

Automating Neurological Disease Diagnosis Using Structural MR Brain Scan Features

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CS229 Final Project

Introduction

Nine percent of those aged 65 or older and about one third of those aged 85 or older have Alzheimer's disease.¹ The incidence of Alzheimer's is expected to triple from 2010 to 2050.² 1.1% of American adults are Schizophrenic.³ Both these diseases are currently diagnosed primarily by a clinical mental health exam. Alzheimer's and recently Schizophrenia have both been shown to have a strong neuroanatomical footprint that appears in MRI.^{4,5} We seek to automate diagnosis and screening of these diseases using structural MRI brain scan features.

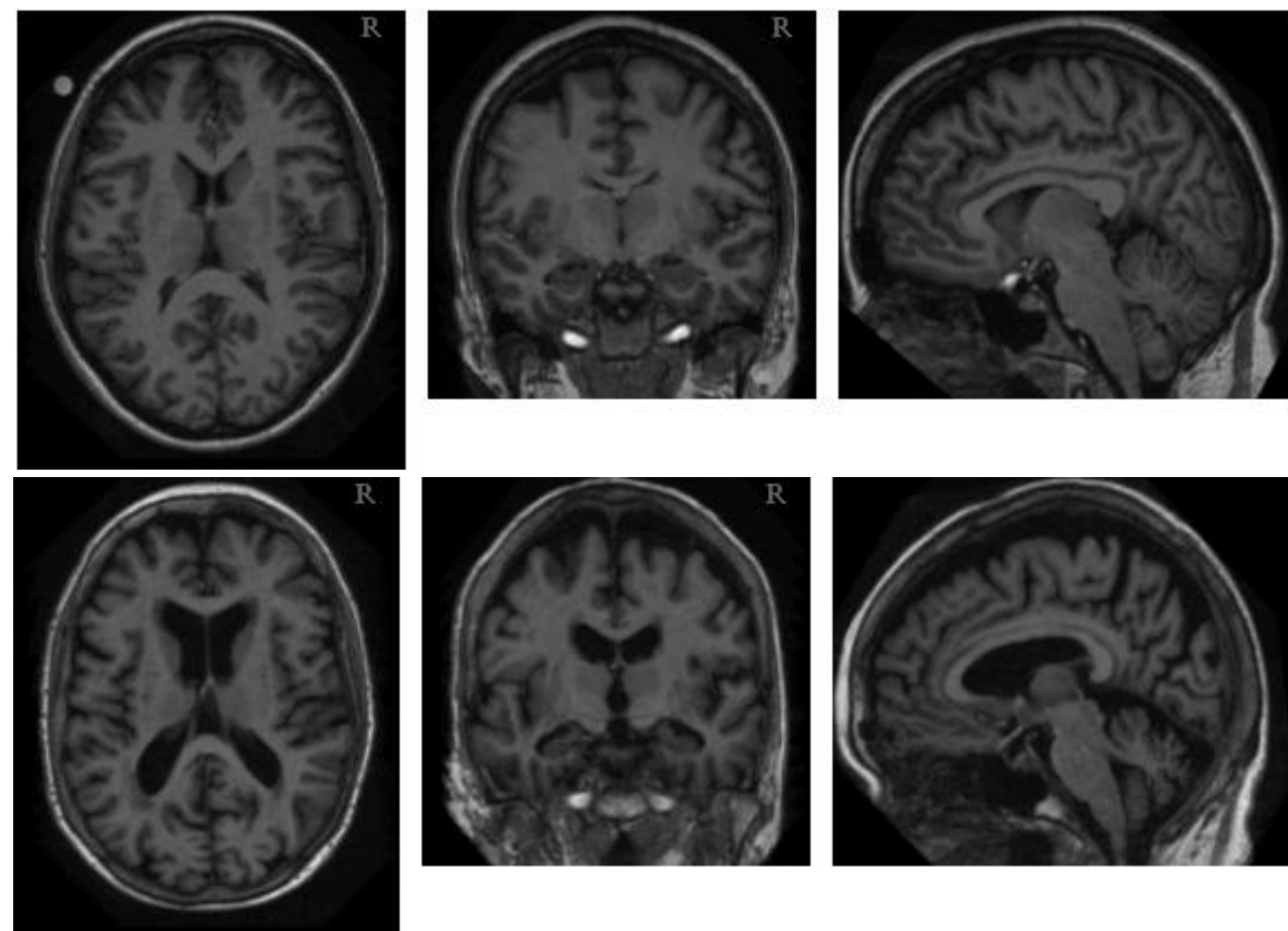


Figure 1: Top row: healthy brain without Alzheimer's Disease. Bottom row: brain with advanced stage of Alzheimer's Disease (Case 2 in OASIS dataset). We can clearly see cortical shrinkage, hippocampus shrinkage and enlarged ventricles in Row 2 as compared to Row 1.

Data

Datasets and extracted features provided by Athinoula A. Martinos Center for Biomedical Imaging.⁶

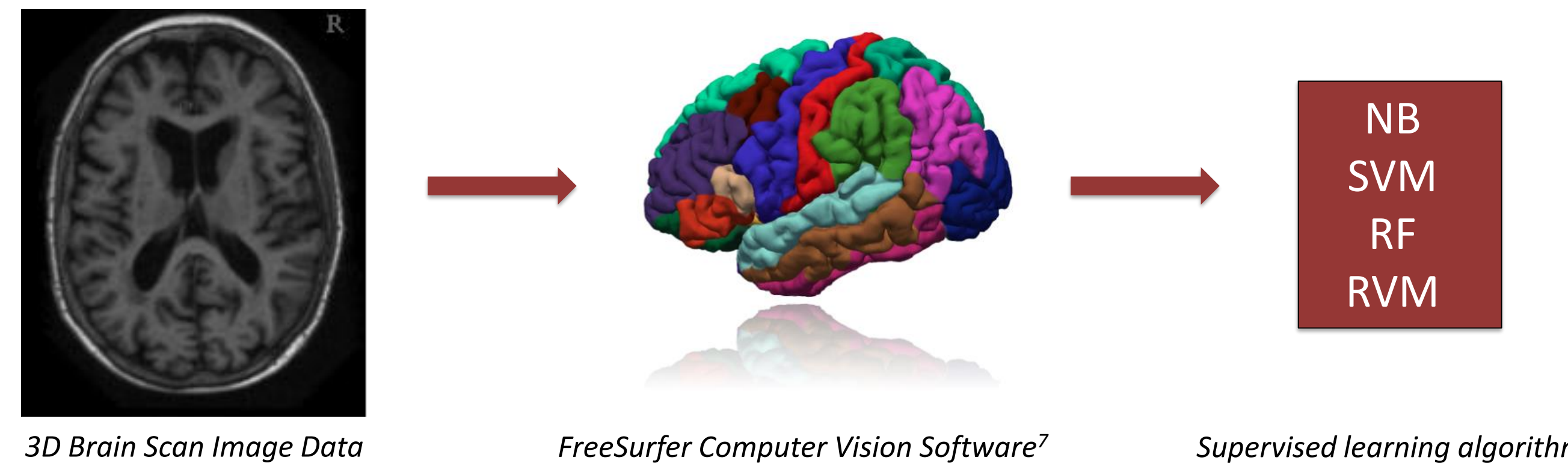
- MIND Clinical Imaging Consortium (MCIC) Schizophrenia Data
- Open-Ended Series of Imaging Studies (OASIS) Alzheimer's Disease Data (Case 1: Mild Alzheimer's (defined as Clinical Dementia Rating > 0, Case 2: Advanced Stage Alzheimer's (defined as Clinical Dementia Rating > 0))

For each of these we used, we used the feature sets:

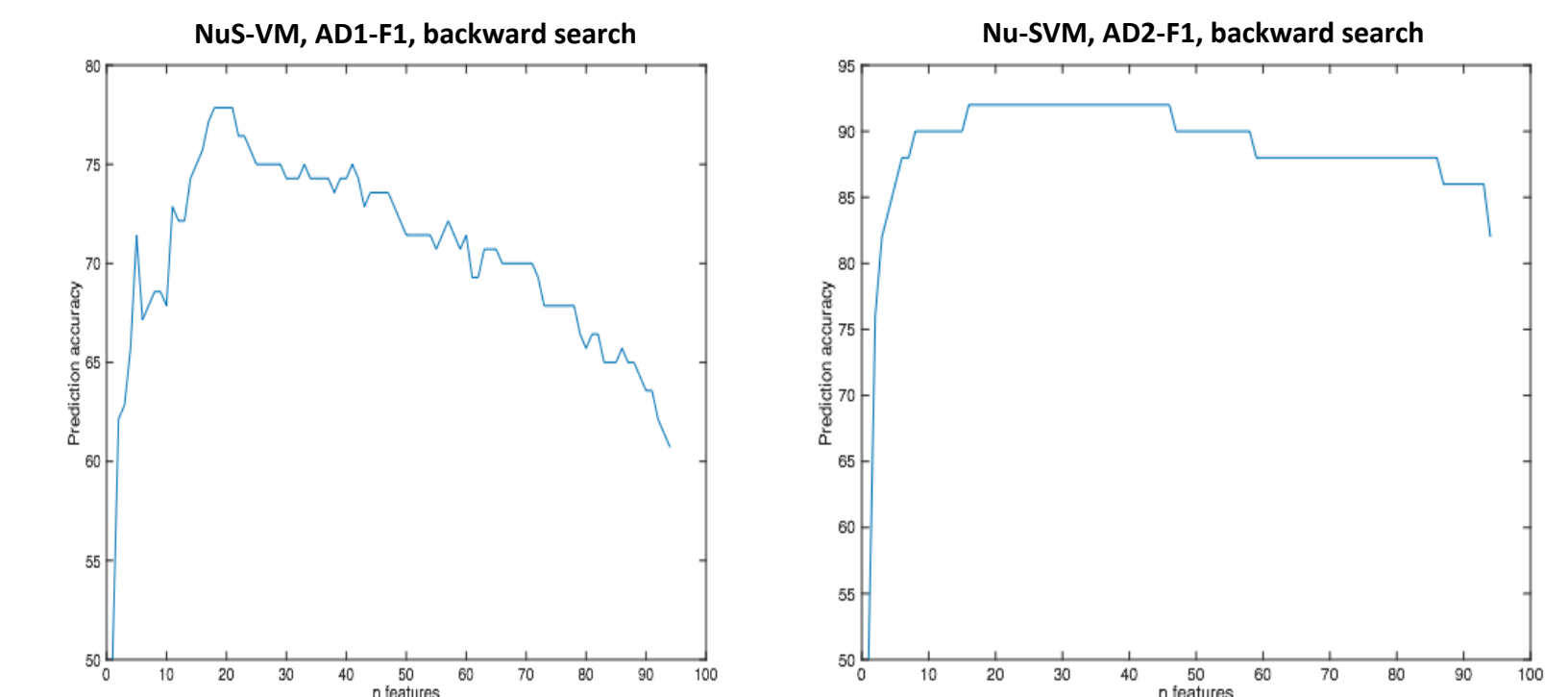
- Volumes of 45 Anatomical Structures (e.g. cerebral cortex, lateral ventricle) combined with 68 thicknesses of cortical parcellations (e.g. anterior frontal)
- 20,484 values of cortical thickness smoothed with Gaussian kernel

Methods

The provided features were extracted from brain MR scans using FreeSurfer⁷ computer vision software by [6]. We take these binary-labeled feature-sets and first get preliminary results using Naïve Bayes. Later we move onto running and optimizing linear and Gaussian kernel SVMs, as well as the Nu-SVM. Finally we apply random forest classifiers and are still deriving results using a Relevance Voxel Machine.



Feature Selection



Feature selection was done using both backward and forward search, and was also attempted both before and after optimizing the hyper-parameters. Results above illustrate variation observed in the smoothness of the search plots. Choice of number of features was much clearer for the less noisy plots (left) and appears to correspond to higher accuracy

Algorithm testing results

The table below provides a comparison of the best results achieved after running and optimizing (for hyper-parameters and numbers of features where computationally feasible) the above algorithms on the given datasets. We use 5-fold cross-validation throughout (the standard provided by the Machine Learning Challenge, which uses a dataset that is a subset of what we use here).

	SCZ – F1	SCZ – F2	AD1 – F1	AD1 – F2	AD2 – F1	AD2 – F2
NB	0.72	0.73	0.79	0.77	0.90	0.93
GNB	0.62	0.60	0.63	0.67	0.76	0.74
Linear SVM	0.66	0.60	0.71	0.66	0.80	0.72
Nu SVM	0.80	0.59	0.78	0.71	0.92	0.76
RF	0.55	0.52	0.61	0.52	0.59	0.60

Conclusions

Nu-SVM performs well across the data sets. Surprisingly, simple Naïve Bayes with binning the continuous features at their medians also performs strongly, even surpassing Nu-SVM for some feature and data sets. Overall, our results show that it is possible to diagnose Schizophrenia and Alzheimer's with fairly high accuracy using machine learning applied to structural brain MR information. Our results confirm prior findings of the significant neuroanatomical footprint of these disease. Our work also suggests that further increasing diagnosis accuracy is a promising direction for future work.

References

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