Machine learning to predict brain amyloid pathology in pre-dementia Alzheimer's Disease using QEEG feature with genetic algorithm

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Introduction

- Alzheimer's disease is one of the major cause of dementia. Currently, Beta-Amyloid is a representative diagnostic index of Alzheimer's disease[1].
- Although Amyloid PET is commonly used to detect Amyloid, its high-cost and radioactivity restrict patients to take it[2].
- Researches have proven that EEG have potentiality as a biomarker and can be used to classify brain diseases[3].
- We found different QEEG pattern between Amyloid(+) and Amyloid(-) group, suggesting the validity of QEEG as a biomarker.

Methods

- Data & Pre-Processing

Normal(+)	Normal(-)	MCI(+)	MCI(-)	total
146	34	29	34	243

Tbl 1. the number of data

- Total 243 Eye-closed Resting-state EEG data
- 80% data for Train, 20% data for Test
- 19 channels based on international 10-20 system
- Bad epoch rejection and ICA method using iSyncBrain®
- Absolute/Relative power of 19 channels and 8 frequency bands. Therefore, 304(2*19*8) features In total.

- Feature Selection & Modeling

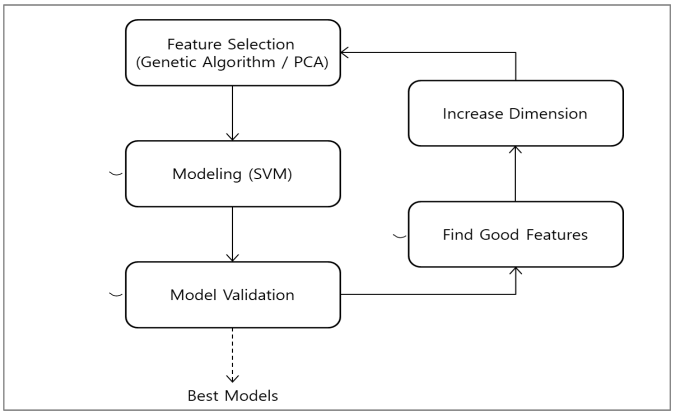
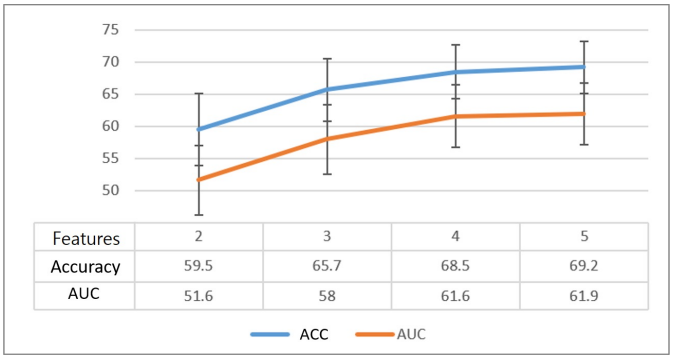


Fig1. The schematic diagram of feature selection and modeling

- Goal 1 is to classify Normal Amyloid (+) vs Normal Amyloid (-)
- Goal 2 is to classify MCI Amyloid (+) vs MCI Amyloid (-)
- SVM (polynomial) based classification model
- Increasing the number of features from 3, and 4, then 5
- Features selection with Genetic Algorithm
- ensembled multiple models and build a scoring system

We tried all combinations of 3 features and selected top 20% features that shows better accuracy [good features]. Then, only using these good features, we tried all combinations of 4 features and repeated same process.

Results



Features	2	3	4	5
Accuracy	59.5	65.7	68.5	69.2
AUC	51.6	58	61.6	61.9

Fig 2. Models performance with different number of features

We found the average accuracy and AUC increased as the number of features Increased.

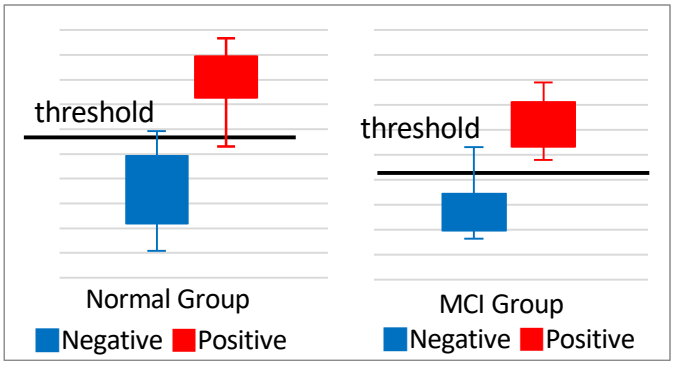


Fig 3. Box plot of Amyloid classification score

Normal	True Positive	True Negative
Predicted Positive	10	2
Predicted Negative	3	33

MCI	True Positive	True Negative
Predicted Positive	11	3
Predicted Negative	2	32

Tbl 2. Confusion matrix of classification

Best Normal Model Showed 92.6% sensitivity, 89.0% specificity and 90.5% accuracy. Best MCI Model Showed 82.5% sensitivity, 86.7% specificity and 85% accuracy.

Conclusions

- We suggests Genetic Algorithms can be useful for feature selection of QEEG, in that it can reasonably cut the number of feature combinations in brain signals.
- We confirmed QEEG can be used as a biomarker for beta-Amyloid. As QEEG is more accessible than PET, QEEG biomarkers can reduce the cost of diagnosis.

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