

Design of convolutional neural networks for automatic detection of Alzheimer's disease

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Agenda



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 - Problem Statement
 - Paper Methodology
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 - Results
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Problem Statement

- Alzheimer's disease is a **progressive neurodegenerative disorder** that is difficult to diagnose at an early stage.
- Current diagnostic methods are time-consuming, expensive, and are not sensitive enough to detect the disease in its early stages.
- Early detection and diagnosis are crucial for effective treatment and management of the disease.
- There is a growing interest in developing automated methods for Alzheimer's disease detection using machine learning.
- The goal is to design an optimized CNN model that can **accurately classify** brain **MRI scans** as either Alzheimer's or healthy controls, thus improving early detection and diagnosis of Alzheimer's disease.

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Related Work

- Initial works applied simple classifiers such as **support vector machines** on features obtained from **volumetric** measurements of the **hippocampus** (Gerardin et al. (2009)) and other brain areas (Plant et al. (2010)).
- Gupta et al. (2013) used pretraining based on a sparse autoencoder to perform classification on the Alzheimer's Disease Neuroimaging Initiative (ADNI) dataset.
- Hon and Khan (2017) applied state-of-the-art architectures such as VGG (Simonyan and Zisserman (2014)) and Inception Net (Szegedy et al. (2015)) on the OASIS dataset (Marcus et al. (2010)).
- Cheng et al. (2017) proposed a more computationally-efficient approach based on large 3D patches processed by individual CNNs, which are then combined by an additional CNN to produce the output.
- Lian et al. (2018) proposed a related hierarchical CNN architecture that automatically identifies significant patches. **Siamese networks** were applied by Khvostikov et al. (2018) to distinguish regions of interest around the hippocampus fusing data from multiple imaging modalities.

Challenges

- Many existing works suffer from data leakage due to flawed data splits, biased transfer learning, or the absence of an independent test set. In the absence of data leakage, CNNs achieved an accuracy of 72-86% when distinguishing between AD and healthy controls
- A significant **drop in test accuracy** (to **52** % for the three-class classification problem considered in the present work) was reported when there was **no patient overlap** between the training and test sets.



Paper Methodology

In this paper we focus on learning using structural brain MRI (T1-weighted scans) to differentiate between:

- Cognitively Normal aging (CN)
- Alzheimer's Disease (AD)
- Mild Cognitive Impairment (MCI)

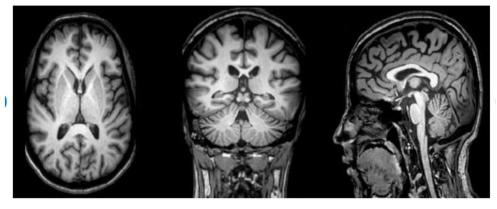
The key components of the architecture are:

- Instance Normalization, an alternative to batch normalization introduced originally in the context of style transfer.
- Use of Small-Sized Kernels in the first layer to avoid downsampling.
- Wide Architectures with large numbers of filters and relatively fewer layers.
- Using **Age** of the patient as an additional feature to the network through an **embedding** inspired by a recent technique from natural language processing



Dataset

- We use T1-weighted structural MRI scans from the **ADNI** (Alzheimer's Disease Neuroimaging Initiative) dataset which have undergone specific image preprocessing steps including **multiplanar reconstruction** (MPR), and corrections of image distortions and non uniformities.
- In total, over **3000** preprocessed scans were used.
- Labels in the ADNI dataset are extracted based on the scores obtained on memory tasks, corrected by education level and other criteria, some of which are subjective.
 - AD (mildly demented patients diagnosed with AD)
 - MCI (mildly cognitively-impaired patients in prodromal phase of AD)
 - **CN** (elderly control participants)
- MRI scanner can generate three types of orientations of human head as shown
 - (a) Axial
 - (b) Coronal
 - (c) Sagittal



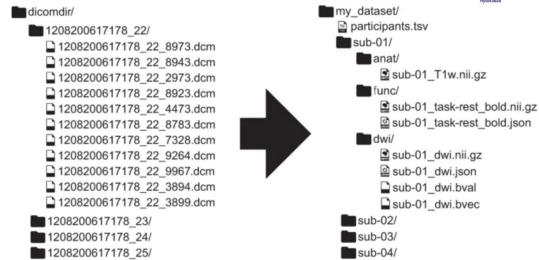
Axial Coronal Sagittal

Data Preprocessing

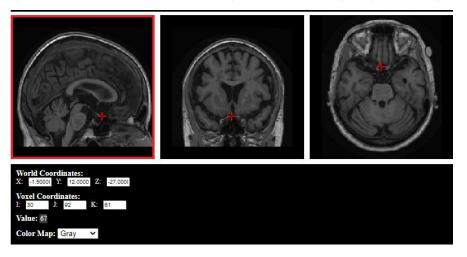
- We first split patients into training, validation and test sets. Then we use Clinica software to register the scans to a Dartel template computed exclusively from the training data and normalize them to the Montreal Neurological Institute (MNI) coordinate space.
- The validation and test data are not used to compute any templates in order to avoid data leakage.
- The input to the Clinica software is the ADNI scans converted to BIDS (brain imaging data structure) format.
- The output is a 3D Image of dimensions 121×145×121
 voxels along sagittal, coronal and axial dimensions
 respectively.

BIDS Structured Dataset





BIDS is a format for standardizing and describing outputs of neuroimaging experiments (left) in a way that is intuitive to understand and easy to use with existing analysis tools (right).





Data Split

• Due to preprocessing and registration errors, the final number of scans in our dataset is **2702**. The subjects in the dataset are split between **training** (70%), **validation** (15%) and **test** (15%) sets.

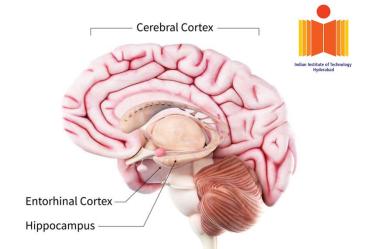
Split	Class	Num. subjects	Num. Scans	Mean Age (std)
	CN	140	567	77.0 (5.4)
Train	MCI	248	840	75.9(7.3)
	AD	193	527	76.7 (7.4)
	CN	33	126	77.2 (5.6)
Val	MCI	39	138	73.3(7.2)
	AD	41	124	76.1 (8.3)
Test	CN	24	105	79.0 (6.1)
	MCI	43	140	76.7(6.5)
	AD	45	135	76.4(5.1)

Demographics of our training, validation and test sets after preprocessing.

Proposed Model

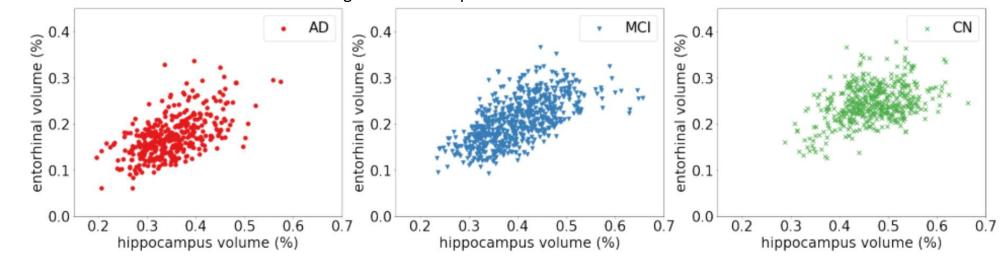
Hippocampus: Hippocampus is a complex S-shaped brain structure embedded deep into temporal lobe. It has a major role in **learning** and **memory**. Studies have shown that it gets affected in a variety of neurological and psychiatric disorders.

Entorhinal: The entorhinal cortex is the gateway for information entering and leaving the hippocampal formation.



Scatterplots of the values of two popular hand-crafted features associated to AD diagnostics: Normalized **Hippocampus volumes** and **Entorhinal volumes**

The features are informative (AD patients tend to have smaller volumes with respect to healthy controls), but they do not enable accurate classification due to the significant overlap between the three classes.



Proposed Model

- The above finding motivates learning discriminative features automatically. Our proposed methodology achieves this using a deep convolutional neural network, inspired by their success in computer vision.
- The proposed architecture is a 3D CNN model, composed of convolutional, normalization, activation and max-pooling layers.
- We outline several design choices that significantly boost the performance of the network for the task of differentiating between CN, AD, and MCI patients

Block	Layer	Type	Output size
	Inputs		$96 \times 96 \times 96$
1	Conv3D InstanceNorm3D ReLU	k1-c4·f-p0-s1-d1	$96 \times 96 \times 96$
	MaxPool3D	k3-s2	$47\times47\times47$
2	Conv3D InstanceNorm3D ReLU	k3-c32· f -p0-s1-d2	$43\times43\times43$
	MaxPool3D	k3-s2	$21\times21\times21$
3	Conv3D InstanceNorm3D ReLU	k5-c64· <i>f</i> -p2-s1-d2	$17 \times 17 \times 17$
	MaxPool3D	k3-s2	$8 \times 8 \times 8$
4	Conv3D InstanceNorm3D ReLU	k3-c64· <i>f</i> -p1-s1-d2	$6 \times 6 \times 6$
	MaxPool3D	k5-s2	$5 \times 5 \times 5$
FC1		1024	
FC2		3	
Softmax		3	

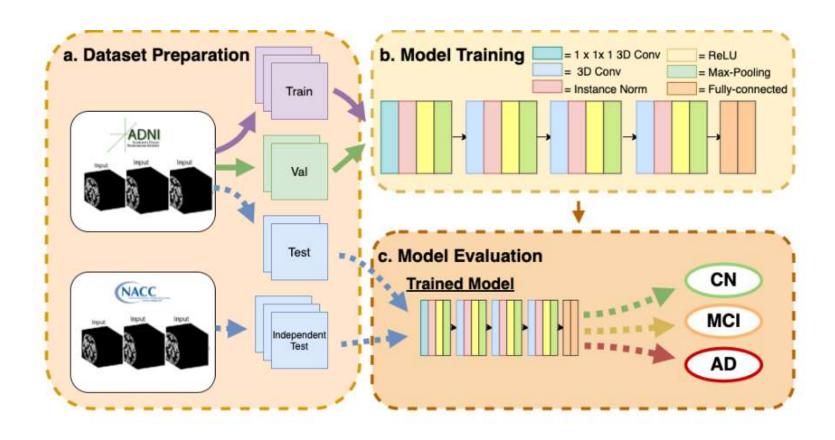
The backbone architecture. k = kernel size, c = number of channels as a multiple of the**widening factor f**, <math>p = padding size, s = stride and d = dilation.

The **age encoding**, if used, is forward propagated through two linear layers with layer normalization before being added to the output of **FC1**





Architecture

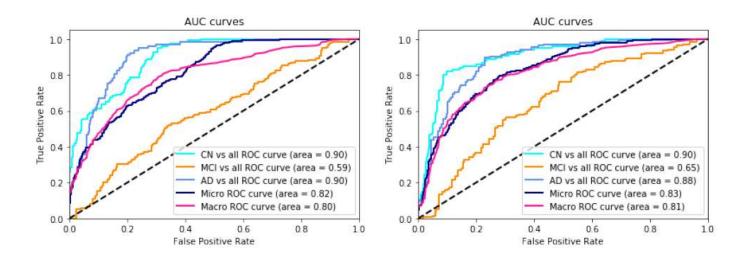


Results



Metric

- Our primary metric in this work is standard classification accuracy (Acc). As the test set is not necessarily balanced, we also use balanced classification accuracy (Bal-Acc) which is calculated as the average of the recall of each class.
- We also compute area under the ROC curves (AUCs), which are widely used for measuring the predictive accuracy of binary classification problems
- We also calculate micro and macro averages, denoted as Micro-AUC and Macro-AUC respectively.
- Below are the ROC curves obtained on the validation and test set. The model achieves around **90** % **AUC** when distinguishing **CN** or **AD** from the other two classes, and **59 65** % when distinguishing **MCI** from the other two classes.



ROC curves on the **validation set** (left) and **test set** (right). Differentiating CN or AD from all other classes results in high AUCs while detecting MCI remains a difficult task.

Results



Comparison with other models

- Our proposed model significantly outperforms previously reported results, as well as the baseline SOTA architectures.
- Incorporating age through the proposed encoding improves performance moderately.

Method	Accuracy	Balanced Acc	Micro-AUC	Macro-AUC
ResNet-18*	50.8%	Œ	ä	-
ResNet-18 pretrained*	56.8%	25	-	-
ResNet-18 $3D^{\diamond}$	$52.4 \pm 1.8\%$	53.1%	-	-
ResNet-18 3D	$50.1\pm1.1\%$	$51.3 \pm 1.0\%$	$71.2 \pm 0.4\%$	$72.4 \pm 0.7\%$
AlexNet 3D	$57.2 \pm 0.5\%$	$56.2 \pm 0.8\%$	$75.1 \pm 0.4\%$	$74.2 \pm 0.5\%$
$\operatorname{proposed}^{\bullet}$	$66.9 \pm 1.2\%$	$67.9 \pm 1.1\%$	$82.0 \pm 0.7\%$	$78.5 \pm 0.7\%$
$proposed^{\bullet} + Age$	$68.2 \pm 1.1\%$	$70.0 \pm 0.8\%$	$82.0 \pm 0.2\%$	$80.0\pm0.5\%$

^{*} Results on 2D ResNets initialized with or without pretrained weights on Imagenet reported by Valliani and Soni (2017).

Comparison of the published models to our best proposed models. + Age means that the model incorporates age encodings.

^{* 3}D ResNet with mild modifications, see Fung et al. (2019) for details. The balanced accuracy is computed using the confusion matrix in the paper.



Instance Normalization

- Use of Instance Normalization instead of commonly used batch normalization.
- In Instance Normalization, mean and variance are calculated for each individual channel for each individual sample across both spatial dimensions.
- Below, we show that applying **instance** normalization consistently **outperforms batch** normalization for our task of interest.

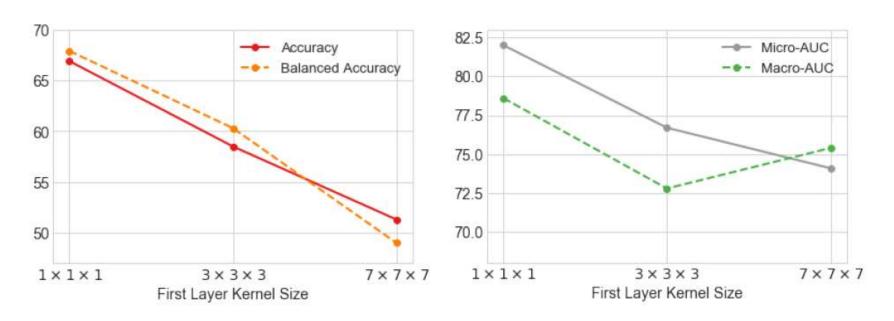
Method	Accuracy	balanced Acc	Micro-AUC	Macro-AUC
$\times 4$ with IN	$63.2 \pm 1.0\%$	$63.3 \pm 0.9\%$	$80.5 \pm 0.5\%$	$\textbf{77.0} \pm \textbf{0.7}\%$
$\times 4$ with BN	$61.8\pm1.1\%$	$62.2 \pm 1.1\%$	$77.0\pm0.5\%$	$73.0\pm0.6\%$
$\times 8$ with IN	$66.9 \pm 1.2\%$	$67.9 \pm 1.1\%$	$82.0 \pm 0.7\%$	$78.5 \pm 0.7\%$
$\times 8$ with BN	$58.8 \pm 0.9\%$	$60.7\pm0.7\%$	$75.9\pm0.7\%$	$73.1\pm0.8\%$
ResNet-18 with IN	$52.3 \pm 0.8\%$	$52.7 \pm 1.1\%$	$\textbf{74.1} \pm \textbf{0.7}\%$	$73.1 \pm 0.9\%$
ResNet-18 with BN $$	$50.1\pm1.1\%$	$51.3\pm1.0\%$	$71.2\pm0.4\%$	$72.4\pm0.7\%$

Comparison of batch normalization (BN) and Instance normalization (IN) layers on the backbone architecture with widening factor of 4 and 8 and on ResNet-18.



Small-sized kernels

- Use of small sized kernel in first layer to avoid early spatial downsampling
- The state of art networks such as ResNet and AlexNet use relatively large kernel sizes and strides in their first layer, which dramatically reduce the spatial dimension of their inputs. However, for our task of interest, early downsampling results in significant loss of performance as shown below.

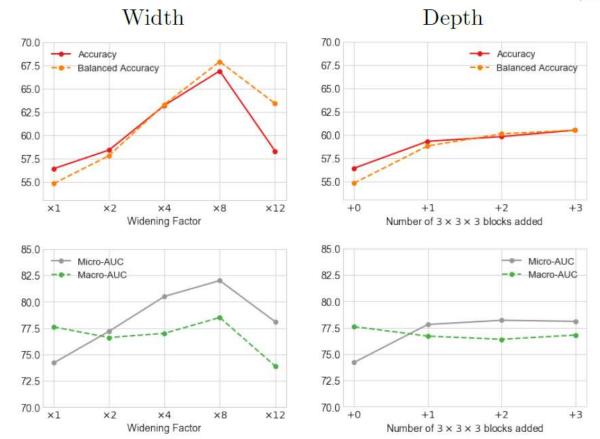


Performances of different first layer kernel sizes. Larger kernel sizes in the first layer result in worse performance.



Wider network

- This architecture design favors a wider architecture that is not too deep.
- It is found that increasing the depth of the model only brings marginal gains, whereas widening the architecture improves performance significantly.
- We also observe that wider networks are often faster and easier to train when compared to deeper networks.



Performance for different widening factors (left) and numbers of additional blocks (right) for backbone architecture. Wider architectures consistently achieve better performance up until a widening factor of x8. Deeper networks only achieve marginal improvement



Age Encodings

- Brains typically **shrink** to some degree in **healthy aging**. This might confuse the model since Alzheimer's disease has a similar effect.
- In order to integrate age information, we encode each age value into a vector and combine the vector with the output of the convolutional layers. we use sinusoidal functions to implement the encoding.

Layer	Output size
Linear	512
LayerNorm	512
Linear	1024

 $AE(age,2i) = sin(age/10000^2i/dmodel)$

 $AE(age,2i+1) = cos(age/10000^2i/dmodel)$

where i = 0, 1, 2, ... dmodel/2 -1 is the dimension and dmodel is the size of the encodings.

• We further transform the age encodings using a few fully connected layers to match the scales and sizes with the visual representation.

Method	Accuracy	Balanced Acc	Micro-AUC	Macro-AUC
No age information Proposed age encoding Baseline age encoding	$66.9 \pm 1.2\%$	$67.9 \pm 1.1\%$	$82.0 \pm 0.7\%$	$78.5 \pm 0.7\%$
	$68.2 \pm 1.1\%$	$70.0 \pm 0.8\%$	$82.0 \pm 0.2\%$	$80.0 \pm 0.5\%$
	$61.5 \pm 1.4\%$	$62.6 \pm 1.0\%$	$78.6 \pm 1.2\%$	$78.3 \pm 1.1\%$

Comparison of different ways of incorporating the age information using the proposed architecture

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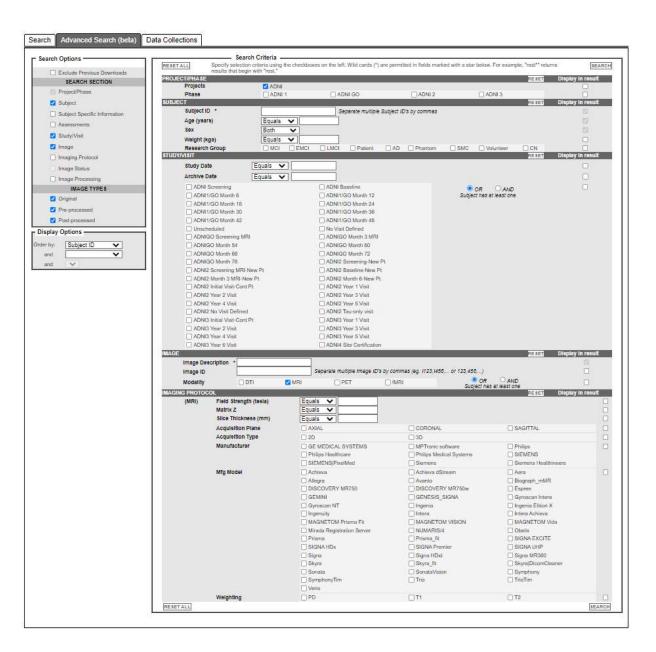
Implementation

- Data Collection
- Code Execution
 - Data Preprocessing
 - Model Training
- Results

Data Collection: from ADNI

The Image and Data Archive (IDA) is a secure online resource for archiving, exploring and sharing neuroscience data.

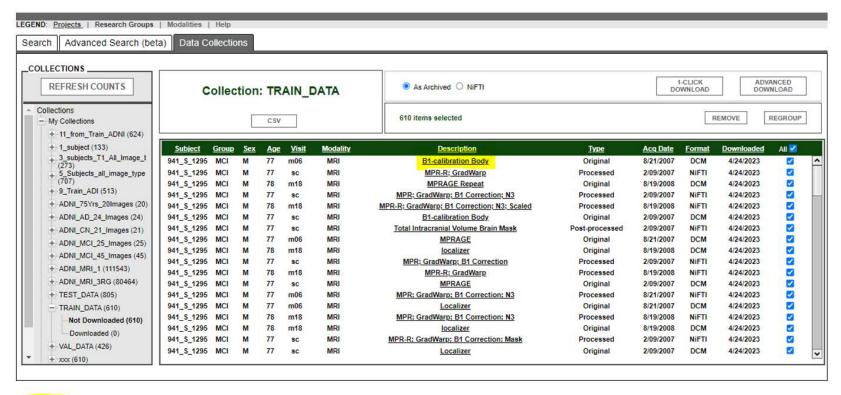
Downloaded Alzheimer's Disease Neuroimaging Initiative (ADNI) from the Image and Data Archive (IDA)





Data Collection: Raw Data with Labels









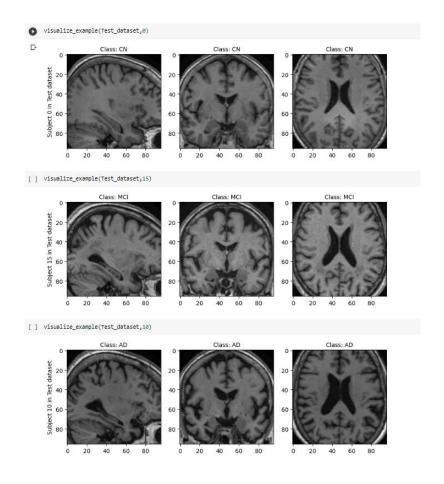
Data Preprocessing: dcm to BIDS t1-volume

```
(clinica-venv) cs22mds15012@instance-2:~$ clinica -v convert adni-to-bids '3 subjects T1 All Image t/ADNI
/home/cs22mds15012/clinica-venv/lib/python3.8/site-packages/clinica/iotools/converters/adni to bids/adni
  adni merge = pd.read csv(adni merge path)
                                                                                                                                                                                                    AmitDoda — MATLAB_maci64 - clinica run t1-volume ./BIDS_DIRECTORY ./BIDS_PROCESSED TRAIN -tsv ./Train_ADNI.tsv -wd ./WD_train
2023-04-26 18:58:37,485:DEBUG:/home/cs22mds15012/BIDS
                                                                                                                                                                       inv) kalaiyarasangKalaiyarasans-MacBook-Pro-2 AmitDoda % clinica run tl-volume './BIDS_DIRECTORY' './BIDS_PROCESSED' 'TRAIN' -tsv './Train_ADNI.tsv' -wd './WD
                                                                                                                                                                      13-64-24 14-58-48, 224-11MFG:The t1-volume pipeline is divided into 4 parts:

t1-volume-tissue-segmentation pipeline: Tissue segmentation, bias correction and spatial normalization to MNI space
                                                                                                                                                                      [Node] Setting-up "t1-volume-tissue-segmentation.2-SpmSegmentation" in "/Users/kalaiyarasan/Documents/AmitDoda/WD_train/t1-volume-tissue-segmentation/46
                                                                                                                                                                             [Node] Executing "2-SpmSegmentation" <nipype.interfaces.spm.preprocess.NewSegment>
                                                                                                                                                                       trode; Executing 2-Symbolymentation Chipppe.interfaces.sym.pic
3424-15:05:06,34 hipppe.workflow INFO:
[Node] Finished "2-SymSegmentation", elapsed time 278.984879s.
                                                                                                                                                                       3424-15:05:06,136 nipype.workflow INFO:
                                                                                                                                                                             [Node] Setting-up "t1-volume-tissue-segmentation.2-SpmSegmentation" in "/Users/kalaiyarasan/Documents/AmitDoda/WD_train/t1-volume-tissue-segmentation/545
                                                                                                                                                                       3424-15:05:06,141 nipype.workflow INFO:
                                                                                                                                                                             [Node] Executing "2-SpmSegmentation" <nipype.interfaces.spm.preprocess.NewSegment>
                                                                                                                                                                       3424-15:06:53,266 nipype.workflow INFO:
                                                                                                                                                                       [Node] Finished "2-SpmSegmentation", elapsed time 107.124026s. 3424-15:06:54,419 nipype.workflow INFO:
                                                                                                                                                                             [Node] Setting-up "t1-volume-tissue-segmentation.2-SpmSegmentation" in "/Users/kalaiyarasan/Documents/AmitDoda/WD_train/t1-volume-tissue-segmentation/3fd/
                                                                                                                                                                       3424-15:06:54,426 nipype.workflow INFO:
                                                                                                                                                                       [Node] Executing "2-SpmSegmentation" <nipype.interfaces.spm.preprocess.NewSegment>
424-15:88:40,874 nipype.workflow INFO:
                                                                                                                                                                       [Node] Finished "2-SpmSegmentation", elapsed time 106.447917s. 3424-15:88:42,671 nipype.workflow INFO:
                                                                                                                                                                             [Node] Setting-up "t1-volume-tissue-segmentation.2-SpmSegmentation" in "/Users/kalaiyarasan/Documents/AmitDoda/WD_train/t1-volume-tissue-segmentation/ef2f
                                                                                                                                                                        424-15:08:42,677 nipype.workflow INFO:
                                                                                                                                                                      #A24-15:08:42,677 nipype.workflow INFO:
[Node] Executing "2-5pmSegmentation" <nipype.interfaces.spm.preprocess.NewSegment>
#A24-15:18:23,124 nipype.workflow INFO:
[Node] Finished "2-5pmSegmentation", elapsed time 100.446552s.
#A24-15:18:24,983 nipype.workflow INFO:
[Node] Setting-up "ti-volume-tissue-segmentation.2-SpmSegmentation" in "/Users/kalaiyarasan/Documents/AmitDoda/WD_train/ti-volume-tissue-segmentation/a5202
 023-04-26 18:59:14,721:DEBUG:T1 conversion done.
 home/cs22mds15012/clinica-venv/lib/python3.8/site-packages/clinica/iotools/bids_utils.py:114: DtypeWarni
                                                                                                                                                                       3424-15:10:24,910 nipype.workflow INFO:
  file to read = pd.read csv(file to read path)
                                                                                                                                                                      [Node] Executing "2-SpmSegmentation" 
(Indee] Executing "2-SpmSegmentation" 
(Indee] Finished "2-SpmSegmentation", elapsed time 109.01262s.
home/cs22mds15012/clinica-venv/lib/python3.8/site-packages/clinica/iotools/bids_utils.py:114: DtypeWarni/
  file to read = pd.read csv(file to read path)
```

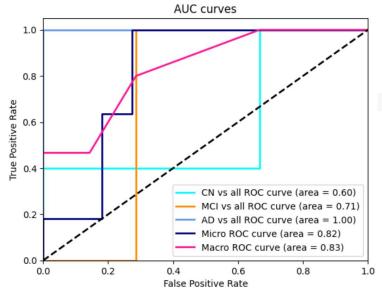
dcm to BIDS BIDS t1-volume

Code Execution: Loading pretrained model and evaluating on small test set



participant_id	session_id	diagnosis	mmse	cdr cdr_sb	age	examination_date	earliest_time	age_rounde
sub-ADNI033S1016	ses-M00	CN	29.0	0.0 0.0	78.3	2006-11-13	2006-11-13	78.5
sub-ADNI033S1016	ses-M06	CN	27.0	0.0 0.0	78.8	2007-05-30	2006-11-13	79.0
sub-ADNI033S1016	ses-M12	CN	30.0	0.0 0.0	79.3	2007-11-28	2006-11-13	79.5
sub-ADNI033S1016	ses-M24	CN	28.0	0.0 0.0	80.3	2008-12-03	2006-11-13	80.5
sub-ADNI033S1016	ses-M36	CN	29.0	0.0 0.0	81.3	2009-12-02	2006-11-13	81.5
sub-ADNI033S1016	ses-M48	CN	30.0	0.0 0.0	82.2	2010-11-10	2006-11-13	82.5
sub-ADNI130S1290	ses-M00	AD	25.0	0.5 4.0	79.3	2007-02-27	2007-02-27	79.5
sub-ADNI130S1290	ses-M06	AD	21.0	0.5 4.0	79.8	2007-09-10	2007-02-27	80.0
sub-ADNI130S1290	ses-M12	AD	19.0	1.0 5.0	80.3	2008-02-29	2007-02-27	80.5
sub-ADNI126S0606	ses-M00	AD	23.0	0.5 3.5	68.5	2006-08-02	2006-08-02	68.5
sub-ADNI126S0606	ses-M06	AD	25.0	1.0 5.0	69.0	2007-02-05	2006-08-02	69.0
sub-ADNI126S0606	ses-M12	AD	25.0	1.0 5.0	69.4	2007-08-02	2006-08-02	69.5
sub-ADNI126S0606	ses-M24	AD	22.0	1.0 7.0	70.4	2008-07-24	2006-08-02	70.5
sub-ADNI128S1407	ses-M00	MCI	24.0	0.5 2.5	74.6	2007-06-25	2007-06-25	74.5
sub-ADNI128S1407	ses-M06	MCI	26.0	0.5 2.5	75.1	2008-01-28	2007-06-25	75.0
sub-ADNI128S1407	ses-M24	MCI	23.0	0.5 3.5	76.7	2009-08-27	2007-06-25	77.0
sub-ADNI029S0866	ses-M00	CN	28.0	0.0 0.0	80.0	2006-10-05	2006-10-05	80.0
sub-ADNI029S0866	ses-M06	CN	29.0	0.0 0.0	80.4	2007-04-04	2006-10-05	80.5
sub-ADNI029S0866	ses-M12	CN	29.0	0.0 0.0	80.9	2007-10-04	2006-10-05	81.0
sub-ADNI029S0866	ses-M24	CN	30.0	0.0 0.0	82.0	2008-10-09	2006-10-05	82.0
sub-ADNI029S0866	ses-M36	CN	29.0	0.0 0.0	83.0	2009-10-22	2006-10-05	83.0
sub-ADNI094S1397	ses-M00	AD	24.0	1.0 4.5	55.1	2007-05-15	2007-05-15	55.0
sub-ADNI094S1397	ses-M06	AD	22.0	1.0 4.5	55.5	2007-11-13	2007-05-15	55.5
sub-ADNI094S1397	ses-M12	AD	11.0	1.0 9.0	56.1	2008-05-15	2007-05-15	56.0
sub-ADNI133S0792	ses-M18	MCI	30.0	0.5 0.5	74.9	2008-03-17	2006-09-25	75.0
sub-ADNI133S0792	ses-M00	MCI	30.0	0.5 1.0	73.5	2006-09-25	2006-09-25	73.5
sub-ADNI133S0792	ses-M06	MCI	29.0	0.5 0.5	73.9	2007-03-21	2006-09-25	74.0
sub-ADNI133S0792	ses-M12	MCI	29.0	0.5 0.5	74.4	2007-09-25	2006-09-25	74.5
cub=ADNT13390792	ses=M24	MCT	28 0	0 5 1 0	75 /	2008-09-18	2006-09-25	75 5





test_model(all_acc, all_balanced_acc,all_auc)

Mean Acc 0.6636363636363638 STD Acc 0.0416597790450531

Mean Balanced Acc 0.666666666666667 std Balanced Acc 1.1102230246251565e-16

Micro mean: 0.8181818181818181
Micro std: 0.021943666193969844
Macro mean: 0.7962648809523809
Macro std: 0.026552204998858332

Code Execution

Config file

```
cat config.yaml
file_name: ./saved_model/1007_pooling_age
 data_root_dir: data/
 dir_to_scans: ./FULL_DATA/subjects
 dir_to_tsv: ./FULL_DATA/TSV_FOR_TRAIN
 batch_size: 4
 val_batch_size: 2
 workers: 2
 percentage_usage: 1.0
exp_name: 1007_pooling_age
visdom:
 port: 8064
 server:
model:
 arch: ours
 input_channel: 1
 nhid: 512
 feature_dim: 1024
 n label: 3
 expansion: 8
 num blocks: 0
 type_name: conv3x3x3
 norm_type: Instance
adv_model:
 nhid: 36
 out_dim: 12
mmse_model:
 nhid: 64
training_parameters:
 use_age: False
 pretrain: #dir to saved model here
 max_iter: 16000
 start_epoch: 0
 epochs: 30
 print_freq: 5
 max_grad_12_norm:
 report_interval: 100
 snapshot_interval: 1000
optimizer:
 method: SGD
   lr: 0.01
   weight_decay: 0.000
```



Model Training from scratch on small train sample

Validation [0/7]	Time 0.692 (0.692)	Data 0.432 (0.432)	Loss 5.7886 (5.7886
Validation [5/7]	Time 0.272 (0.343)	Data 0.000 (0.073)	Loss 0.0057 (3.267)
Epoch [20]: Validat saved_model	ion Accuracy 58.333		
Epoch: [21][0/9]	Time 2.235 (2.235)	Data 1.045 (1.045)	Loss 0.1744 (0.1744
Epoch: [21][5/9]	Time 1,172 (1,347)	Data 0.000 (0.175)	Loss 0.4384 (0.2719
Validation [0/7]	Time 0.715 (0.715)	Data 0.455 (0.455)	Loss 9.9523 (9.952)
Validation [5/7]	Time 0.267 (0.347)	Data 0.000 (0.077)	Loss 0.0020 (5.210)
Epoch [21]: Validat saved_model	,000 00 00		
Epoch: [22][0/9]	Time 2.167 (2.167)	Data 0.978 (0.978)	Loss 0.1323 (0.132
Epoch: [22][5/9]	Time 1.175 (1.337)	Data 0.000 (0.165)	Loss 0.7827 (0.646)
Validation [0/7]	Time 0.808 (0.808)	Data 0.547 (0.547)	Loss 6.1226 (6.1226
Validation [5/7]	Time 0.271 (0.360)	Data 0.000 (0.092)	Loss 0.0897 (3.1200
Epoch [22]: Validat saved_model	ion Accuracy 66,667		
Epoch: [23][0/9]	Time 2.797 (2.797)	Data 1.584 (1.584)	Loss 0.1585 (0.1585
Epoch: [23][5/9]	Time 1.157 (1.439)	Data 0.000 (0.266)	Loss 0.3422 (0.5861
Validation [0/7]	Time 0.799 (0.799)	Data 0.546 (0.546)	Loss 7.8977 (7.8977
Validation [5/7]	Time 0.270 (0.360)	Data 0.000 (0.091)	Loss 0.0197 (4.1058
Epoch [23]: Validat saved_model			
Epoch: [24][0/9]	Time 2.844 (2.844)	Data 1.611 (1.611)	Loss 0.0783 (0.0783
Epoch: [24][5/9]	Time 1.173 (1.447)	Data 0.000 (0.269)	Loss 0.1149 (0.3799
Validation [0/7]	Time 0.769 (0.769)	Data 0.509 (0.509)	Loss 8.7516 (8.7516
Validation [5/7]	Time 0.272 (0.375)	Data 0.000 (0.105)	Loss 0.0316 (4.408)
Epoch [24]: Validat saved_model	8		
Epoch: [25][0/9]	Time 2.822 (2.822)	Data 1.591 (1.591)	Loss 0.0349 (0.0349
Epoch: [25][5/9]	Time 1.174 (1.448)	Data 0.000 (0.266)	Loss 0.9839 (0.3059
Validation [0/7]	Time 1.175 (1.175)	Data 0.916 (0.916)	Loss 7.9771 (7.977)
Validation [5/7]	Time 0.268 (0.489)	Data 0.000 (0.225)	Loss 0.0050 (4.0618
Epoch [25]: Validat saved_model	ion accuracy 66.66/		
Epoch: [26][0/9]	Time 2.173 (2.173)	Data 0.974 (0.974)	Loss 0.1579 (0.1579
Epoch: [26][5/9]	Time 1.185 (1.342)	Data 0.000 (0.164)	Loss 0.2858 (0.1972
Validation [0/7]	Time 1.014 (1.014)	Data 0.762 (0.762)	Loss 11.1706 (11.17
Validation [5/7]	Time 0.273 (0.401)	Data 0.000 (0.128)	Loss 0.0037 (5.6385
Epoch [26]: Validat saved_model	55 To 100		W 2002222 V2 1000
Epoch: [27][0/9]	Time 2.218 (2.218)	Data 1.012 (1.012)	Loss 0.0727 (0.0727
Epoch: [27][5/9]	Time 1,177 (1,347)	Data 0.000 (0.169)	Loss 0.0721 (0.1090
Validation [0/7]	Time 0.802 (0.802)	Data 0.540 (0.540)	Loss 7.9799 (7.9799
Validation [5/7]	Time 0.273 (0.360)	Data 0.000 (0.091)	Loss 0.0196 (4.2744
Epoch [27]: Validat saved_model			
Epoch: [28][0/9]	Time 2.103 (2.103)	Data 0.911 (0.911)	Loss 0.0367 (0.0367
Epoch: [28][5/9]	Time 1.176 (1.327)	Data 0.000 (0.153)	Loss 0.0449 (0.8310
Validation [0/7]	Time 0.847 (0.847)	Data 0.585 (0.585)	Loss 5.6035 (5.6035
Validation [5/7] Epoch [28]: Validat	Time 0.270 (0.371) ion Accuracy 58.333	Data 0.000 (0.098)	Loss 0.0109 (2.8687
saved_model	Time 2 130 (2 130)	Data 0 033 (0 033)	LOSS & BAFF /0 04FF
Epoch: [29][0/9]	Time 2.130 (2.130) Time 1.175 (1.339)	Data 0.933 (0.933) Data 0.000 (0.161)	Loss 0.0455 (0.0455 Loss 0.1777 (0.1726
Epoch: [29][5/9] Validation [0/7]	Time 1.175 (1.339)	Data 0.461 (0.461)	LOSS 0.1/// (0.1/20 LOSS 4.8243 (4.8243
Validation [6/7]	Time 0.718 (0.718)	Data 0.461 (0.461)	LOSS 4.8243 (4.8243 LOSS 0.1197 (2.3942

Model Achieved 66.67 % Validation accuracy in 30 epochs

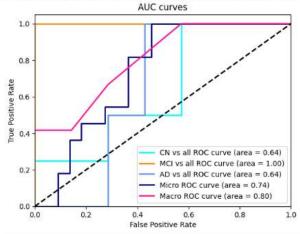
Results on small test set



· Results on Test Data using model trained from scratch

```
y [26] all_acc, all_balanced_acc, all_auc = evaluation_models(model_file_name,Test_loader, expansion_list = [8], use_age = True, norm_type= 'Instance')
```

Iteration: 0 ['model.image_embedding_model.conv.conv0_s1.weight', 'model.image_embedding_model.conv.conv0_s1.bias', 'model.image_embedding_model.conv.conv1_s1.weight', 'model ['image_embedding_model.conv.conv0_s1.weight', 'image_embedding_model.conv.conv1_s1.weight', 'image_embedding_embedding_mod



[27] test_model(all_acc, all_balanced_acc,all_auc)

Mean Acc 0.5181818181818181 STD Acc 0.09136250564655354

Micro mean: 0.7413223140495867 Micro std: 0.025080976703295024 Macro mean: 0.8282440476190475 Macro std: 0.03992617133905823

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Challenges

- Good amount of medical domain knowledge is needed.
- The ADNI MRI dataset is very bulky.
- Medical imaging requires good amount of preprocessing which is time consuming and compute expensive operation.

Novelty/ Future Work

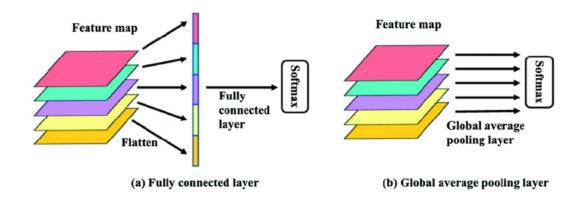


Proposal: Use of **Global Average Pooling** (GAP) layer instead of fully connected layers FC1, FC2

Improved Performance: Medical images often contain a large number of small and subtle features which can be effectively captured by GAP, which computes the average value of each feature map.

Efficient Training: The use of GAP can reduce the computational cost of the network, which can help to reduce the training time.

Interpretability: GAP can provide interpretability by understanding the contribution of each feature map to the final classification decision.



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Conclusion

- In this paper, a novel 3D CNN architecture is developed to perform three-way classification between patients with Alzheimer's disease, patients with mild cognitive impairment, and healthy controls.
- The architecture combines different elements (instance normalization, small kernels, wider layers, and an encoding of the patient's age) to achieve a significant gain in classification accuracy, demonstrated on completely held-out dataset.

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Thank You