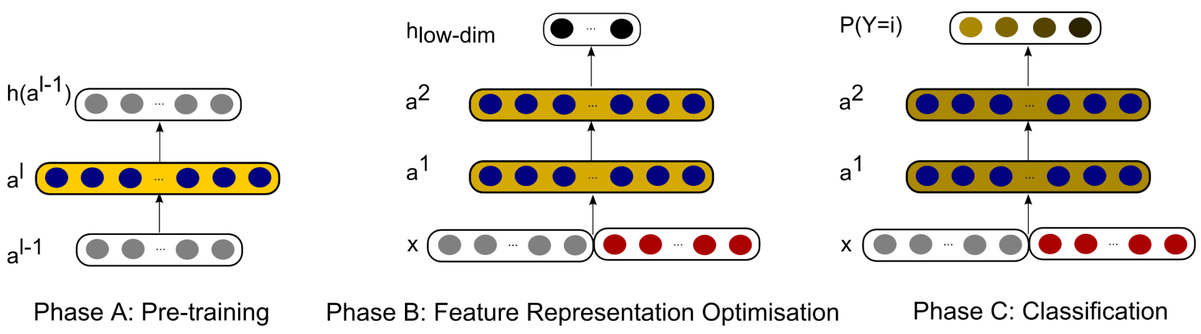
Multi-Phase Neuroimaging Feature Learning for Neurodegenerative Disease Diagnosis

Siqi Liu, PhD Student
Supervisor: Weidong (Tom) Cai, Sonia Pujol, Ron Kikinis*, David Feng*
School of Information Technologies
FACULTY OF ENGINEERING & INFORMATION TECHNOLOGIES

Introduction

- To aid the clinical decision making, feature learning methods have been applied on finding the correlations between the high dimensional features extracted from neuroimaging data recently.
- Low-dimensional biomarkers, such as the Mini-Mental-State-Examination (MMSE) and the cerebrospinal fluid measurements (CSF), are known as supportive diagnostic tools for clinic diagnosis of brain diseases, accompanied with the high-dimensional neuroimaging biomarkers, such as Magnetic Resonance Image (MRI) and Positron Emission Tomography (PET).
- In an attempt to utilise the low-dimensional biomarkers we proposed a Multi-Phase Neuroimaging Feature (MPNF) framework that have low-dimensional biomarkers embedded in the feature representation learning rather than directly using them as features.

Method



Phase A: Pre-training Phase B: Feature Representation Optimisation Phase C: Classification

Phase A: SAE Pre-Training

- Phase A depicts the unsupervised layer-wised pre-training of the feature representation network which learns a manifold to reconstruct the features at the previous layer. The objective function can be demonstrated as

$$L(W,b,x,z) = \min_{W,b} ||h(W,b,x) - x||_2^2 + \lambda ||W||_2^2$$

where h(…) is the reconstruction of the activations on the neurons of the previous layer.

Phase B*: Feature Augmentation

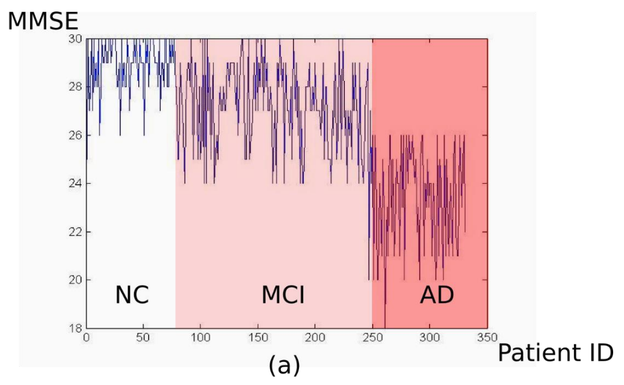
- The parameters of the auto-encoders learned by Phase A are unfolded and stacked in Phase B. In Phase B, the feature representation network is enhanced by training to output the low-dimensional features. The outputs of Phase B are the low-dimensional biomarkers estimated with the extracted high-level features, where Linear Regression $h(W,a^{(l)}) = Wa^{(l)} + b$ is used.

Phase C: Supervise Fine-tuning

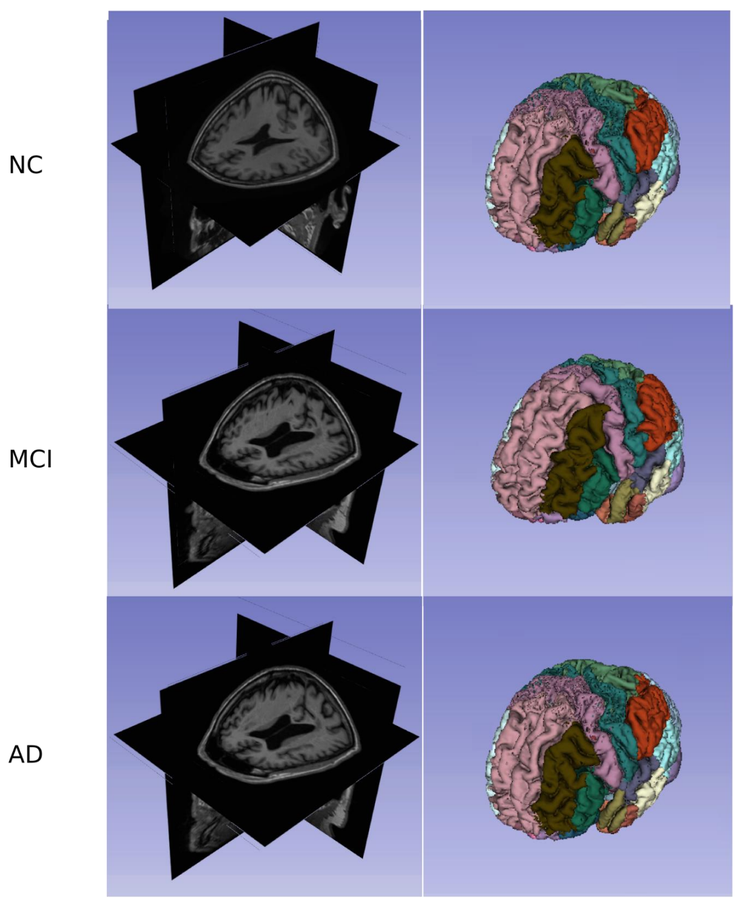
- In Phase C, after replacing the output layer with softmax regression, the entire structure is finally fine-tuned for the purpose of classification. The learnt features in Phase C are expected to be more sensitive to the training labels since the hidden layers could learn high-level disorder-specific features. The diagnosis probability can be shown as

$$P(Y=i|x) = \frac{e^{W^i a + b^i}}{\sum_j e^{W^i a + b^i}}$$

where a is the feature vector obtained by the fine-tuned SAE. Y is assigned to possible stages of a particular disease, such as NC, MCI and AD of AD progression. The prediction P(Y=i|x) with the highest probability is chosen as the final decision. The network is then fine-tuned by back-propagating the classification loss with the pre-labelled training subjects as a supervised classification neural network.



(a)



(b)

The comparison between the variations of low-dimensional biomarkers and neuroimaging data. (a) is the plot of MMSE scores. (b) are slices and MAPER whole brain mask models from ADNI baseline cohort, generated using 3D Slicer 4.3.1.

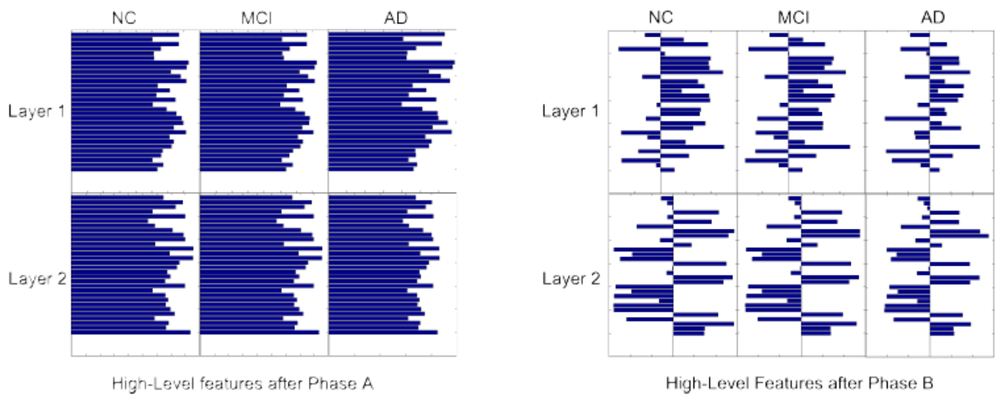
Results

The performance (%) of the AD binary classification between NC and AD. The first two columns are precisions on each class. The last three columns depict the overall performance (accuracy, sensitivity and specificity).

	NC	AD	ACC	SEN	SPE
MKSVM	89.10 ± 1.26	90.13 ± 1.02	89.60 ± 0.91	89.09 ± 1.39	90.10 ± 1.12
SAE	89.39 ± 10.73	85.67 ± 14.94	88.20 ± 7.68	87.66 ± 9.50	87.50 ± 15.04
Proposed	91.17 ± 8.54	88.35 ± 8.17	90.11 ± 3.06	84.45 ± 10.51	93.89 ± 6.31

The performance (%) of the trinary AD classification between NC, MCI and AD. The first three columns are precisions on each class. The last three columns depict the overall performance (accuracy, sensitivity and specificity).

	NC	MCI	AD	ACC	SEN	SPE
MKSVM	47.53 ± 2.59	57.29 ± 0.90	49.74 ± 2.33	53.2 ± 1.27	44.59 ± 2.89	85.00 ± 1.92
SAE	46.97 ± 21.71	61.87 ± 12.26	60.78 ± 15.88	58.57 ± 9.21	49.16 ± 16.60	83.53 ± 6.56
Proposed	49.00 ± 22.42	61.29 ± 12.94	61.52 ± 13.87	59.19 ± 9.20	50.98 ± 16.08	84.36 ± 6.71



The examination of the high-level features extracted by Phase A and Phase B (applied MMSE scores) of MPFR. These features were obtained by a network with 2 hidden layers of 30 neurons each.

Conclusion

In this study, we presented a novel framework, the Multi-Phase Feature Representation (MPFR), for the feature representation of neuroimaging data. It differs between the conventional deep learning architecture by learning features to output low-dimensional biomarkers before the deep network is fine-tuned with classification labels. The preliminary results showed that MPFR framework outperformed SAE as well as the state-of-the-art classification method (Multi-Kernel SVM) and had a great potential to embed other low-dimensional biomarkers in feature representation learning without constraining the size of available training data.

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