

# Global Disease Index, a novel tool for MTL atrophy quantification





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We propose an improvement of the methodology described in Chincarini et al. (2011), [1]. This is a novel automatic analysis technique based on local analysis on structural MRI. Here, 9 volumes of interest (VOI) are selected, extracted from target scan, and filtered with several different intensity and textural filters. Filtered regions are then analyzed with a Random Forest (RF) classifier to prune less relevant features for the discrimination between Cognitively Normal (CN) and Alzheimer's Disease (AD) subjects. Features subset is subsequently processed with a combination of Support Vector Machines (SVM) and Random Forest (RF), to give the final classification index. This value ranges from -1 (AD-like condition) to 1 (normalcy). Other values are to represent intermediate conditions (MCI).

Sex [M/F]

95/95

5/4

3/6

#### Subjects: TRAIN & TEST

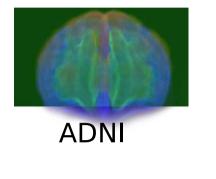
Training dataset consisted in 581 1.5T T1-weighted MR scans; 30 of which provided within CADDementia challenge and the other data coming from ADNI database. The procedure has been tested on 354 test subjects from CADDementia challenge

Age [y]

 $76.6 \pm 5.5$ 

 $68 \pm 8.5$ 

66.1 ± 5.2



CADD

Cohort

CN

MCI

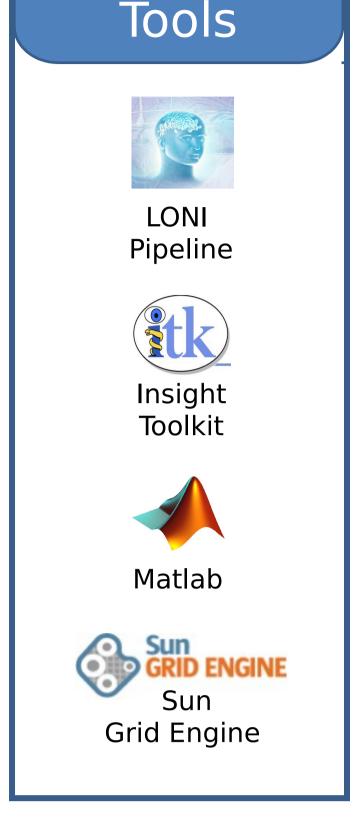
AD

CN	12	$62.3 \pm 6.2$	9/3	
Cohort	Sample size	Age [y]	Sex [M/F]	
AD	166	75.5 ± 7.4	71/45	
IVICI	195	70.0 ± 7.8	00/79	

Sample size

190

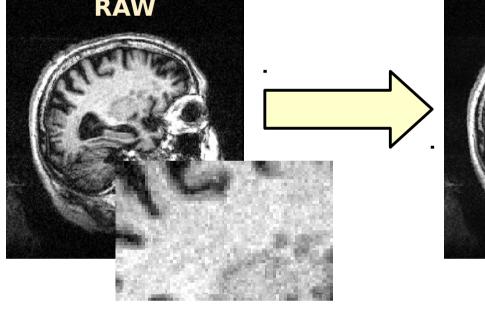
AD cohort includes 50 MCI subjects who converted to clinical dementia after a 2-y follow-up

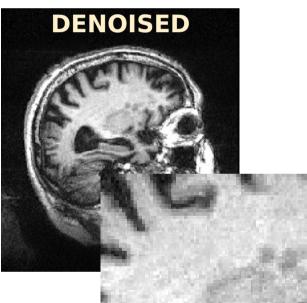


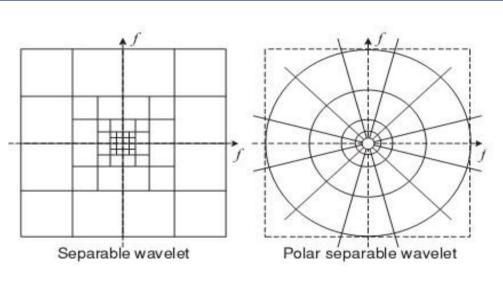
## Preprocessing

Uniformity across different sites and machineries is achieved by means of a denoise filter in the Steerable Pyramid configuration. This filter performs a polar-separable decomposition in the frequency domain, thus allowing independent representation of scale and orientation. The 3 noise thresholds (one for each image dimension) have been set to an identical value corresponding to the means of the thresholds found for 654 images in a previous study, in which thresholds were calculated as functions of the inflection point of the SSI curve between orignal and denoised image

 $SSIM(x,y) = \frac{(2\mu_x \mu_y + c_1)(2\sigma_{xy} + c_2)}{(\mu_x^2 + \mu_y^2 + c_1)(\sigma_x^2 + \sigma_y^2 + c_2)}$ **DENOISED** 







Wavelet-based filters: Sparse representation

Scale & dir dependent

0.8

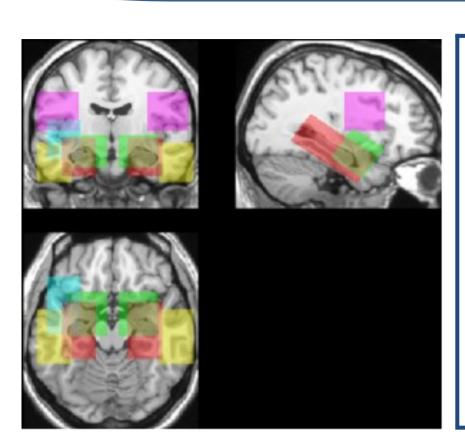
Sensitivity o o o o

0.0

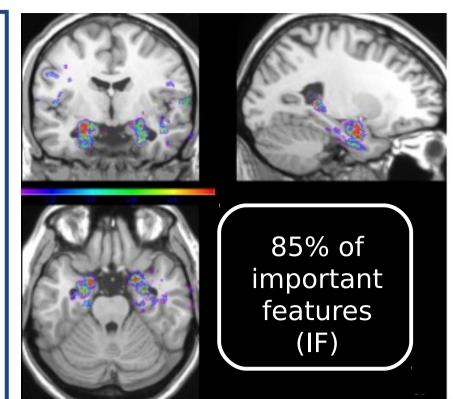
Spatial normalization of denoised images is carried out in 2 steps. A rigid 7 and a 12 degrees-of-freedom transformations are performed with Insight Toolkit (ITK) in order to map incoming MRIs onto the Montreal Neurological Institute's (MNI) ICBM152 reference. Scans are also resampled with a 1mm<sup>3</sup> isotropic grid.

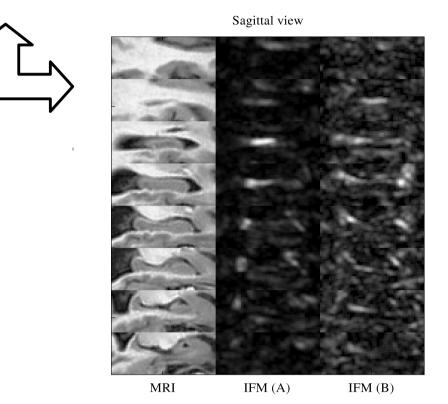
This procedure yielded a mis-registration rate of approximately 4%

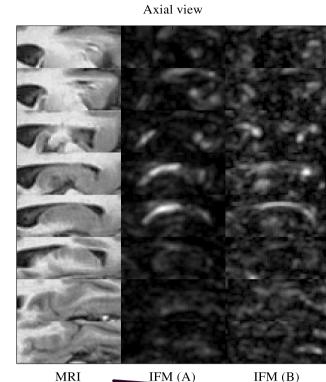
#### Feature selection

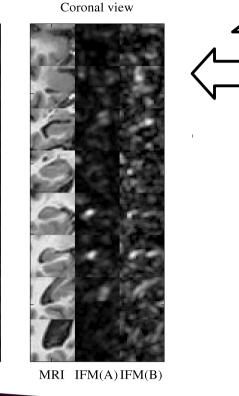


VOIs are then filtered with 18 filters in order to enhance textural / intensity features. Most relevant features (IF) are selected with Random Forest, that is able to order each feature's weight in CN vs AD discrimination





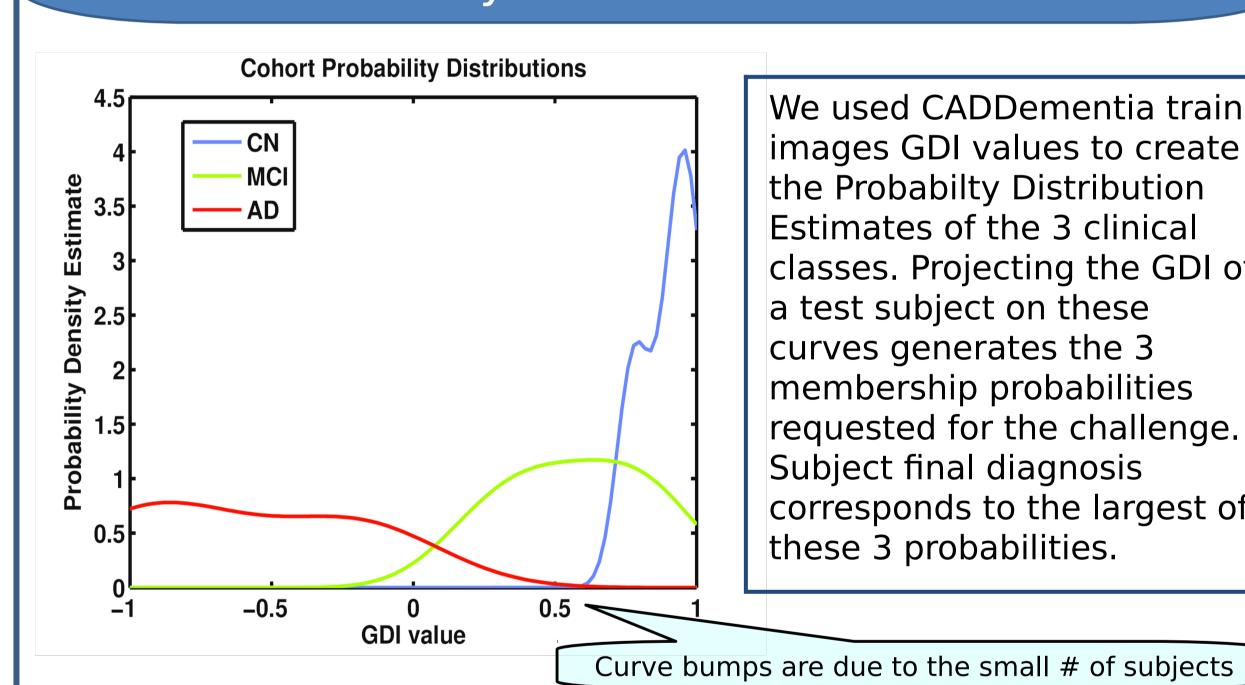




Sagittal / Axial / Coronal view of different employed filters (Gaussian mean, standard deviation, range, entropy, mexican hat,..) output computed on an hippoocampal box

A reduct subset of the Important Features is fed into a Support Vector Machines (SVM) and a Random Forest (RF) classifiers, the two outcomes are combined with a weighted mean providing the final Global Disease Index (GDI) score. Classifiers are trained on 551 ADNI images. The subset of these multiple, highly localized image-based relevant features is found in [1] proved to to be responsible for the overall clinical diagnosis and prognosis.

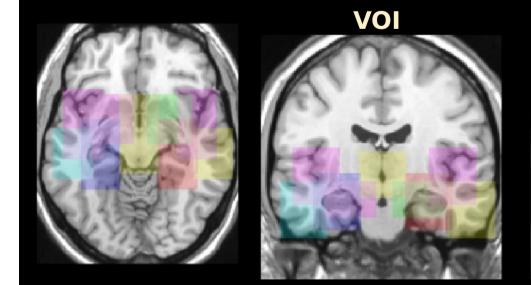
## Probability Distribution Estimates

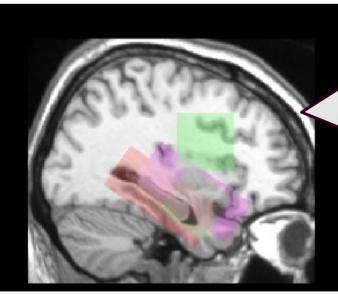


We used CADDementia train images GDI values to create the Probabilty Distribution Estimates of the 3 clinical classes. Projecting the GDI of a test subject on these curves generates the 3 membership probabilities requested for the challenge. Subject final diagnosis corresponds to the largest of these 3 probabilities.

The proposed algorithm is fully automated and requires an average CPU-time (single core) of computation of about 45 minutes per subject.

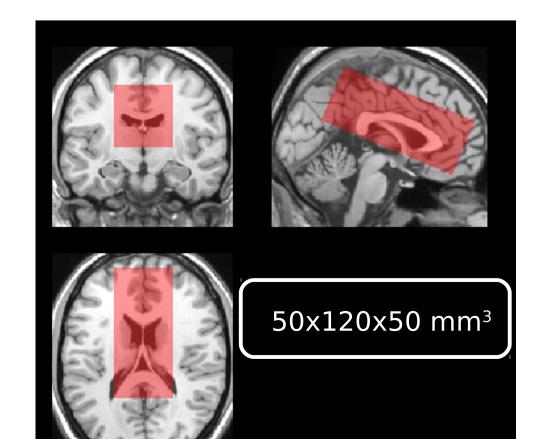
## VOI extraction & normalization





**Hippocampus &** entorhinal cortex **Amigdala** 

Parallelepiped-shaped volumes (VOI) are rigidly registered on target normalized scan. 8-10 references for each template VOI are employed to ensure a good registration even in case of severe degeneration. 7 VOI (critical regions in AD onset) and 2 (relatively spared ones) are chosen.



Extracted regions are intensity normalized by means of a region-based algorithm. A VOI is outlined around ICBM152 template's Corpus Callosum, it is then segmented in CSF/GM/WM, and the 3 cluster means are computed. Target VOI corresponding intensity values are non-linearly matched to the ones of ICBM152. This mapping is extended to intermediate intensities with a smooth piece-wise polynomial curve.

Scans are now well overlapping and content comparable

[1] A. Chincarini, P. Bosco, P. Calvini, G. Gemme, M. Esposito, C. Olivieri, L. Rei, S. Squarcia, G. Rodriguez, R. Bellotti, P. Cerello, I. De Mitri, A. Retico, F. Nobili; "Local MRI analysis approach in the diagnosis of early and prodromal AD". Neurolmage, 58 (2011) 469-480.

# Results

CN (AUC = 93.5%)

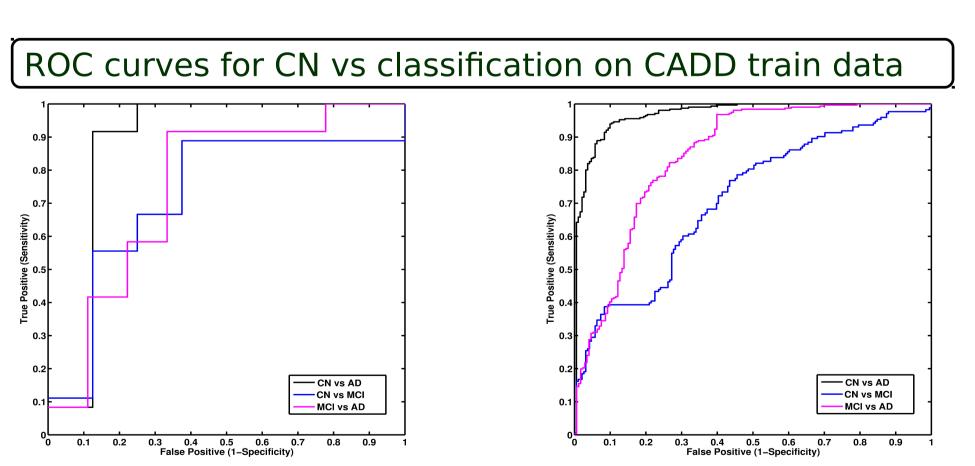
MCI (AUC = 69.8%)

AD (AUC = 92.6%)

1.0

8.0

0.6



MCI detection is low

because of the

of this class's GDI

0.4

1-Specificity

heterogeneity

0.2

GDI methodology is able to discriminate on CADDementia train data with: AUC = 0.93 for CN vs AD (sensitivity = 0.92 @ specificity = 0.88) AUC = 0.78 for CN vs MCI (sensitivity = 0.92 @ specificity = 0.67) AUC 0.8 for MCI vs AD distinction (sensitivity = 0.89 @ specificity = 0.62)

Slightly better results are obtained for ADNI data in leave-20-out ROC curves for one-vs-all classification on CADD train data crossvalidation: AUC=0.97 for CN vs AD (sens=0.94 @ spec=0.90) CN vs MCI: 0.71 (sens = 0.77 @ spec = 0.78)AD vs MCI: AUC = 0.85

(sensi 0.86 @ spec = 0.64)

GDI blind classification of the test population delivers  $146 \text{ CN (GDI} = 0.85 \pm 0.06),$ 125 MCI (GDI =  $0.51 \pm 0.16$ )

83 AD (GDI =  $-0.31 \pm 0.29$ )

Overall one-vs-all classification accuracy of 0.73