specificity and 65% positive predictive value (adjusted for 33.6% prevalence of progressors) (***Korolev et al., 2017***). We also report the highest positive predictive value compared to the current state-of-the-art predictive model using A$\beta$ PET scans, which reported 74% (adjusted) positive predictive value (***Mathotaarachchi et al., 2017***). Finally, our results also reproduced our past work which developed a model that optimizes specificity and positive predictive value (***Dansereau et al., 2017***). Our performance is close to the 90% positive predictive value reported by ***Dansereau et al.*** (***2017***) using a combination of structural and functional MRI measures and a two-stage predictive model, with the limitation of a smaller sample size (N=56 MCI patients) due to limited availability of functional MRI data in ADNI.

An ideal model to predict conversion to AD dementia would have both high sensitivity and high specificity, meaning it would be able to detect all progressor MCI and reject all stable MCI individuals. However, there is a balance between sensitivity and specificity that should be considered depending on the context. In the case of progression to AD dementia, the pathophysiological heterogeneity of clinical diagnosis will prevent highly accurate prediction linking brain features to clinical trajectories. We argue that, faced with heterogeneity, it is necessary to sacrifice sensitivity to focus on a subgroup of individuals with similar brain abnormalities. In a predictive model, one needs to choose a threshold to control the proportions of false positives and false negatives. A receiver operating characteristic (ROC) curve illustrates the trade off between the true positive and false positive rates as the threshold for positivity changes and is often used to determine an optimal threshold. Generally, increasing the threshold leads to higher specificity and lower sensitivity. The high specificity of our two-stage model indeed came at a cost of reduced sensitivity (55.1% in ADNI1 and 47.3% in ADNI2 for classifying pMCI vs sMCI), which is much lower than sensitivity values of 64%-95% reported by other groups (***Dansereau et al., 2017***). The two stage procedure, based on prediction stability, did not offer gains compared to a simpler SVM model, if the threshold of the SVM model could be selected *a priori* to match the specificity of the two stage procedure (see ROC curves in Figure 3 in supplementary material). The two-stage prediction model offered the advantage of a principled approach to train the prediction model in a high-specificity regime, based on stability. The choice of a L1 regularized logistic regression also lead to a compact and interpretable subset of features for the HPS.

Favoring specificity over sensitivity could be useful in settings where false positives need to be minimized and positive predictive value needs to be high, such as expensive clinical trials. Here, with our HPS VCOG model, we report the high positive predictive values for progression to AD from the MCI stage (up to 87.8%, adjusted for 33.6% prevalence of progressors). Importantly, the proposed HPS+ model used tools that are already widely used by clinicians. The present work could be used as a screening tool for recruitment in clinical trials that target MCI subjects who are likely to progress to dementia within three years. The implementation of an automated selection algorithm could also result in groups of MCI subjects with more homogeneous brain pathology. However, we note that HPS+ subjects did not all present with significant amyloid burden (92.0% and 68.4% of HPS+ subjects in ADNI1 and ADNI2 respectively, Figure 3), which means that not all HPS+ individuals are likely to have prodromal AD, even when progressing to AD dementia.

When we trained our model with cognitive features only, tests for general cognition, memory, and executive function were chosen as the strongest predictors of AD dementia. Our COG HPS model thus supports previous research that reported general cognition, memory, and executive function as important neuropsychological predictors of dementia (***Dickerson et al., 2007***; ***Belleville et al., 2017***; ***Tabert et al., 2006***; ***Korolev et al., 2016***). Compared to the state-of-the-art multi-domain cognition-based predictive model, which reported 87.1% specificity and 81.8% positive predictive

value (77.5% when adjusted to 33.6% pMCI prevalence) (***Belleville et al., 2014***), our COG HPS model achieved similar performance reaching between 87.5%-95% specificity and 72.3%-85.1% (adjusted) positive predictive value. As general cognition was the strongest feature in our model to predict progression, this supports previous findings that MCI patients with deficits across multiple domains are at the highest risk for dementia (***Tabert et al., 2006***; ***Mitchell et al., 2009***).

For our VBM model, we extracted a number of gray matter atrophy subtypes that recapitulated previously reported subtypes, namely the medial temporal lobe and parietal dominant subtypes (***Noh et al., 2014***; ***Hwang et al., 2016***; ***Park et al., 2017***; ***Varol et al., 2017***), which were associated strongly with a diagnosis of AD dementia. Weights for the parietal dominant and medial temporal lobe subtypes (Subtypes 1 and 6 from Figure1b, respectively) contributed substantially to the highly predictive signature in the VBM model. The atrophy pattern of subtype 6 is spatially similar to the spread of neurofibrillary tangles in Braak stages III and IV (***Braak and Braak, 1991***), which may support previous findings that tau aggregation mediates neurodegeneration (***Spillantini and Goedert, 2013***). The contributions of the parietal dominant and medial temporal lobe subtypes in the VBM model are also in line with previous works, which have reported that cortical thickness and volumes of the medial temporal lobes, inferior parietal cortex, and precuneus are strong predictors of progression to dementia (***Korolev et al., 2017***; ***Eskildsen et al., 2013***).

When combined with cognitive tests in the VCOG model, the structural subtypes were given marginal weights. This suggests some redundancy between atrophy and cognition, and that cognitive features have higher predictive power than structural features in the ADNI MCI sample. This conclusion is consistent with the observation that the COG model significantly outperformed the VBM model, similar to previous work (***Korolev et al., 2017***). Although cognitive markers were stronger features, the VCOG model assigned large negative weights for the structural subtypes 3, which showed greater relative GMV in the temporal lobes, and 7, which showed greater relative GMV in the parietal, occipital, and temporal lobes. This means that these features were predictive of stable MCI in the VCOG model, in line with previous work showing that atrophy in these regions is predictive of progression to dementia (***Korolev et al., 2017***; ***Eskildsen et al., 2013***). Furthermore, we demonstrated that combining MRI data with cognitive markers significantly improves upon a model based on MRI features alone. This result is again in line with the literature (***Korolev et al., 2016***; ***Moradi et al., 2015***), yet was shown for the first time for a model specifically trained for high positive predictive value. Note that in the current study, the predictive model was trained exclusively on images acquired on 1.5T scanners from ADNI1. Good generalization to ADNI2 with 3T scanners demonstrates robustness of imaging structural subtypes across scanner makes.

While the VCOG model identified the majority of MCI subjects who were highly likely to progress to dementia, there were sizable groups of subjects who were uniquely identified as progressors by the unimodal signatures. For example, out of all the MCI subjects that were picked up by the three HPS models, 12.9% and 35.3% of subjects from ADNI1 and ADNI2 respectively were identified as progressors exclusively by the VBM HPS model (Supplementary Figure 5). Although these subjects presented an AD-like brain atrophy pattern, they may exert compensatory mechanisms or have a high cognitive reserve that may allow them to maintain a higher level of cognitive function than subjects who were also selected by the COG signature. Out of all the HPS+ MCI subjects across the three models, the COG HPS model also exclusively labeled 20.4% and 10.8% of subjects from ADNI1 and ADNI2 respectively as progressors (Supplementary Figure 5). As these subjects were not labeled by the VBM model, they may represent subjects who have patterns of neurodegeneration that are atypical of AD or subjects who have a non-AD pathology. Structural MRI and cognition therefore provide complementary information about AD risk, and it appears that brain atrophy can add to the predictive value of cognitive markers. Our results converge with clinical practices that utilize both neuropsychological testing and brain imaging to inform diagnosis and prognosis, although our approach has the added benefits of being data-driven, automated and optimized for high positive predictive value.

The VCOG highly predictive signature might reflect a late disease stage. We looked at the ratio of

early to late MCI subjects in the ADNI2 sample (note that ADNI1 did not have early MCI subjects). Of the MCI subjects identified as HPS+ by the VCOG model, 84.4% were late MCI subjects, compared to a rate of 34.9% of late MCI subjects in the entire ADNI2 MCI sample (Supplementary Figure 2). In both ADNI1 and ADNI2, the VCOG HPS+ subjects had on average the worst baseline cognition and the worst cognitive decline over time (see Figure 3g and Supplementary Figure 1). The HPS+ subjects in ADNI1 also had significantly greater amounts of A$\beta$ and tau pathology compared to the whole sample, although these findings were not replicated in ADNI2 (Figure 3d,e). Given that the majority of HPS+ subjects were late MCI subjects and had worse cognition, the two-stage predictive model appears to be effective at identifying individuals at later disease stages who are at the cusp of progressing to dementia. This result is to be expected since the model was built on cognitive variables that are designed to separate cognitively normal and individuals with dementia at certain cut-offs. This approach may not be optimal for early detection of future cognitive decline. Training a model to classify MCI progressors and non-progressors to dementia could be done in order to capture future progressors in earlier preclinical stages (e.g. early MCI). Finally, we focused on structural MRI and neuropsychological batteries as features in our models due to their wide availability and established status as clinical tools. However, we believe adding other modalities such as PET imaging, CSF markers, functional MRI, genetic factors, or lifestyle factors could result in higher predictive power, especially at earlier preclinical stages of AD.

## Conclusion

In summary, we developed a highly precise and specific model to predict progression from MCI to AD dementia within a time span of three years. Using structural MRI and neuropsychological markers, we trained a model to recognize an anatomical and cognitive signature that is highly predictive of AD dementia by learning the difference between AD patients and controls. We validated the model in three independent samples, a second sample of AD patients and controls, and two separate cohorts that contained both stable MCI patients and MCI patients who progressed to dementia. The model was able to predict progression to dementia in MCI patients with up to 93.1% positive predictive value and up to 96.7% specificity. Our model could potentially improve subject selection in clinical trials and identify individuals at a higher risk of AD dementia for early intervention in clinical settings.

## Methods and Materials

### Data

Data used in the preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu). The ADNI was launched in 2003 as a public-private partnership, led by Principal Investigator Michael W. Weiner, MD. The primary goal of ADNI has been to test whether serial 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 Alzheimer's disease (AD). For up-to-date information, see www.adni-info.org. We took baseline T1-weighted MRI scans from the ADNI1 (228 CN, 397 MCI, 192 AD) and ADNI2 (218 CN, 354 MCI, 103 AD) studies. For a detailed description of MRI acquisition details, see http://adni.loni.usc.edu/methods/documents/mri-protocols/. All subjects gave informed consent to participate in these studies, which were approved by the research ethics committees of the institutions involved in data acquisition. Consent was obtained for data sharing and secondary analysis, the latter being approved by the ethics committee at the CRIUGM. For the MCI groups, each individual must have had at least 36 months of follow-up for inclusion in our analysis. We also further stratified the MCI groups into stable (sMCI), who never received any change in their diagnosis, and progressors (pMCI), who received a diagnosis of AD dementia within 36 months of follow-up. pMCI who progressed to AD dementia after 36 months were excluded. After applying these inclusion/exclusion criteria, we were left with 280 and 268 eligible MCI subjects

**Table 1.** Demographic information for post-QC subjects in ADNI1 and ADNI2.

| ADNI1 | CN | sMCI | pMCI | AD |
|---|---|---|---|---|
| **N** | 205 | 89 | 155 | 172 |
| **Age ± SD** | 76.1 ± 5.0 | 73.9 ± 7.6 | 74.2 ± 7.1 | 75.3 ± 7.5 |
| **Female %** | 51.7 | 40.4 | 41.9 | 50.0 |
| **APOE4+ %** | 27.8 | 37.1 | 68.4 | 66.3 |
| **ADAS13 ± SD** | 9.5 ± 4.3 | 14.4 ± 5.5 | 21.3 ± 5.2 | 28.7 ± 7.1 |
| **MMSE ± SD** | 29.1 ± 1.0 | 27.7 ± 1.7 | 26.7 ± 1.7 | 23.4 ± 2.0 |
| **ADNI2** | **CN** | **sMCI** | **pMCI** | **AD** |
| **N** | 188 | 182 | 55 | 90 |
| **Age ± SD** | 72.8 ± 6.1 | 70.8 ± 7.3 | 72.1 ± 7.1 | 74.6 ± 7.9 |
| **Female %** | 54.0 | 47.3 | 49.1 | 45.6 |
| **APOE4+ %** | 29.4 | 36.3 | 65.4 | 70.4 |
| **ADAS13 ± SD** | 9.1 ± 4.2 | 11.8 ± 5.3 | 21.4 ± 6.5 | 31.9 ± 8.7 |
| **MMSE ± SD** | 29.1 ± 1.1 | 28.4 ± 1.5 | 27.3 ± 1.9 | 23.1 ± 2.3 |

ADAS13 = Alzheimer's Disease Assessment Scale - Cognitive subscale (13 items); MMSE = Mini Mental State Examination

in ADNI1 and ADNI2 respectively.

## Structural features from voxel-based morphometry

Images were processed and analyzed with the NeuroImaging Analysis Kit (NIAK) version 0.18.1 (https://hub.docker.com/r/simexp/niak-boss/), the MINC toolkit (http://bic-mni.github.io/) version 0.3.18, and SPM12 (http://www.fil.ion.ucl.ac.uk/spm/software/spm12/) under CentOS with Octave (http://gnu.octave.org) version 4.0.2. Preprocessing of MRI data was executed in parallel on the Cedar supercomputer (https://docs.computecanada.ca/wiki/Cedar), using the pipeline system for Octave and Matlab - PSOM (***Bellec et al., 2012***). Each T1 image was linearly co-registered to the Montreal Neurological Institute (MNI) ICBM152 stereotaxic symmetric template (***Fonov et al., 2011***), using the CIVET pipeline (***Ad-Dab'bagh et al., 2006***), and then re-oriented to the AC-PC line. Each image was segmented into grey matter, white matter, and CSF probabilistic maps. The DARTEL toolbox (***Ashburner, 2007***) was used to normalize the grey matter segmentations to a predefined grey matter template in MNI152 space. Each map was modulated to preserve the total amount of signal and smoothed with with a 8 mm isotropic Gaussian blurring kernel. After quality control of the normalized grey matter segmentations, we were left with 621 subjects in ADNI1 (out of 700, 88.7% success rate) and 515 subjects in ADNI2 (out of 589, 87.4% success rate). See Table 1 for demographic information of post-QC subjects.

We extracted subtypes to characterize variability of grey matter distribution with the CN and AD samples from ADNI1. In order to reduce the impact of factors of no interest that may have influenced the clustering procedure, we regressed out age, sex, mean grey matter volume (GMV), and total intracranial volume (TIV), using a mass univariate linear regression model at each voxel. We then derived a spatial Pearson's correlation coefficient between all pairs of individual maps after confound regression. This defined a subject x subject (377 x 377) similarity matrix which was entered into a Ward hierarchical clustering procedure (Figure 1a). Based on visual inspection of the similarity matrix, we identified 7 subgroups (Figure 1b). Each subtype was defined as the average map of each subgroup. For each subject, we computed spatial correlations between their map and each subtype, which we call weights (Figure 1a). The weights formed a $n$ subject x $n$ subtypes matrix, which was included in the feature space for all predictive models including VBM throughout this work.

## Cognitive features

We took baseline neuropsychological scores for each subject from several cognitive domains: memory from the composite score ADNI-MEM (***Crane et al., 2012***), executive function from the composite score ADNI-EF (***Gibbons et al., 2012***), language from the Boston Naming Test (BNT), visuospatial from the clock drawing test, and global cognition from the Alzheimer's Disease Assessment Scale-Cognitive (ADAS13). We chose measures that span multiple cognitive domains as it has been suggested that the use of a combination of neuropsychological measures is likely the best approach to predicting incipient dementia (***Belleville et al., 2017***). These scores were included as features for the predictive models involving cognition.

## Prediction of easy AD dementia cases in ADNI1

We trained a SVM model with a linear kernel, as implemented by Scikit-learn (***Pedregosa et al., 2011***) version 0.18 to classify AD vs CN from ADNI1 to get a baseline prediction accuracy. A tenfold cross-validation loop was used to estimate the performance of the trained model. Classes were balanced inversely proportional to class frequencies in the input data for the training. A nested cross-validation loop (stratified shuffle split with 50 splits and 20% test size) was used for the grid search of the hyperparameter $C$ (grid was $10^{-2}$ to $10^{1}$ with 15 equal steps). We randomly selected subsamples of the dataset (retaining 50% of participants in each subsample) to replicate the SVM training 500 times. For each 50% subsample, a separate SVM model was trained to predict AD or CN in ADNI1. Predictions were made on the remaining 50% of the sample that was not used for training. For each subject, we calculated a hit probability defined as the frequency of correct classification across all SVM replications in which the test set contained that subject. Easy AD cases were defined as individuals with 100% hit probabilities with the AD label. Next, we trained a logistic regression classifier (***Fan et al., 2008***), with L1 regularization on the coefficients, to predict the easy AD cases. A stratified shuffle split (500 splits, 50% test size) was used to estimate the performance of the model for the grid search of the hyperparameter $C$ (grid was $10^{-2}$ to $10^{1}$ with 15 equal steps). See (***Dansereau et al., 2017***) for more information about this two-step prediction. We used the whole CN and AD sample from ADNI1 to obtain three highly predictive signatures (HPS), one using VBM subtypes (VBM only), one using cognitive features (COG only), and one using the combination of VBM and cognitive features (VCOG). In all three signatures, age, sex, mean GMV, and TIV were also included as features.

## Prediction of progression to AD dementia from the MCI stage in ADNI1

The logistic regression trained on AD vs CN was used to identify MCI patients who have a HPS of AD dementia in ADNI1. We re-trained our models on AD vs CN after optimizing our hyperparameters (resampling size and resampling ratio) in order to maximize specificity and positive predictive value while keeping a minimum of 30% sensitivity for our classification of sMCI (n=89) vs pMCI (n=155) in ADNI1. This was done for all three signatures. In brief, we used the AD and CN sample from ADNI1 as a training set, the MCI subjects from ADNI1 as a validation set, and ADNI2 served as our test set.

## Statistical test of differences in model performance

We used Monte-Carlo simulations to generate confidence intervals on the performance (i.e. positive predictive value, specificity and sensitivity) of both base SVM and HPS models for their predictions of AD vs CN and pMCI vs sMCI. Taking the observed sensitivity and specificity, and using similar sample sizes to our experiment, we replicated the number of true and false positive detection 100000 times using independent Bernoulli variables, and derived replications of positive predictive value, specificity and sensitivity. By comparing these replications to the sensitivity, specificity and positive predictive value observed in both models, we estimated a p-value for differences in model performance (***Phipson and Smyth, 2010***). A p-value smaller than 0.05 was interpreted as evidence of a significant difference in performance, and 0.001 as strong evidence. We also used this approach to compare the performance of the combined features (VCOG) to the models containing VBM

features or cognitive features only. Note that, based on our hypotheses regarding the behaviour of the HPS model, the tests were one-sided for increased specificity and positive predictive value, and one-sided for decreased sensitivity.

### Statistical tests of association of progression, AD biomarkers, and risk factors in HPS+ MCI subjects

Based on the classifications resulting from the base SVM and HPS models, we separated the MCI subjects into three different groups: 1) HPS+, subjects who were selected by the HPS model as hits, 2) Non-HPS+, subjects who were selected by the base SVM model as hits but were not selected by the HPS model, and 3) Negative, subjects who were not selected as hits by either algorithm.

We tested statistically if the HPS+ subgroup was enriched for progression to dementia, APOE4 carriers, females, and subjects who were positive for A$\beta$ and tau pathology. Positivity of AD pathology was determined by CSF measurements of A$\beta$ 1-42 peptide and total tau with cut-off values of less than 192 pg/mL and greater than 93 pg/mL respectively (***Shaw et al., 2009***). We implemented Monte-Carlo simulations, where we selected 100000 random subgroups out of the original MCI sample. By comparing the proportion of progressors, APOE4 carriers, females, A$\beta$-positive, and tau-positive subjects in these null replications to the actual observed values in the HPS subgroup, we estimated a p-value (***Phipson and Smyth, 2010***) (one sided for increase). A p-value smaller than 0.05 was interpreted as evidence of a significant enrichment, and 0.001 as strong evidence.

One-way ANOVAs were used to evaluate differences between the HPS groupings with respect to age. Post-hoc Tukey's HSD tests were done to assess pairwise differences among the three classes (HPS+, Non-HPS+, Negative). These tests were implemented in Python with the SciPy library (***Jones et al., 2001***) version 0.19.1 and StatsModels library (***Seabold and Perktold, 2010***) version 0.8.0.

To explore the impact of HPS grouping on cognitive trajectories, linear mixed effects models were performed to evaluate the main effects of and interactions between the HPS groups and time on ADAS13 scores up to 36 months of follow-up. The models were first fit with a random effect of participant and then were fit with random slopes (time | participant) if ANOVAs comparing the likelihood ratio suggested a significant improvement in model fit. All tests were performed separately on the ADNI1 and ADNI2 datasets. These tests were implemented in R version 3.3.2 with the library nlme version 3.1.128 (***Pinheiro et al., 2018***).

### Public code and data

The code used in this experiment is available on a Github repository: https://github.com/SIMEXP/vcog_hps_ad.

## Acknowledgments

We would like to thank Sylvia Villeneuve, Alexa Pichet-Binette and Jacob Vogel for providing us with data to help start our preliminary analyses for this project. We would like to thank Hien Nguyen for advising us on parts of the statistical analyses.

Data collection and sharing for this project was funded by the Alzheimer's Disease Neuroimaging Initiative (ADNI) (National Institutes of Health Grant U01 AG024904) and DOD ADNI (Department of Defense award number W81XWH-12-2-0012). ADNI is funded by the National Institute on Aging, the National Institute of Biomedical Imaging and Bioengineering, and through generous contributions from the following: AbbVie, Alzheimer's Association; Alzheimer's Drug Discovery Foundation; Araclon Biotech; BioClinica, Inc.; Biogen; Bristol-Myers Squibb Company; CereSpir, Inc.; Cogstate; Eisai Inc.; Elan Pharmaceuticals, Inc.; Eli Lilly and Company; EuroImmun; F. Hoffmann-La Roche Ltd and its affiliated company Genentech, Inc.; Fujirebio; GE Healthcare; IXICO Ltd.; Janssen Alzheimer Immunotherapy Research & Development, LLC.; Johnson & Johnson Pharmaceutical Research & Development LLC.; Lumosity; Lundbeck; Merck & Co., Inc.; Meso Scale Diagnostics,

LLC.; NeuroRx Research; Neurotrack Technologies; Novartis Pharmaceuticals Corporation; Pfizer Inc.; Piramal Imaging; Servier; Takeda Pharmaceutical Company; and Transition Therapeutics. The Canadian Institutes of Health Research is providing funds to support ADNI clinical sites in Canada. Private sector contributions are facilitated by the Foundation for the National Institutes of Health (www.fnih.org). The grantee organization is the Northern California Institute for Research and Education, and the study is coordinated by the Alzheimer's Therapeutic Research Institute at the University of Southern California. ADNI data are disseminated by the Laboratory for Neuro Imaging at the University of Southern California.

The computational resources used to perform the data analysis were provided by Compute Canada (www.computecanada.org). This project was funded by NSERC grant number RN000028 and the Canadian Consortium on Neurodegeneration in Aging (CCNA, www.ccna-ccnv.ca), through a grant from the Canadian Institutes of Health Research and funding from several partners including SANOFI-ADVENTIS R&D. AT is supported by a bursary from the Centre de recherche de l'institut universitaire de gériatrie de Montréal and the Courtois foundation. CD is supported by a salary award from the Lemaire foundation and Courtois foundation. PB is supported by a salary award from "Fonds de recherche du Québec – Santé" and the Courtois foundation.

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# Appendix 1

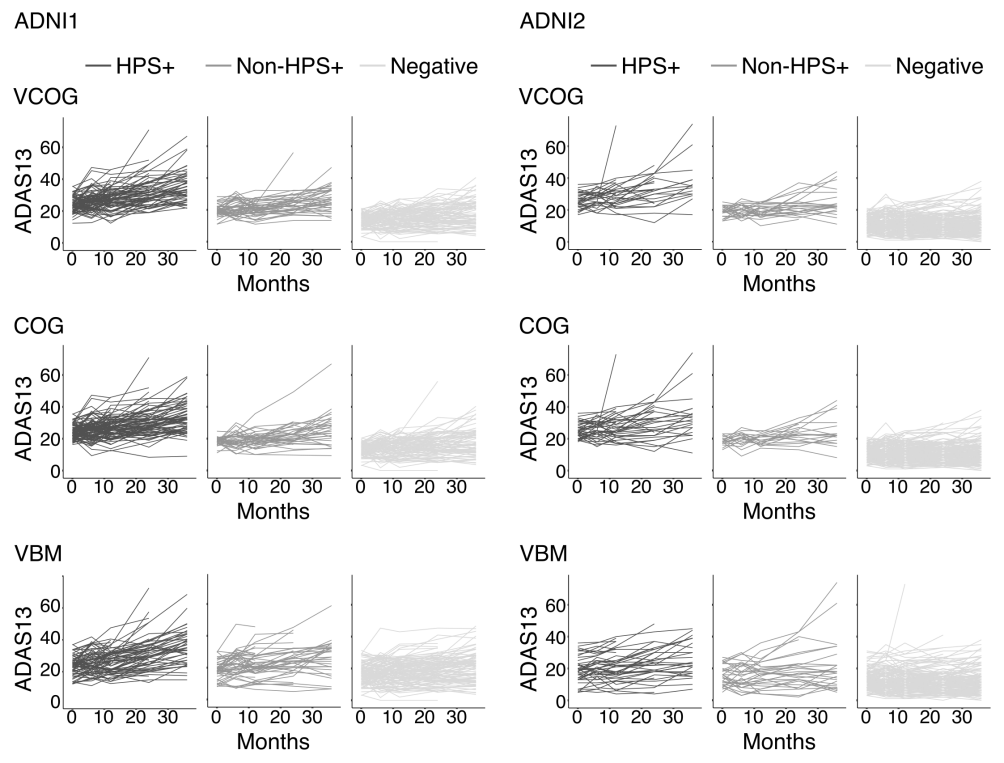
## Supplementary results

### Comparison of COG, VBM and VCOG HPS+ subjects

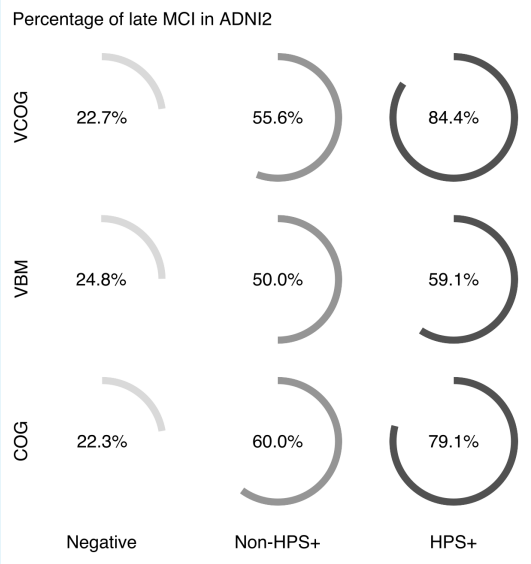
We found substantial overlap of subjects labeled as HPS+ in the MCI cohorts across the VBM, COG and VCOG signatures (Supplementary Figure 5). There were very few subjects that were labeled as HPS+ exclusively by the VCOG signature. As to be expected, the majority of subjects labeled as HPS+ by the VCOG signature (ADNI1: 97.7%; ADNI2: 100%) were also labeled as HPS+ by either the VBM only or COG only signatures or both. Of the subjects that were labeled as HPS+ by the VBM only signature, 23.6% and 55.2% in ADNI1 and ADNI2 respectively were identified exclusively by the VBM HPS. There were relatively few subjects (7 and 2 subjects in ADNI1 and ADNI2 respectively) that were captured by VBM and VCOG but missed by the COG HPS. The COG HPS actually identified the majority of all HPS+ subjects across the three signatures (ADNI1: 106 of 132 total subjects, ADNI2: 40 of 65 total subjects). From Supplementary Figure 5, we can see that the VCOG HPS acts as a refinement of the COG signature, as the VCOG HPS captures a subset of subjects that were labeled by the COG HPS.

Out of the HPS+ subjects labeled by all three signatures, 97.9% and 93.7% from ADNI1 and ADNI2 respectively progressed to dementia (Supplementary Table 1). These subjects had worse cognition based on the MMSE and higher proportions of APOE4 carriers, A$\beta$ positive and tau positive individuals, compared to the baseline rates in all MCI subjects. Of the HPS+ subjects who were labeled only by the VBM model, 70.6% and 43.4% from ADNI1 and ADNI2 respectively were progressors. This group of subjects had less A$\beta$ and tau positive individuals compared to the baseline rates. Of the HPS+ subjects who were labeled only the COG model, 70.4% and 57.1% from ADNI1 and ADNI2 respectively progressed to dementia. This group appeared to have a greater proportion of A$\beta$ positive individuals compared to the baseline rates in both ADNI1 and ADNI2 cohorts. The majority of these COG HPS+ subjects were also male. Given the distinct characteristics among the exclusively COG, exclusively VBM, and VCOG HPS+ subjects, these groups may represent subgroups with different risks for AD dementia. As it appears that a greater proportion of pMCI is captured when cognitive and structural MRI features are combined, these findings may support joining multiple modalities together in order to achieve higher positive predictive value. However, these results are qualitative and of an exploratory nature due to low sample sizes.

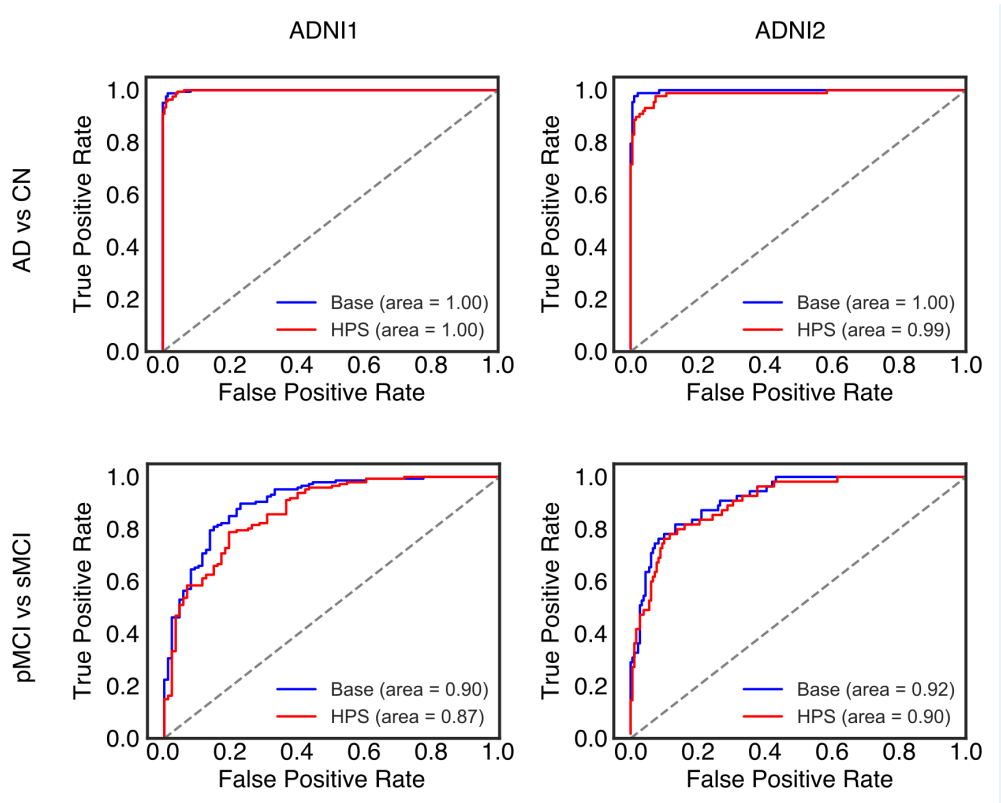
## Supplementary figures



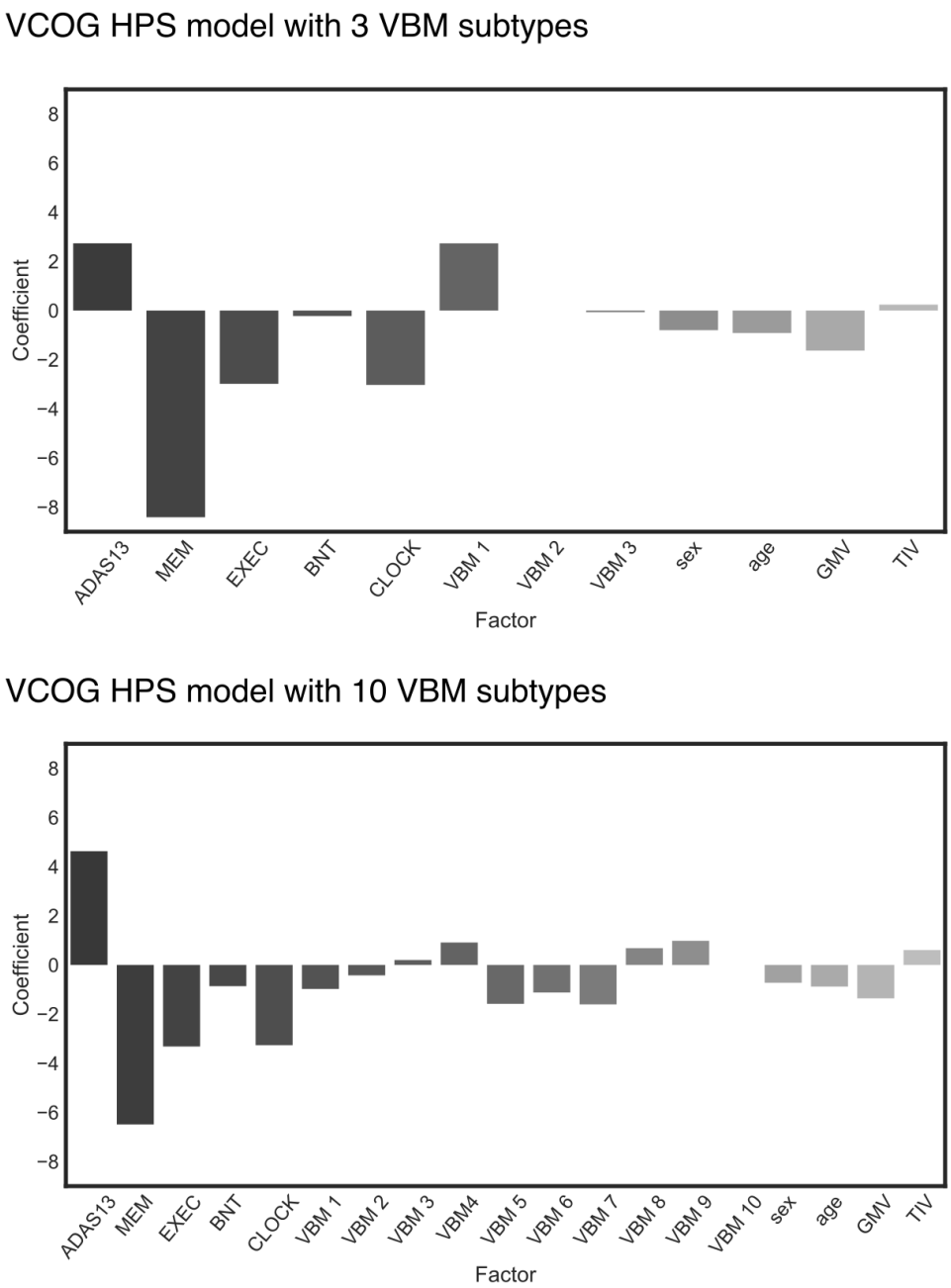

**Appendix 1 Figure 1.** Cognitive trajectories for individual MCI subjects in ADNI1 and ADNI2 grouped by HPS classifications (HPS+, Non-HPS+, Negative) by the VCOG, COG, and VBM high confidence prediction models.



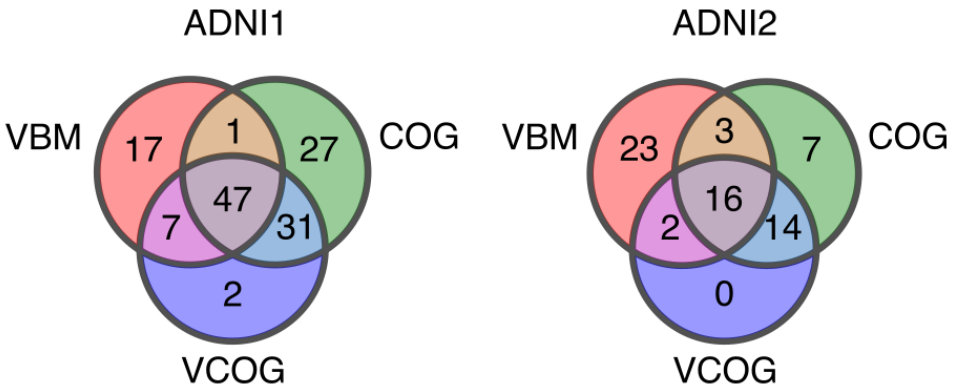

**Appendix 1 Figure 2.** Percentage of late MCI ADNI2 subjects within each HPS grouping (HPS+, Non-HPS+, Negative) across each highly predictive model (VCOG, VBM, COG). In each model, there was a significantly greater proportion of late MCI subjects in the HPS+ class compared to the Negative class (VCOG: $\chi^2 = 51.0, p < 0.001$; VBM: $\chi^2 = 21.8, p < 0.001$; COG: $\chi^2 = 59.9, p < 0.001$).




**Appendix 1 Figure 3.** Receiver operating curves (ROC) for each classification (AD vs CN; pMCI vs sMCI) and model (Base: traditional SVM; HPS: two-stage highly predictive signature) in both ADNI1 and ADNI2 cohorts. The ROC plots are shown for models using the VCOG predictors.




**Appendix 1 Figure 4.** Coefficients of factors in the VCOG HPS models for a model featuring 3 VBM subtypes and a model featuring 10 VBM subtypes.




**Appendix 1 Figure 5.** Venn diagram depicting the number of MCI subjects labeled as HPS+ by the VBM, COG, and VCOG HPS models in ADNI1 and ADNI2.

## Supplementary tables

**Appendix 1 Table 1.** Characteristics of HPS+ subjects from the VBM, COG, and VCOG signatures in ADNI1 and ADNI2 MCI cohorts.

| **ADNI1** | **Baseline** | **VBM** ~~COG~~ ~~VCOG~~ | ~~VBM~~ **COG** ~~VCOG~~ | ~~VBM~~ ~~COG~~ **VCOG** | **VBM** **COG** ~~VCOG~~ | **VBM** ~~COG~~ **VCOG** | ~~VBM~~ **COG** **VCOG** | **VBM** **COG** **VCOG** |
|---|---|---|---|---|---|---|---|---|
| pMCI % | 62.6 | 70.6 | 70.4 | 100 | 100 | 57.1 | 93.5 | 97.9 |
| APOE4 % | 57.0 | 58.8 | 70.4 | 100 | 100 | 71.4 | 71.0 | 63.8 |
| A$\beta$+ % | 76.1 | 50.0 | 91.7 | n/a | 100 | 100 | 88.9 | 91.7 |
| tau+ % | 50.7 | 0.0 | 83.3 | n/a | 0.0 | 50.0 | 66.7 | 66.7 |
| Female % | 40.8 | 41.2 | 29.6 | 50.0 | 0.0 | 42.9 | 61.3 | 36.2 |
| Age | 74.1±7.2 | 74.4±5.5 | 73.9±6.0 | 80.0±6.2 | 79.3 | 69.3±4.1 | 73.9±7.0 | 74.4±7.3 |
| Education | 15.7±2.9 | 17.1±2.1 | 15.7±3.3 | 15.0±1.4 | 20.0 | 16.0±2.6 | 14.3±3.1 | 15.9±2.9 |
| MMSE | 27.0±1.8 | 27.8±1.4 | 27.6±1.2 | 26.5±0.7 | 29.0 | 25.4±0.5 | 25.9±1.5 | 26.0±1.6 |
| **ADNI2** | **Baseline** | **VBM** ~~COG~~ ~~VCOG~~ | ~~VBM~~ **COG** ~~VCOG~~ | ~~VBM~~ ~~COG~~ **VCOG** | **VBM** **COG** ~~VCOG~~ | **VBM** ~~COG~~ **VCOG** | ~~VBM~~ **COG** **VCOG** | **VBM** **COG** **VCOG** |
| pMCI % | 30.6 | 43.5 | 57.1 | n/a | 33.3 | 0.0 | 78.6 | 93.7 |
| APOE4 % | 42.6 | 47.8 | 42.9 | n/a | 33.3 | 50.0 | 57.1 | 68.7 |
| A$\beta$+ % | 69.0 | 75.0 | 100 | n/a | 100 | 100 | 55.6 | 77.8 |
| tau+ % | 39.7 | 42.9 | 25.0 | n/a | 50.0 | 0.0 | 62.5 | 55.6 |
| Female % | 48.1 | 39.1 | 14.3 | n/a | 33.3 | 50.0 | 57.1 | 50.0 |
| Age | 70.7±7.3 | 71.4±5.9 | 74.8±6.6 | n/a | 67.0±13.7 | 73.6±2.5 | 71.7±8.6 | 77.1±4.8 |
| Education | 16.4±2.6 | 16.3±2.6 | 16.9±2.5 | n/a | 15.0±3.6 | 19.0±1.4 | 15.6±2.3 | 15.9±2.8 |
| MMSE | 28.2±1.7 | 28.3±1.5 | 28.0±1.3 | n/a | 28.7±1.5 | 27.5±2.1 | 26.7±1.8 | 26.1±1.7 |

The Baseline column represents values for all MCI subjects.
Age and education are presented in years (mean ± standard deviation).
A$\beta$ and tau CSF measures were available for approximately one third of all subjects across both cohorts.

**Appendix 1 Table 2.** pMCI vs sMCI performance metrics for VCOG HPS models with different number of VBM subtypes.

| **ADNI1** | **3 clusters** | **7 clusters** | **10 clusters** |
|---|---|---|---|
| Specificity | 0.8636 | 0.9310 | 0.8864 |
| Sensitivity | 0.5578 | 0.5510 | 0.5510 |
| Positive predictive value (adjusted) | 0.6743 | 0.8035 | 0.7105 |
| Accuracy | 0.6723 | 0.6936 | 0.6766 |
| **ADNI2** | **3 clusters** | **7 clusters** | **10 clusters** |
| Specificity | 0.9556 | 0.9667 | 0.9556 |
| Sensitivity | 0.4727 | 0.4727 | 0.4364 |
| Positive predictive value (adjusted) | 0.8433 | 0.8777 | 0.8324 |
| Accuracy | 0.8425 | 0.8511 | 0.8340 |

Positive predictive value was adjusted for a 33.6% prevalence of pMCI subjects.