

Research Summary

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3D Regional Shape Analysis of Left Ventricular Using MR Images: Abnormal Myocardium Detection and Classification

- Accepted by IEEE International Symposium on Biomedical Imaging (ISBI)

Problem Setup

- Previous indices (such as wall thickness, strain and curvature) are usually correlated to the AHA 17-segment model and only suitable for ischemic heart disease.
- The primary goal of this study is to propose a novel framework that helps to automatically extract regional 3D indices representing abnormal LV morphology.

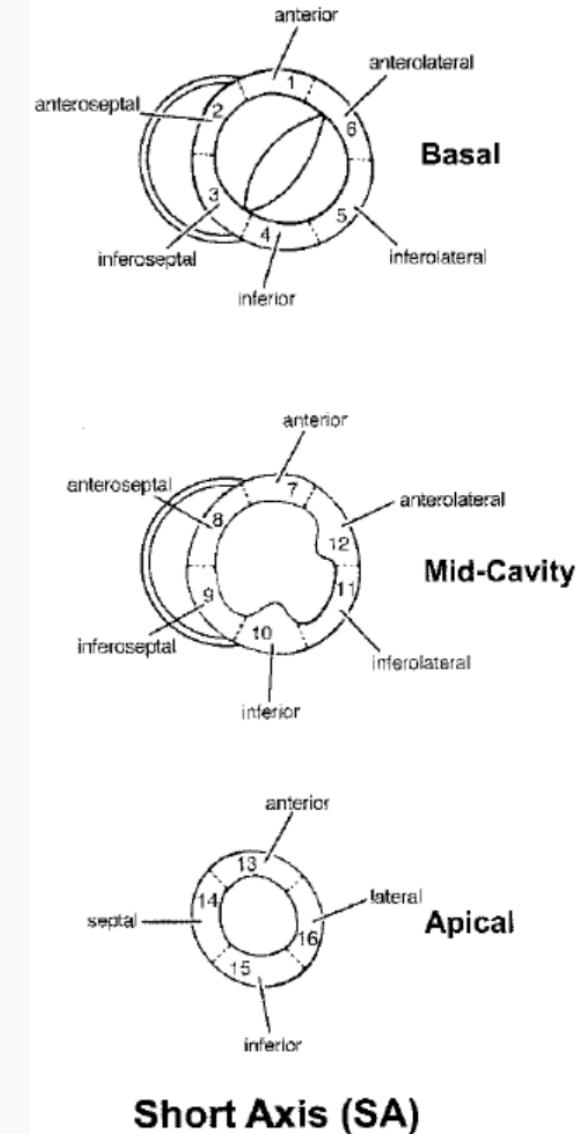
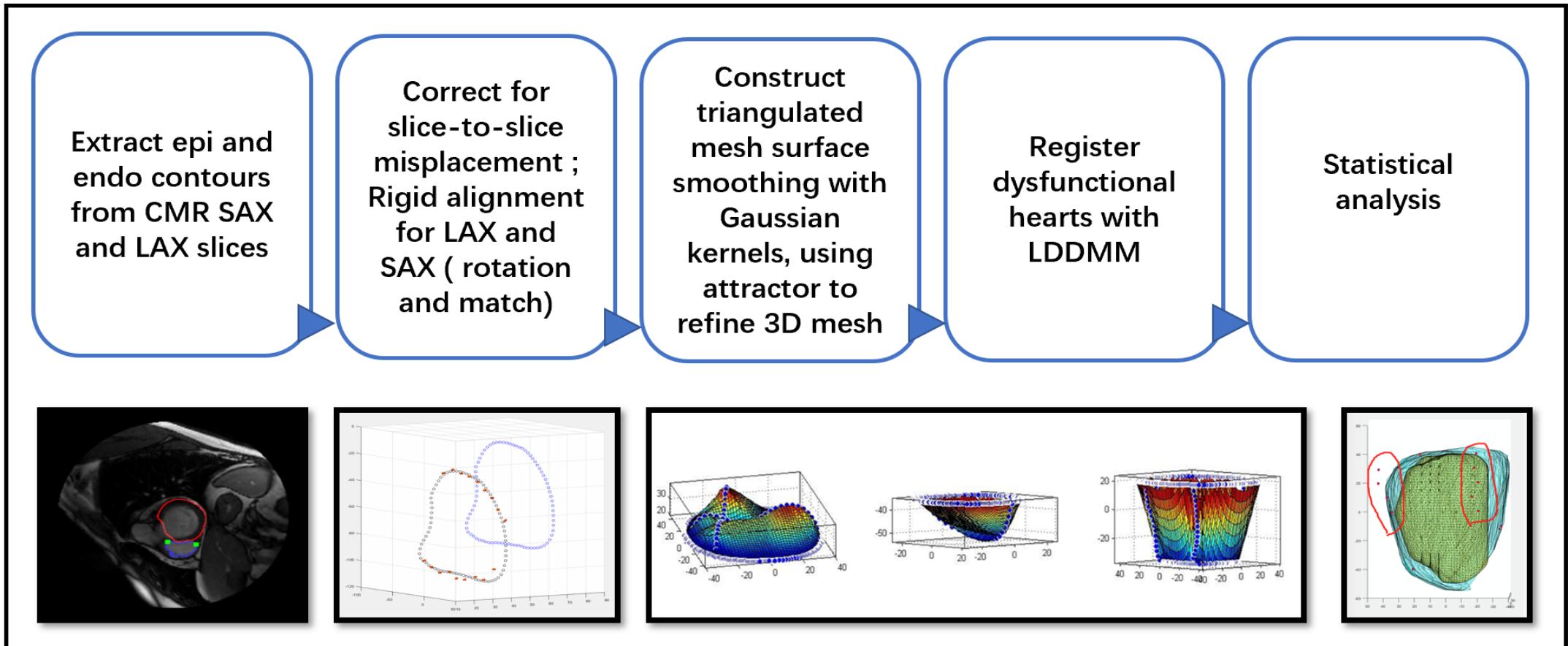


Illustration of AHA 17 Segments

Flow charts of proposed framework



Data Acquisition and Registration

- Our study included 24 subjects from Sunnybrook Cardiac Data. Three different heart failure types are included in the dataset: myocardial infarction (HFI), heart failure without infarction (HFNI) and hypertrophy (HYP) patients.

| | HYP | HFNI | HFI |
|-------------------|----------|---------|----------|
| Male Cases | 5 | 4 | 5 |
| Age(year) | 61(13) | 72(12) | 55.5(13) |
| LVEDV (ml) | 130 (51) | 238(56) | 190(41) |
| LVESV (ml) | 37(21) | 144(43) | 162(52) |

- In our study, LDDMM-ot was used to construct the average normal template, and multi-kernel LDDMM [was used to register all individual 3D model.

Abnormal Regions Visualization on 3D Surfaces

- Multilinear principal component analysis (MPCA) was used to extract the features that contributed the most to group variance.
- The principle features (top 5) extracted by MPCA were retrieved and projected on the original 3D models for visualization.

Decomposition: $v_k = \text{argmax}(Xv)^T(Xv)$

where $\|v\| = 1$, $v^T v_j = 0, j = 1 \dots k - 1$

Reconstruction from the first k features:

$$X' = Xv_1 \dots v_k v_{1 \dots k}^T$$

Disease Classification

- Data: Displacement field calculated from LDDMM algorithm reflected how large a part was different from the normal case.

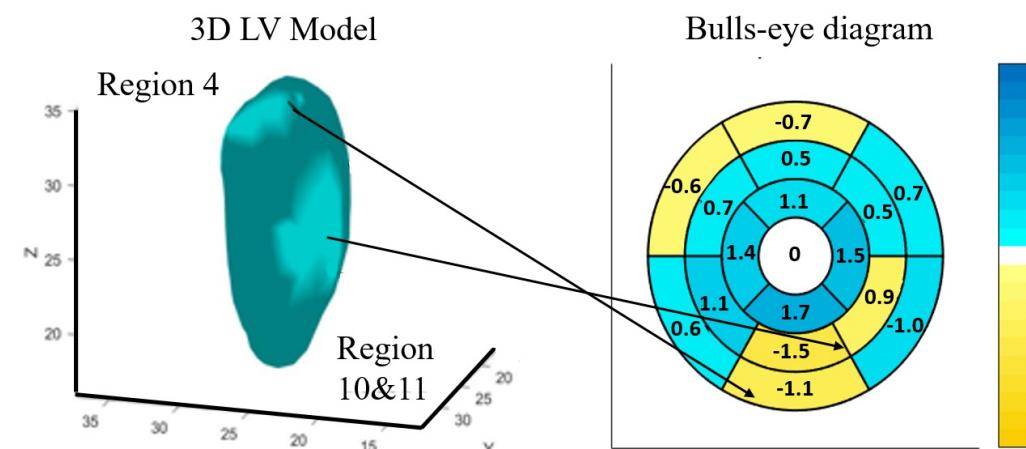
Table 1. Classification Results

| Task | Methods | Leave-one-out Accuracy | Sensitivity (Specificity) |
|-----------|----------------------------|------------------------|---------------------------|
| HFNI-HFI | Global Points Signature | 68.75% | 87.50% (50.00%) |
| | Random Forest | 62.50% | 75.00% (50.00%) |
| | XGBoost | 75.00% | 87.50% (62.50%) |
| | MPCA + LDA + Random Forest | 94.00% | 100% (89.00%) |
| HFI - HYP | Global Points Signature | 62.50% | 75.00% (50.00%) |
| | Random Forest | 62.50% | 50.00% (75.00%) |
| | XGBoost | 62.50% | 62.50% (62.50%) |
| | MPCA + LDA + Random Forest | 94.00% | 100% (89.00%) |
| HFNI-HYP | Global Points Signature | 62.50% | 87.50% (37.50%) |
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| | MPCA + LDA + Random Forest | 94.00% | 89.00% (100%) |

Automatic Detection & Visualization of Abnormal Regions

A hypertrophic cardiomyopathy case was illustrated in Figure 2 as an example. The light blue points on the left represented the first 5 components. And on the right, the regional shape changes based on displacement field were summarized and presented according to conventional 17-segment model.

Few regions of the endocardium appeared to be closer to the central line comparing to normal cases. The neighbor regions accompanied to be further away from the central line. This is consistent with morphology of eccentric hypertrophy and its compensation in LV remodeling

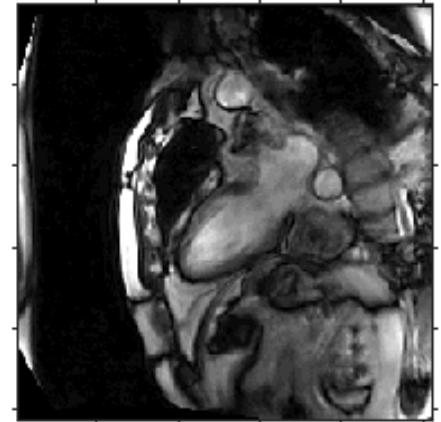


Cardiac Multi-View MR Imaging Segmentation and Domain Adaptation with Marginalized Denoising Autoencoder

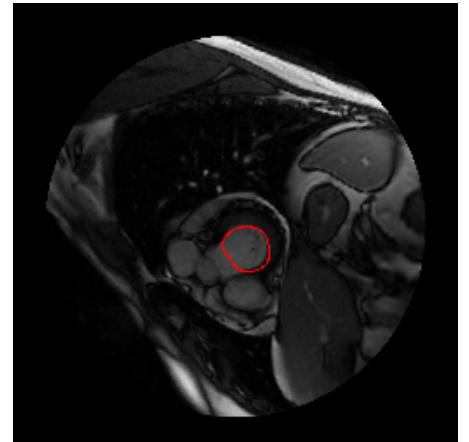
Background

Segmentation of cardiac left ventricle (LV) from cardiac long-axis (LAX) MR Imaging has long been a difficult task because of the following:

- Lack of large dataset for deep learning training: 8~12 short-axis (SAX) images vs. 0~2 LAX images per patient were taken during a clinic check.
- Texture / brightness difference of the MR imaging between different datasets.



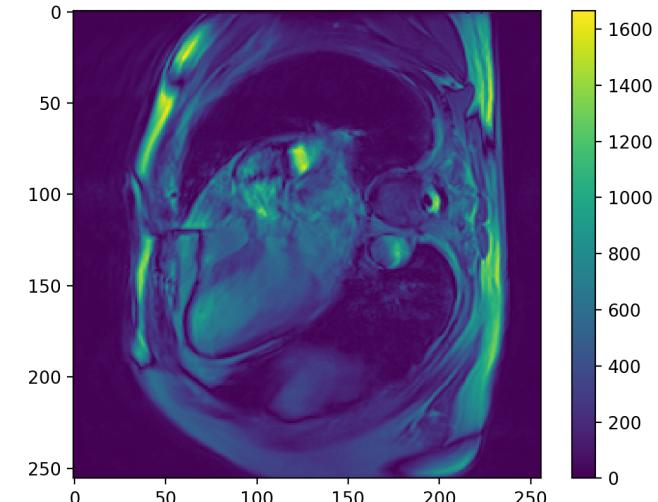
Cardiac Long-axis images



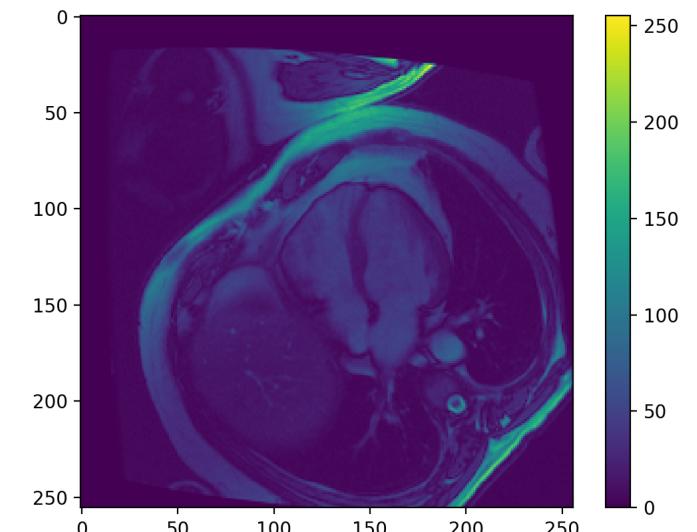
Cardiac short-axis images

Problem Setup

- Sunnybrook cardiac dataset provides 250 SAX and 50 LAX images with ground truth contour.
- Our task is to develop a model to segment left ventricle on both SAX and LAX images obtained from Massachusetts General Hospital (MGH) cardiac dataset.
- This task was viewed as a general domain transformation problem. Improving the similarity of images between different datasets can possibly lead to higher segmentation accuracy.

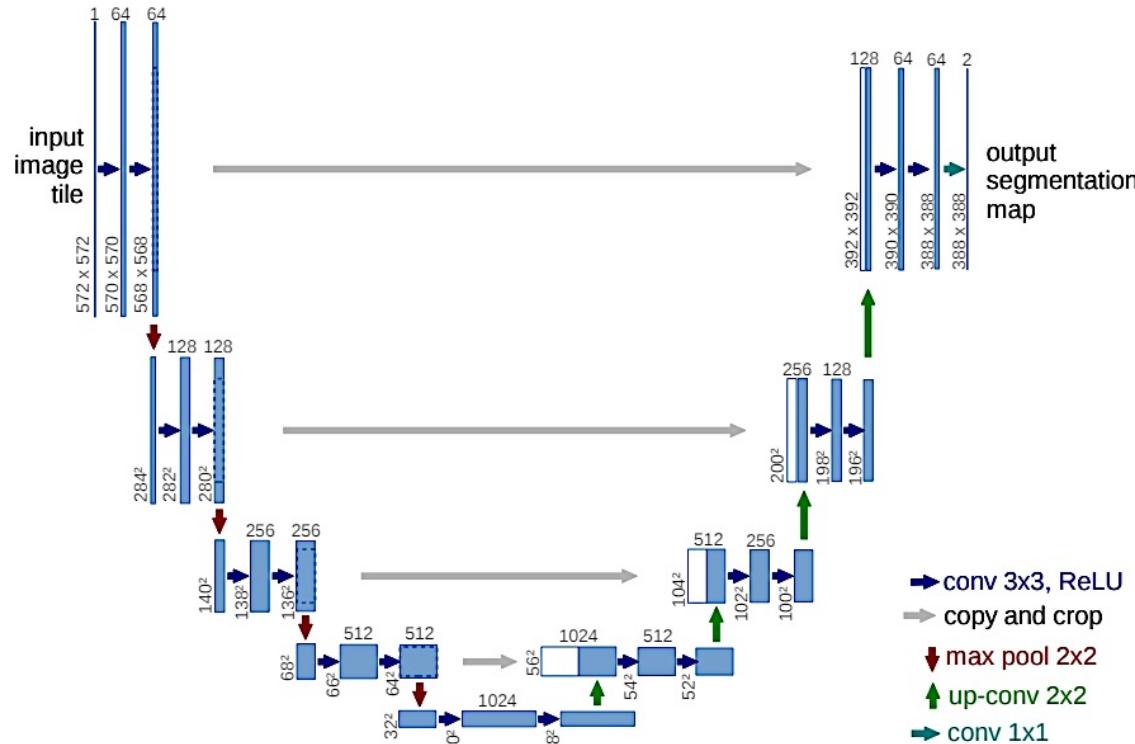


Sunnybrook LAX image



MGH LAX image

Deep Learning Architecture for Segmentation



Cited from:
U-Net: Convolutional Networks for Biomedical Image Segmentation, Olaf Ronneberger, 2015

Architecture:
U-net with pretrained VGG16 checkpoints.

Model 1 (for SAX segmentation):
U-Net trained on Sunnybrook SAX data.

Model 2 (for LAX segmentation):
Train Model 1 on Sunnybrook LAX data.

| Dice Accuracy for LV segment model | | |
|------------------------------------|-----|-----|
| Test data from | SAX | LAX |
| Sunnybrook | 92% | 88% |
| MGH | 65% | 18% |

Large drop

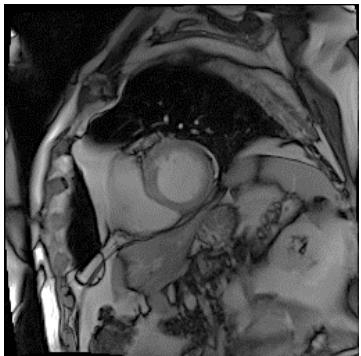
Previous Methods

- Converting two domains into the same one before training the segmentation model: Varghese Alex[2017]. (not desired)
- Texture adaption with Histogram Matching.
- Using edge information to adjust contours given by segmentation mdoels: Huaifei Hu[2014].

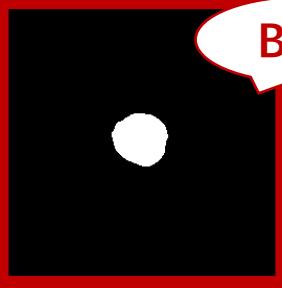
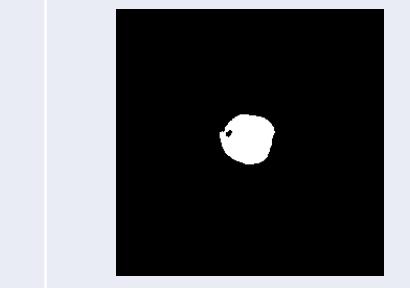
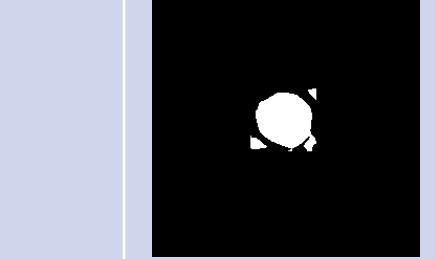
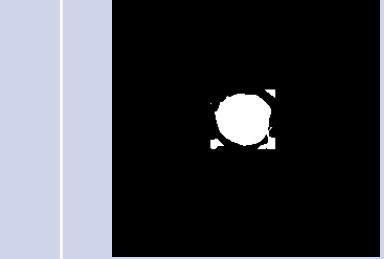
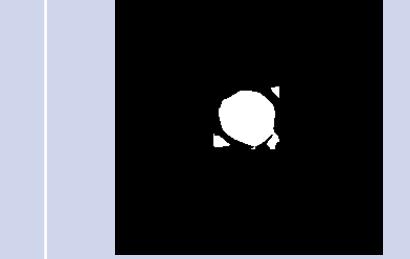
Performance of Previous Methods

Test Sample: MGH SAX data with Dice accuracy of 90%.

Conclusion: Self histogram equilibrium, histogram matching and adding edge information sometimes will not improve the results.

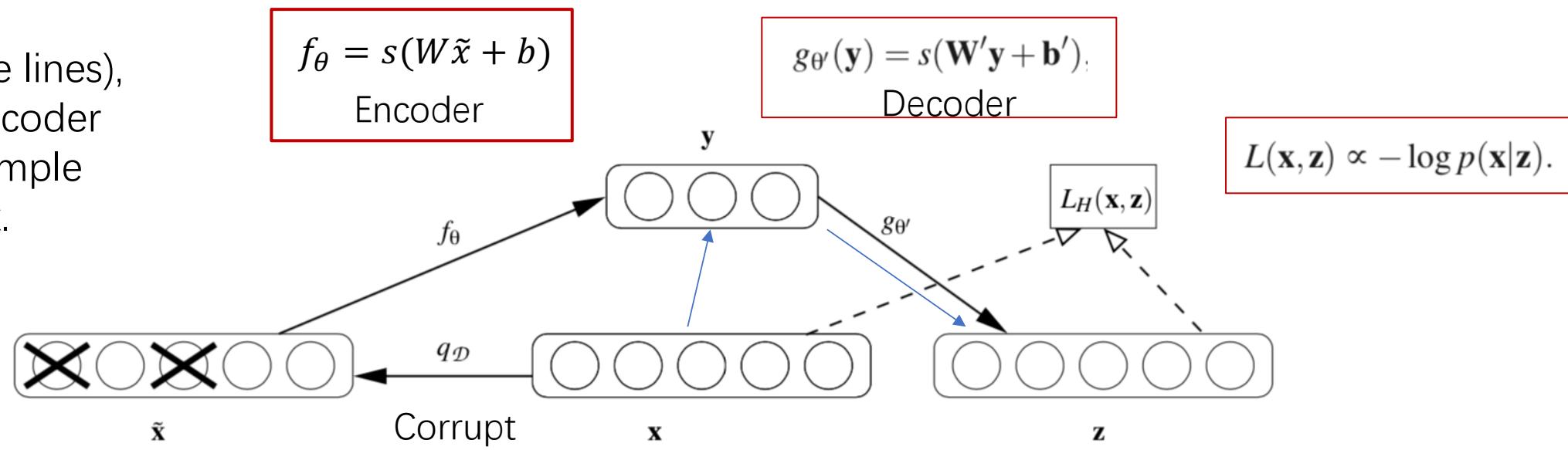


ground truth

| | | Self Equilibrium: False | | Self Equilibrium: True | |
|--|--|---|---|---|---|
| | | Histogram Matching: False | Histo- Matching: True | Histo- Matching: True | Histo- Matching: True |
| Adding Edge Detection Results: False |  Best | | | | |
| |  |  |  |  |  |
| Adding Edge Detection Results: True |  |  |  |  |  |
| |  |  |  |  |  |

Domain Adaptation with De-noising Autoencoder

Compared with
Autoencoder (Blue lines),
Denoising Autoencoder
uses corrupted sample
 \tilde{x} to reconstruct x .



Why this can help with
domain adaptation?



View the whole process as a MCMC simulation of $P(x|\tilde{x})$.
Sample generator is q_D . After training, given random sample from two datasets as \tilde{x} , the projector $f_\theta(g_{\theta'}(\cdot))$ can be found to convert the samples into the common space.

Marginalization and Domain Adaptation

With finite samples, the simulation process can be simplified as Marginalized De-noising Autoencoder (Minmin Chen [2012]):

$$\mathcal{L}_{sq}(\mathbf{W}) = \frac{1}{2mn} \sum_{j=1}^m \sum_{i=1}^n \|\mathbf{x}_i - \mathbf{W}\tilde{\mathbf{x}}_{i,j}\|^2$$

$$\mathcal{L}_{sq}(\mathbf{W}) = \frac{1}{2nm} \text{tr} \left[(\bar{\mathbf{X}} - \mathbf{W}\tilde{\mathbf{X}})^\top (\bar{\mathbf{X}} - \mathbf{W}\tilde{\mathbf{X}}) \right]$$

$\mathbf{W} = \mathbf{P}\mathbf{Q}^{-1}$ with $\mathbf{Q} = \tilde{\mathbf{X}}\tilde{\mathbf{X}}^\top$ and $\mathbf{P} = \bar{\mathbf{X}}\tilde{\mathbf{X}}^\top$.

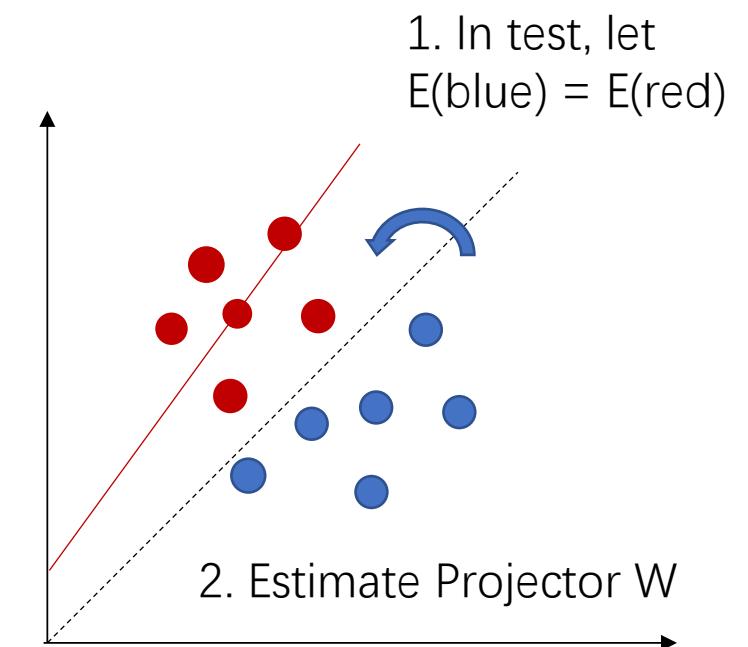
$\mathbf{W} = E[\mathbf{P}]E[\mathbf{Q}]^{-1}$.

$$\mathbf{W} = \frac{N_a \bar{\mathbf{X}}_a + N_b \bar{\mathbf{X}}_b}{N_a + N_b} \tilde{\mathbf{x}}^\top E[\mathbf{Q}]^{-1} = \mathbf{W}_a \quad (\text{if } \bar{\mathbf{X}}_a = \bar{\mathbf{X}}_b)$$

Thus, we can use \mathbf{W} to estimate $P(x_a | \tilde{x})$.

Loss function

Solve as linear regression



Convert MGH dataset (blue points) to look like Sunnybrook dataset (red).
(can be improved)

Application on MGH cardiac data

- Limitation of all types of Autoencoder:

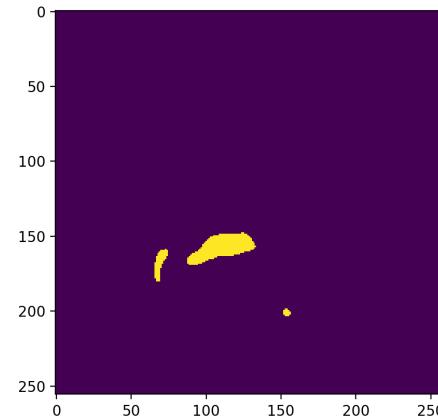
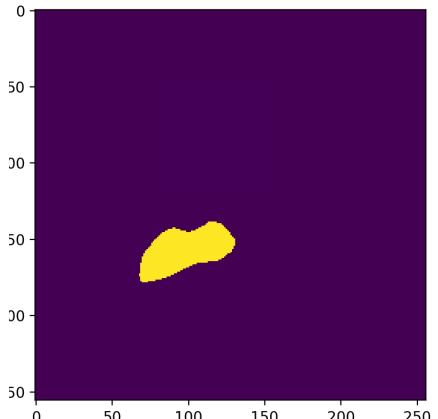
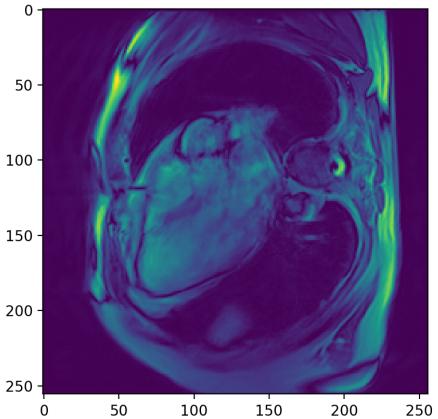
Autoencoder assume that for real-value x , $X|z \sim \mathcal{N}(z, \sigma^2 I)$.

Therefore, it may not perform well on 2D image data.

Following steps were taken to guarantee domain adaptation performance:

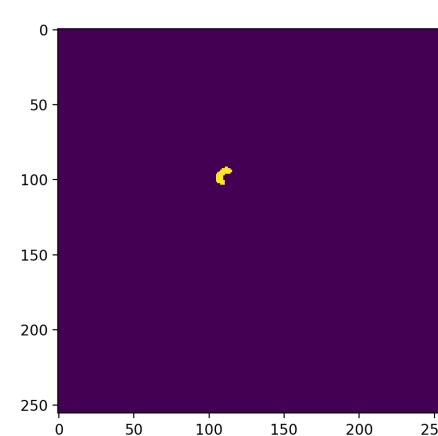
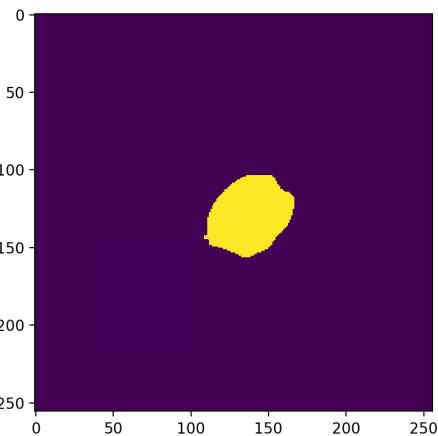
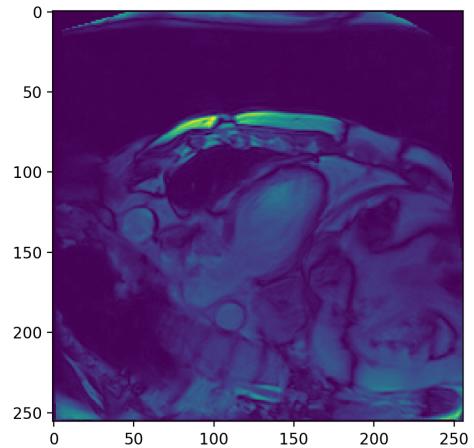
- Step 1: Bin the train/test data into histogram 0~255.
- Step 2: Perform Marginalized Stacked De-noising Auto-encoder (4 layers).
- Step 3: Reconstruction- Covert transformed bins back into images with linear interpolation.

Test Performance



After sDAE (DICE = 78%)

Before sDAE (DICE = 15%)



After sDAE (DICE = 73%)

Before sDAE (DICE = 0%)

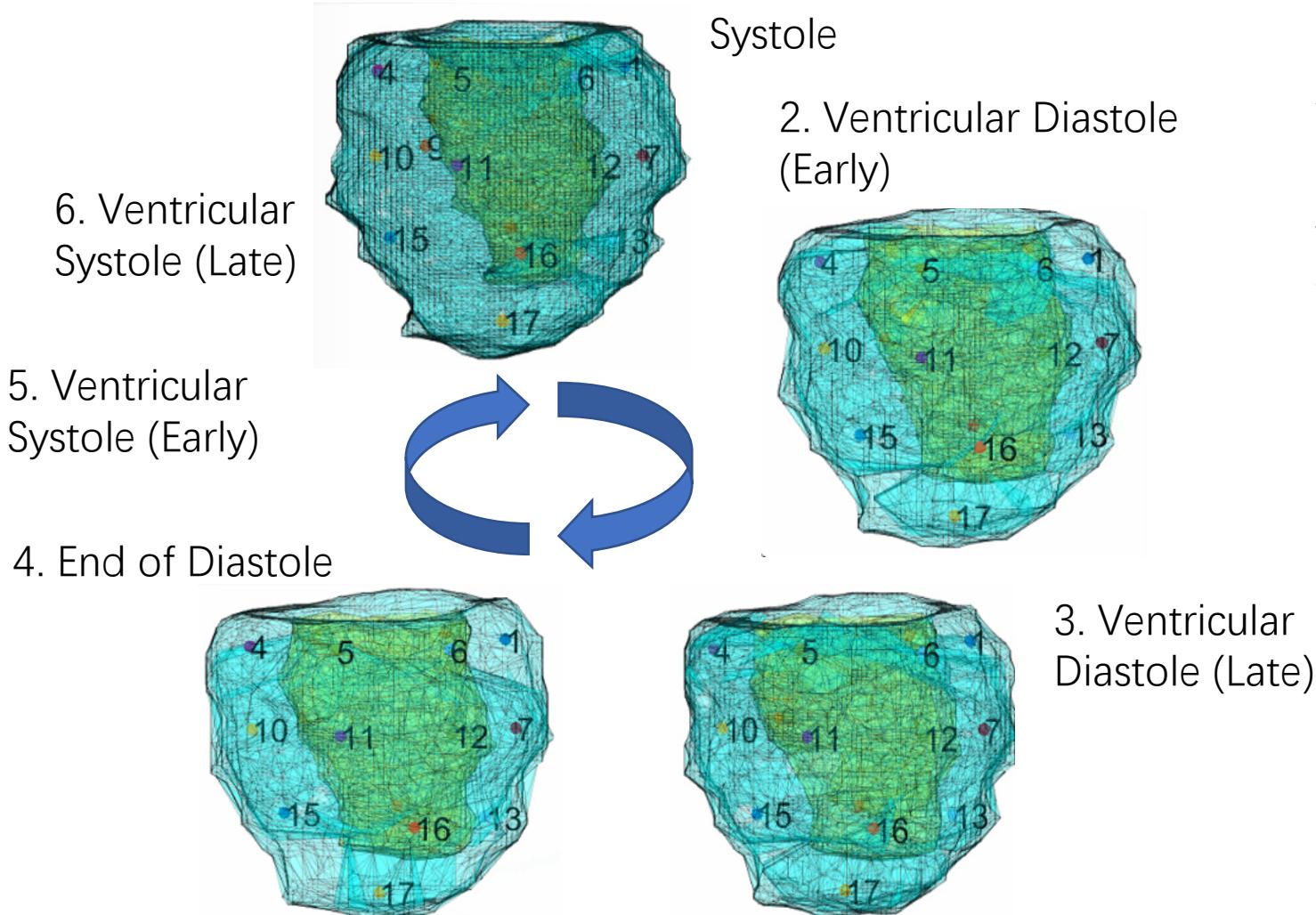
Segmentation performance using U-net improved a lot.

However, random holes may appear on the mask. This problem links with the robustness of the deep learning network.

Novel Marker for the Detection of Difference in Cardiac Working Pattern

Pilot Study at Two Time Points

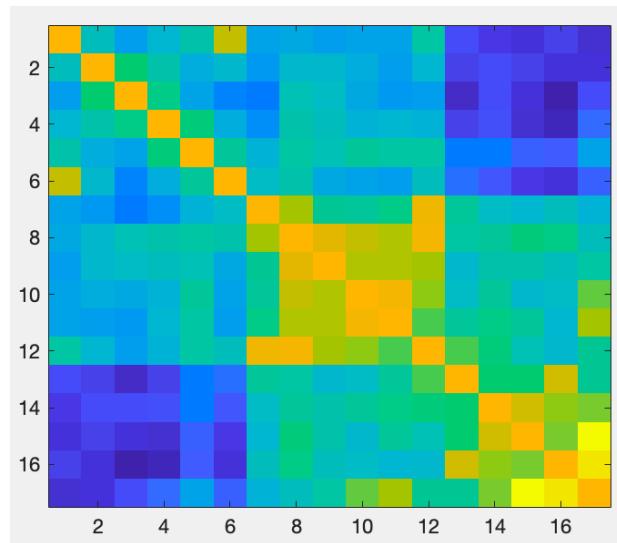
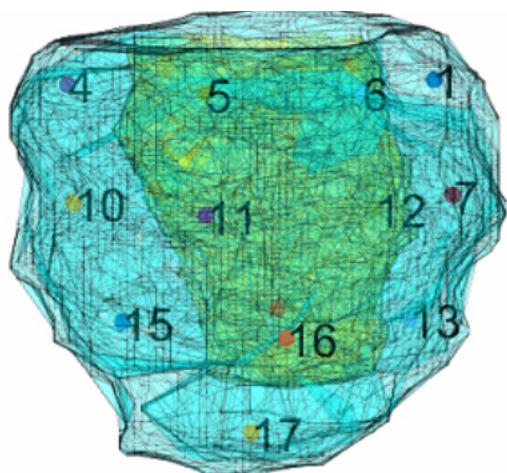
Cardiac Circle



Existing biomarkers for Cardiac Circle:
Volume of Left Ventricle, Cardiac Sphericity.

We proposed a novel biomarker—cardiac skeleton to reveal the working pattern of myocardium through a cardiac circle.

Problem Setup



Skeleton was defined by linking the center points of AHA 17 segments of the myocardium.

This system can be represented by a graph where nodes $V=17$ represent the key points, edges $E = 136$ represent the length of linkages between points.

Goals:

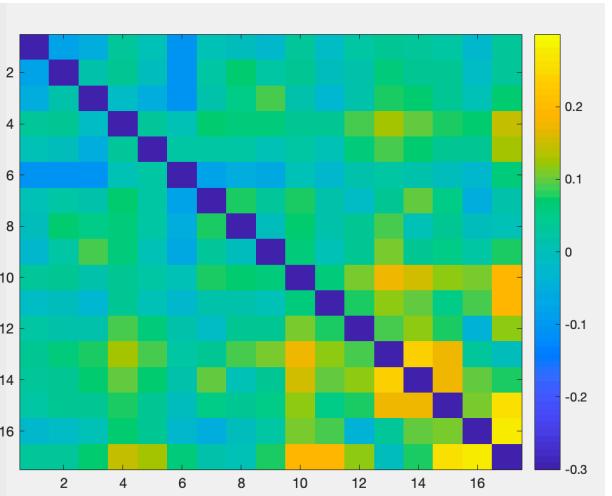
1. Detect changes of working patterns of 17 cardiac regions between two clinic measurements.
2. Link the biomarker with clinic outcomes— Recover or Worsen.

Problem Setup (2)

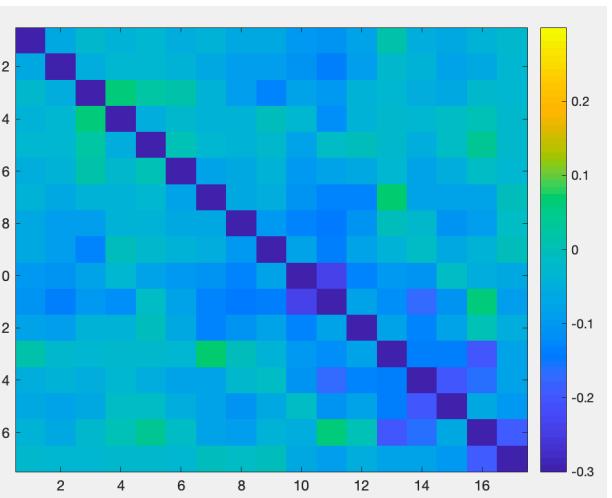
By taking the difference between graphs constructed from time1 and time2 data, the changes of working patterns can be detected and then be used to predict outcome labels.

For different diseases, the functioning mechanism of the heart can be very different, thus it is also of our interest to rank the 17 regions based on the graph and find regions that change the most and the least in each dysfunctional group.

Worsen (Heart gets fatter)



Recover



Difference between graphs at time1 and time2, element-wise divided by individual time1 graph.

Ranking Algorithm Based on Graph Partitioning

Preliminary Definition

Given an undirected graph $G=(V, E)$, where $V=17$ represents unordered cardiac regions, $E = 136$ represents the percentage change of each linkages of the cardiac skeleton, ordering the nodes $V_i > V_j > \dots > V_k > V_m > V_n > V_o$ to enforcing the following:

- 1) The weighted edge value $W_{ij} = E_{ij} / \text{Degree}(V_i) + E_{ij} / \text{Degree}(V_j)$ bigger than W_{km} .
- 2) After coarsening the graph based on 1), $W_{\{ij,km\}} > W_{\{km,no\}}$. This guarantees that not only is W_{ij} the biggest value on the graph, but also $\langle V_i, V_j \rangle$ is the most influential pair among the all.
- 3) If $W_{ij} > W_{km}$ is determined, $V_i > V_j$ if $\text{Degree}(V_i) > \text{Degree}(V_j)$.
- 4) An $O(N^2)$ algorithm to rank the node is to partition the graph based on METIS and sort the current highest layer by weighted edge value at each iteration.

Sudo Code

Compute Degree for each node

Degree= sum(Laplacian) at each row

Repeat

Random start at V_i

If V_i is unmarked:

 Compute weighted edge value between V_i and all the unmarked V_j

$W_{ij} = E_{ij} / \text{Degree}(V_i) + E_{ij} / \text{Degree}(V_j)$

 Select (V_i, V_j) that has the biggest weighted edge value

end if

Sort all the subtrees based on the weights W_{ij} .

(This gives subtrees with higher W_{ij} more chances to be selected earlier).

Until all the nodes are marked

} (*)

Coarse original graph by combining edges started from the same cluster together.

If number(V) in graph != 1:

 repeat (*);

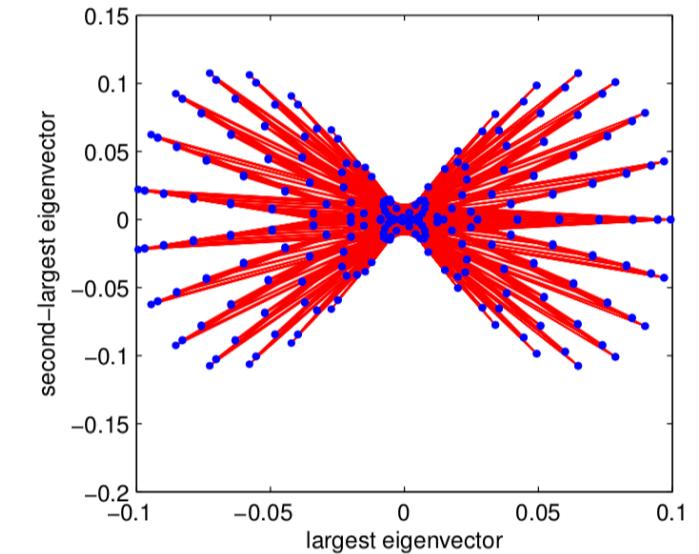
If the degree of right leave $V_i >$ left leave V_j , swipe V_i, V_j ;

Validation of the New Biomarker

- To verify that the edges between 17 segments (132 features) on the skeleton can be used to predict outcome labels (recover or not), ChebNet (Michaël Defferrard [2017]) was used as classifier.
- In graph signal processing theory, the eigenvectors U of the Laplacian L represent a space in which the projection of feature $x^T L x$ represents how far away one sample is from its neighbors, as illustrated in the left figure.
- ChebNet Graph convolutional neural network is defined as $y = g_\theta(L)x = U g_\theta(\Lambda) U^T x = U \sum_{k=0}^{K-1} \theta_k \Lambda^k U^T x$.

↓
Graph convolution operator. If null, it is just $Lx = v(i)-v(j)$

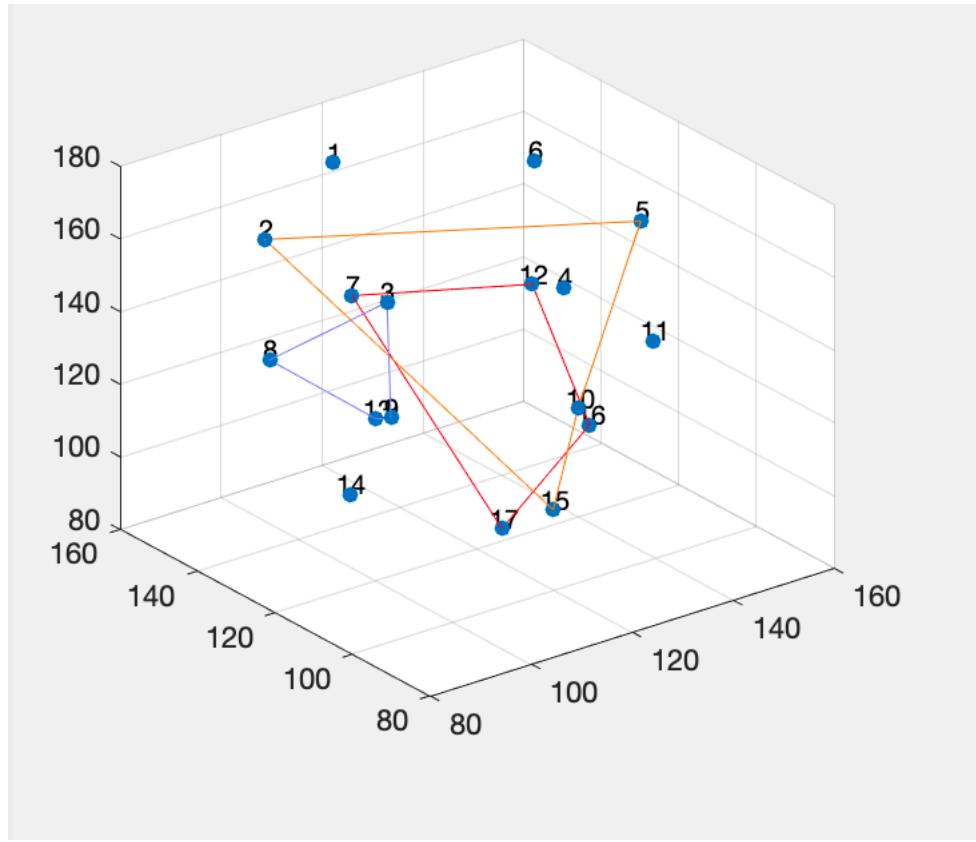
↓
Polynomial parametrized estimation to accelerate the $g_\theta(L)x$ as $\sum_k \theta_k (L)_{i,j}^k$.



Embedding of features with 1st, 2nd eigenvectors of Laplacian as coordinates
(from Standford CS168 notes)

Results

This figure illustrated the clusters found by the ranking algorithm.

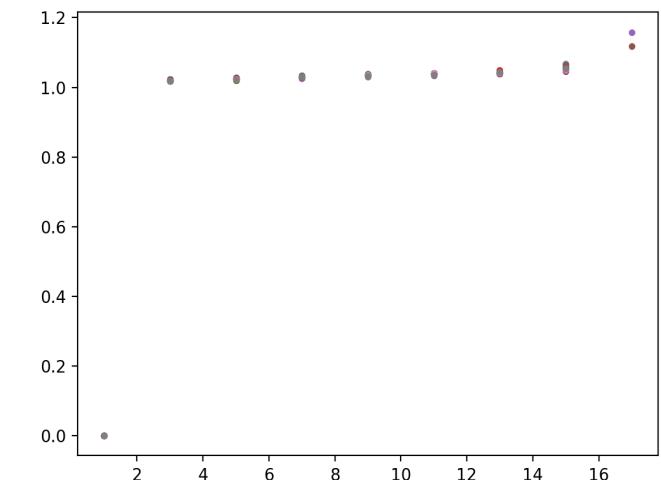


Blue showed the part that has the least (and negative) values. Red and yellow points showed the part that has the biggest positive changes between two measurements.

From the plot, we can clearly tell that the heart was generally enlarged during the two measurement. The blue areas may lose its function and cause the deterioration.

Discussion

- In the pilot study, we only apply Chebnet on the first measurement of all the patients to predict the diagnosis labels (recover or not) because we are still processing MR images. Currently, the accuracy is 78%. If we include longitudinal data, the accuracy should be improved a lot.
- There are negative weights on the graph when we were trying to conduct graph partitioning and ranking, as the positive sum and the negative sum of the partitioned graph can not be optimized at the same time, we chose to record the weights value and preserve clusters that only have positive, or negative values.
- Since there are negative values in the graph, we also tried to calculate eigenvalue of the Laplacian to determine how many clusters can be made. For example, the left figure shows that a) we can make clusters from the graph as eigenvalue₁>0; b) the number of clusters $\frac{1}{2} \times \text{eigenvalues}_2^2 \leq N < 2 \times \text{eigenvalues}_2$, which is 2~3.

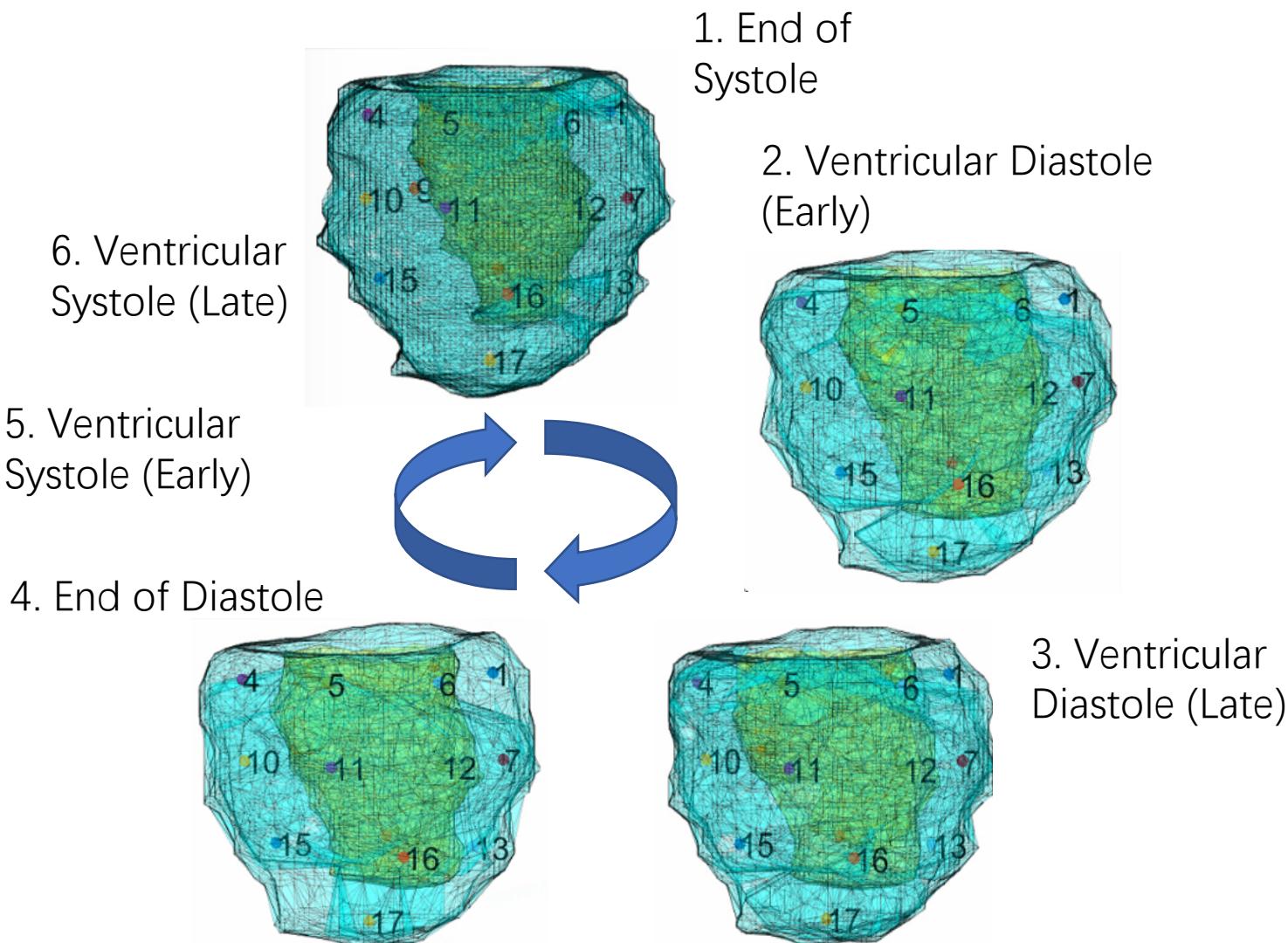


Eigenvalues of Laplacian
of two samples

Invariant Pattern Throughout the Cardiac Circle

Pilot Study at Selected Time Points in a Cardiac Circle

Cardiac Circle

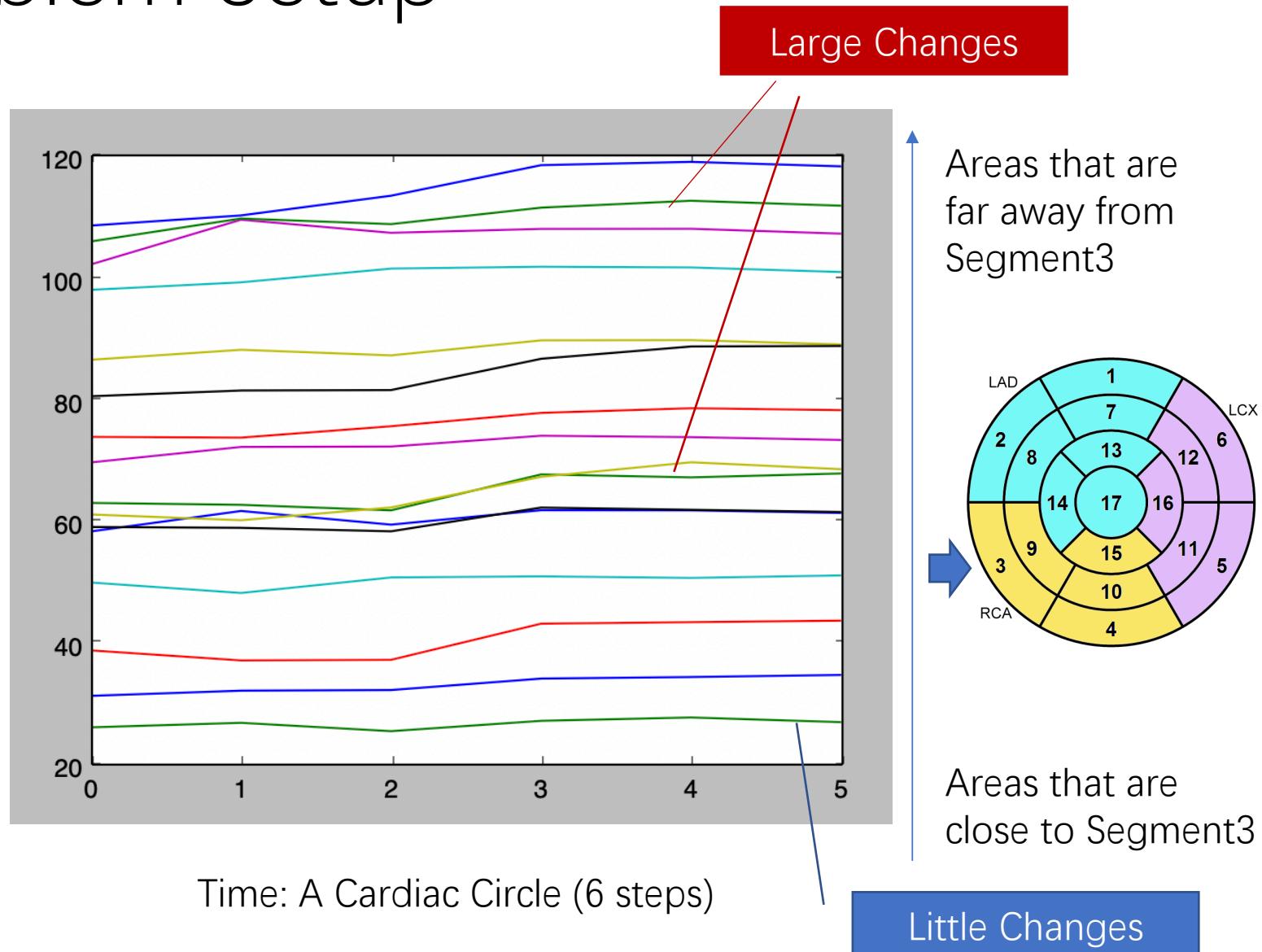


Existing biomarkers for Cardiac Circle:
Volume of Left Ventricle, Cardiac Sphericity.

How to detect abnormally edge changes through a cardiac circle?

Problem Setup

Length of linkages between Segment3 and other parts of the cardiac surface



Basic Assumption

For a region of the cardiac surface (For exp. Segment3 & Segment9), it is abnormal that the very remote segments (like Segment12) change the most during a cardiac circle.



Goal

Build a model to reflect variant / invariant patterns of the linkages.

As a pilot study, we only used one cardiac circle to model the invariant pattern.

Preliminary Definition

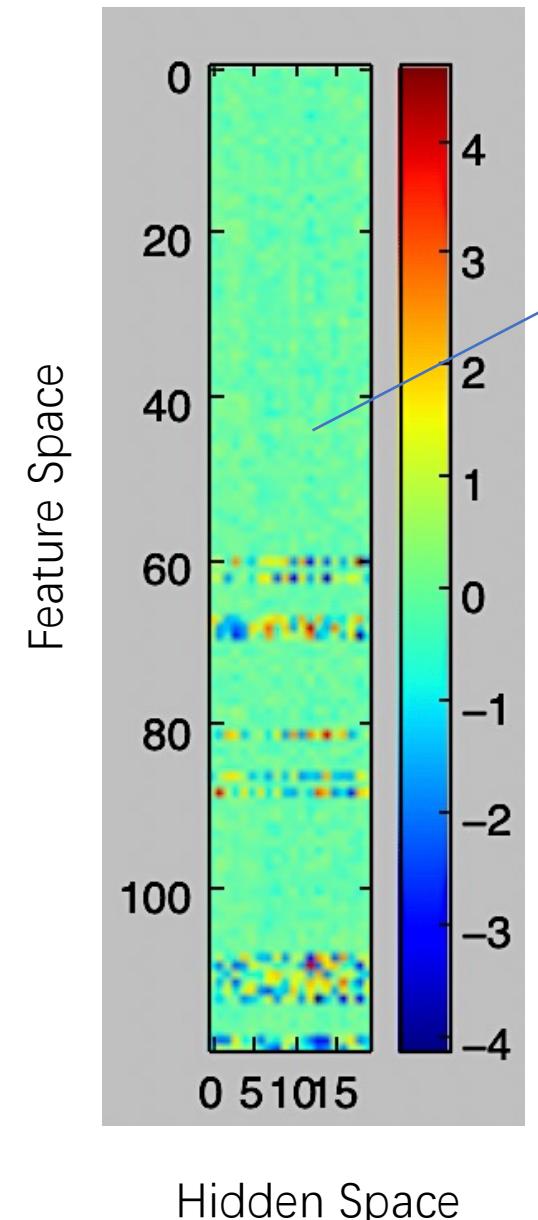
- Consider a system of first-order differential equations: $\dot{x} = F(x)$.
- Define auxiliary scalar function: $q(x) = \frac{1}{2} |F(x)|^2$
- $q(x^*) = 0$ if and only if x^* is a fixed point of F .
- The Hessian of q : $\frac{\partial^2 q}{\partial x_i \partial x_j} = \sum_k^N \frac{\partial F_k}{\partial x_i} \frac{\partial F_k}{\partial x_j} + \sum_k^N \dot{x}_k \frac{\partial^2 F_k}{\partial x_i \partial x_j}$.
- For q to be at a minimum, the gradient $\dot{x}_k = 0$, or that $\frac{\partial F_k}{\partial x_i}(x) = 0$, and $\sum_k^N \dot{x}_k \frac{\partial^2 F_k}{\partial x_i \partial x_j} > 0$, or that \dot{x} is a zero eigenvector of $\frac{\partial F}{\partial x}$.

Method

- Construct Recurrence Neural Network, using Time t edge information to predict t+1 edge value: $X_{t+1} = VS_t(X_t)$
- Hidden layer were defined as $S_t = f(Ux_t + WS_{t-1})$, where f is the ReLu function. The output layer $O_t = VS_t$.
- For feature x_i , this system $\dot{x}_i = F(x) = -x_i + \sum_k^N V_{ik}S_k$.
- The Jacobian of the network is $\frac{\partial F_i}{\partial x_j} = -\delta_{ij} + V_{ij}r'_j$. $\delta_{ij}=1$, if i=j and otherwirse 0.

Results

- As an illustration of this method, we used the linkages starting from Segment3 and Segment9 as inputs and model the motion throughout the cardiac Circle (6 steps).
- Two hidden layers were used in RNN.
- The left plot shows the Jacobian of the network on the first hidden layer. The dimension of the hidden space is 20, the dimension of the feature space is $\max(X)+2$.



Large parts were invariant. This means areas that are close to Segment3 and Segment9 changed less throughout a cardiac cycle, which is abnormally.

Discussion

- With the proposed method, we do not have to model the motion of each edges but still get the invariant patterns.
- The current application has the following problems:
 1. The input feature space is sparse and too many invariant states were found. Currently we only discussed the meaning of the non-zero part of the Jacobian.
 2. If the input space has 120 dimension, the hidden space is not large enough to capture all the changes of state, which is of the dimension of 120^2 .
 3. Only one cardiac cycle was used in this pilot study.

We are trying to collect more data. To improve the current model, we will try to model the diastole (enlarge, state:1) period and find the edges that has the opposition motion (shrink, state:-1).

Detection of Mild Cognitive Impairment using Brain Magnetoencephalography Data

1. Backgrounds, Goals and Tools

Backgrounds

- Dementia of the Alzheimer's type (DAT): disconnection syndrome.
- Mild Cognitive Impairment (MCI): Hypersynchronization over prefrontal and posterior areas could be a hallmark of network disruption at early clinical stages of the disease. [1]
- The physiopathological patterns of this disease could manifest differently at different stages of the disease.

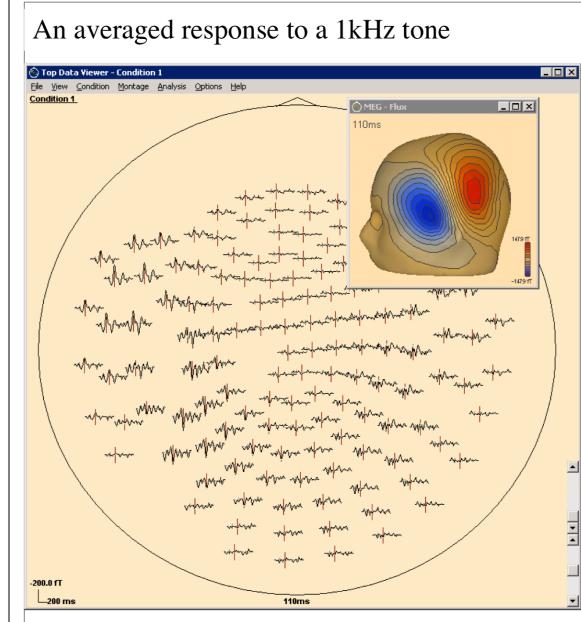
[1] Bajo, R., Castellanos, N.P., Cuesta, P., Aurtenetxe, S., Garcia-Prieto, J., Gil-Gregorio, P., del- Pozo, F., Maestu, F., 2012. Differential patterns of connectivity in progressive mild cognitive impairment. *Brain Connect.* 2 (1), 21–24.

Goals

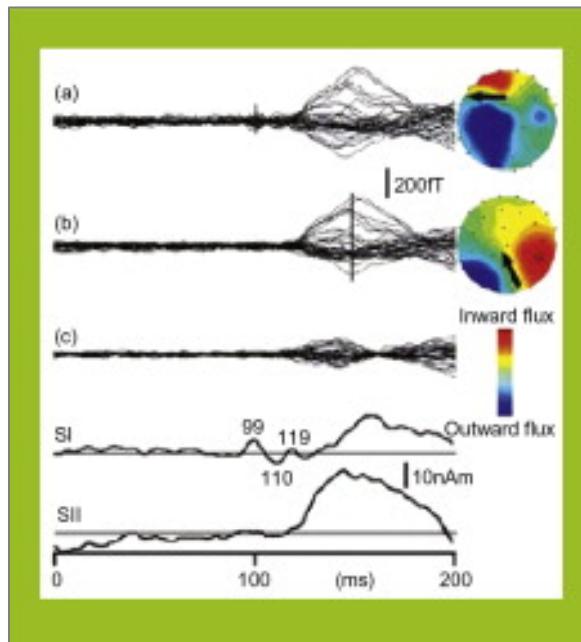
- Detect mild cognitive impairment (MCI) patient from the control group.
- Find powerful physiopathological characteristics of this disease.

Magnetoencephalography (MEG)

- Millisecond temporal resolution, millimeter spatial resolution.
- Populations of neurons are connected into networks.
- MEG is highly sensitive to dendritic (nerve cell) flow at right angles to the walls of the sulci (the cortical folds).
- Magnetic fields pass through skull and various tissues undistorted.
- Our MEG data: blinded study, demographic data were obtained.



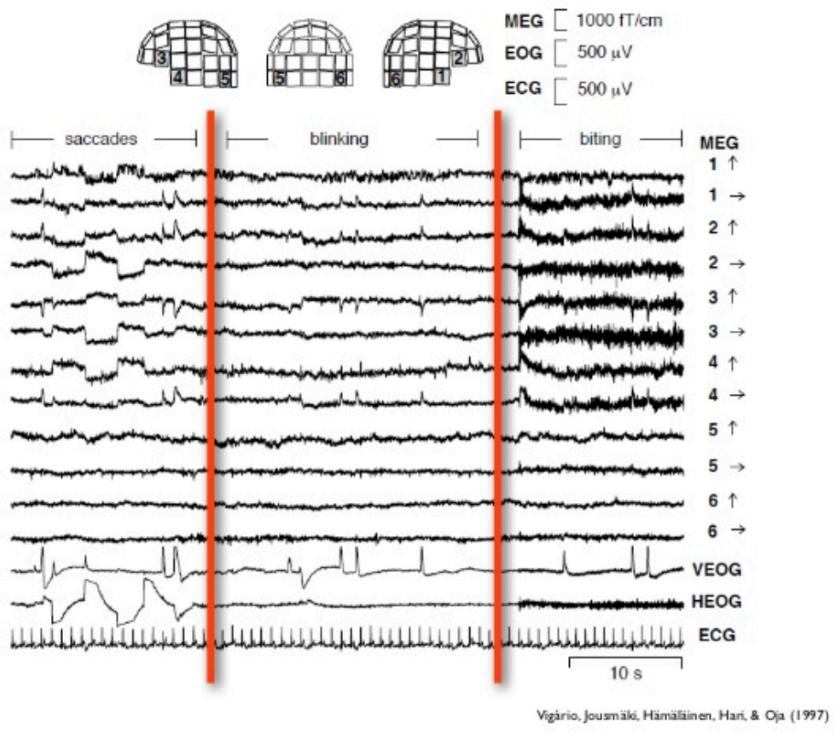
Magnetic field



Noise Type

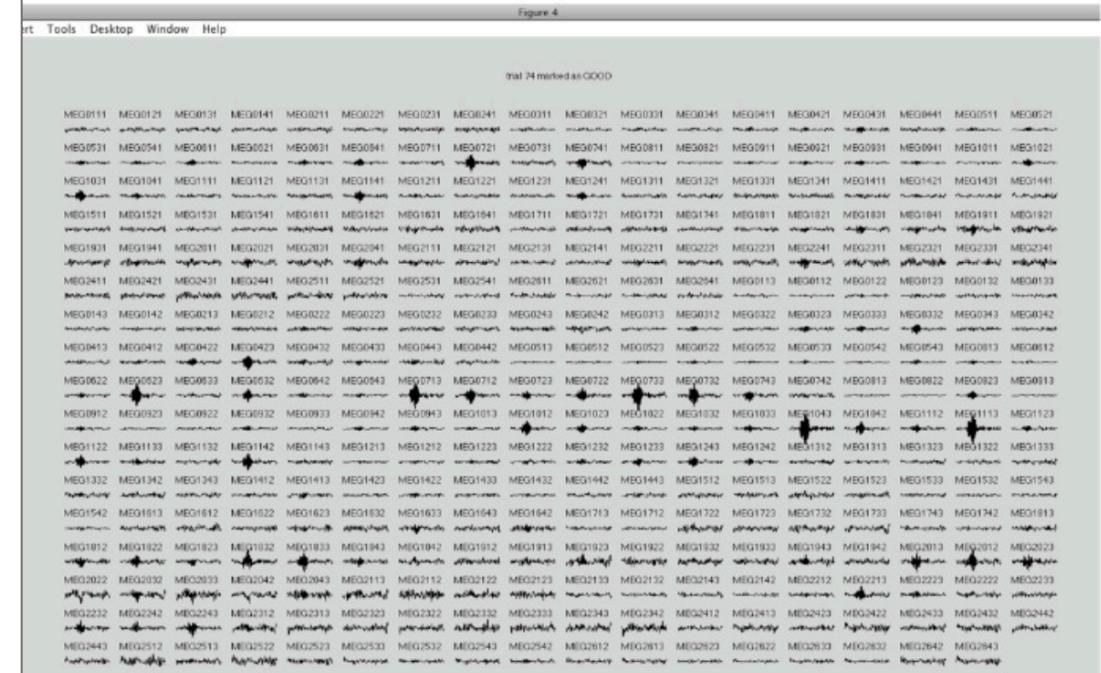
Biological Noise

B



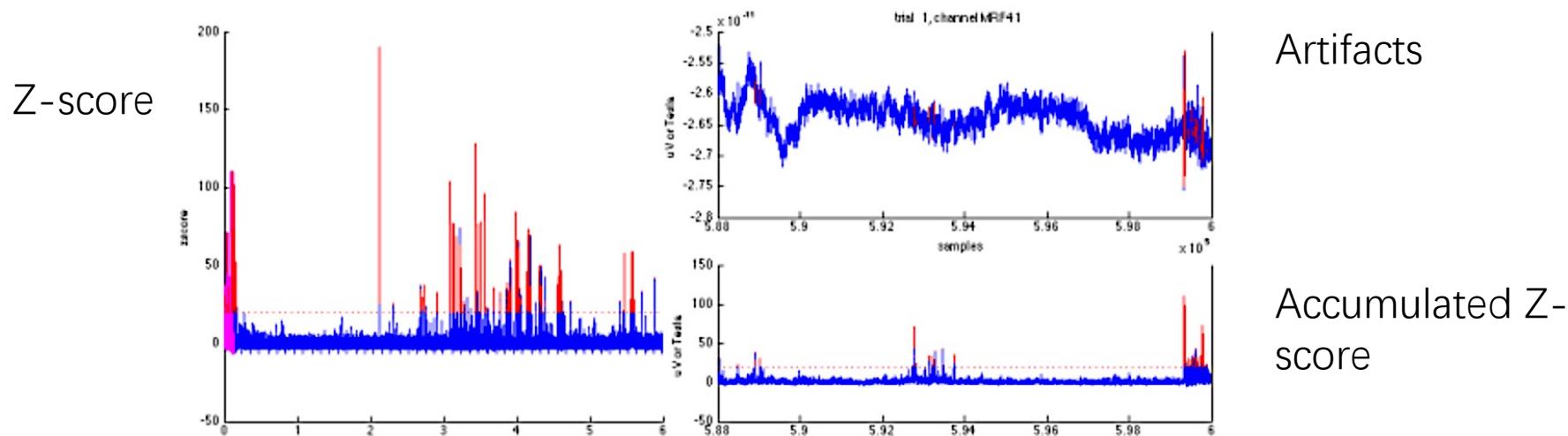
A Environmental Interferences

C Noise from nearby construction



Pre-processing

- Temporal Signal Space Projection: Differentiate unique, time-invariant sources.
- Frequency Filter: Bandpass Filtering with finite impulse response filters.
- Artifacts detection: Thresholding the accumulated z-score.



Connectivity

- Power correlation connectivity (**pairwise correlation**)
- Amplitude correlation connectivity (**pairwise correlation**)
- Coherence connectivity (**pairwise coherence in frequency domain**)
- Cross-spectral density matrix (**autocorrelation with lags**)
- Phase-locking value (**mean phase difference**)
- Weighted pairwise phase consistency (**bias-free mean phase difference**)
- Orthogonal correlation map (**independence of complex series**)
- Mutual Information map



After
Fourier
Transform
-ation

2. Detection of Mild Cognitive Impairment

Graph Signal Processing

A. With Amplitude data
(LOOCV Accuracy: 69%)

1. Chenhui's Method

53 samples * 90 nodes -> correlation metrics C (90*90 dimensions)

$$\rightarrow L = \text{diag}(1+C) - (1+C)$$

\rightarrow Eigenvalue decomposition $L=F\Lambda F'$

\rightarrow take out first 12 eigenvectors and get F' (12*90)

\rightarrow projection energy = $\sum(F'x (12*90) * 90*1))$

or use $\text{trace}(x'Lx)$ as projection energy.

Used on the mean data, which is of 78*306 dimension.

Not enough information contained in
the MEG average data .

Graph Signal Processing

B. View orthogonal-correlation map as a graph: LOOCV 73%

Input: a metric measuring pair-wise distances → Use average G of one group

Or use $\exp(-G)$;

→ $W = \operatorname{argmin} \operatorname{tr}(x' L x) + \text{regularization term (like } \|W\|)$

= $\operatorname{argmin} (\|WX\| + \text{regularization term})$

W weighs of node: 306*306, X pairwise distance metrics 306*306

→ projection energy: $\operatorname{cumsum}(\operatorname{sum}(\|WX\|, 2) / \operatorname{norm}(X))$

or use total cumulative energy residual = $1 - \{\operatorname{cumsum}(\operatorname{sum}(\|WX\|)) / \operatorname{cumsum}(\operatorname{svd}(X^2))\}$

measuring how well the graph fit the new data



Eigenvalue Decomposition.
Avoid projecting correlation matrix onto
the basis.

Graph Signal Processing

C. Graph semi-supervised learning
on MI map: 82%~87% in subgroups

Step 1: Chi-squared feature selection.

Step 2: Learn individual level Laplacian matrix from selected features.

Step 3: Use graph patterns as regularization term in regression to classify two groups.

$$\operatorname{argmin}_{\{y^{\wedge}\}} (\|y^{\wedge} - y\|^2 + \gamma \|L^{1/2}y^{\wedge}\|_2)$$

Accuracy: 70<Age<78, Female: 87%; Age<=70, Female: 82%.

Common Spatial Pattern

- Two covariance matrices

$$\mathbf{R}_1 = \frac{\mathbf{X}_1 \mathbf{X}_1^T}{t_1}$$

$$\mathbf{R}_2 = \frac{\mathbf{X}_2 \mathbf{X}_2^T}{t_2}$$

- Find

$$\mathbf{P}^{-1} \mathbf{R}_1 \mathbf{P} = \mathbf{D}$$

and

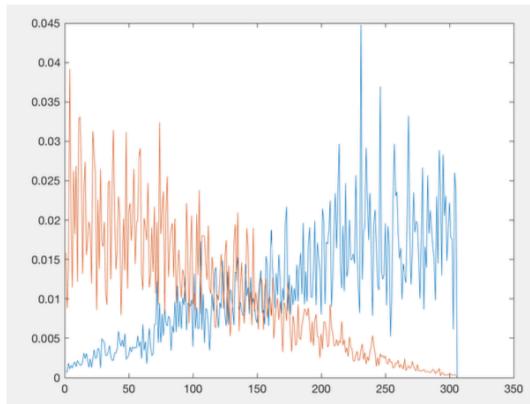
$$\mathbf{P}^{-1} \mathbf{R}_2 \mathbf{P} = \mathbf{I}_n$$

with \mathbf{I}_n the [identity matrix](#).

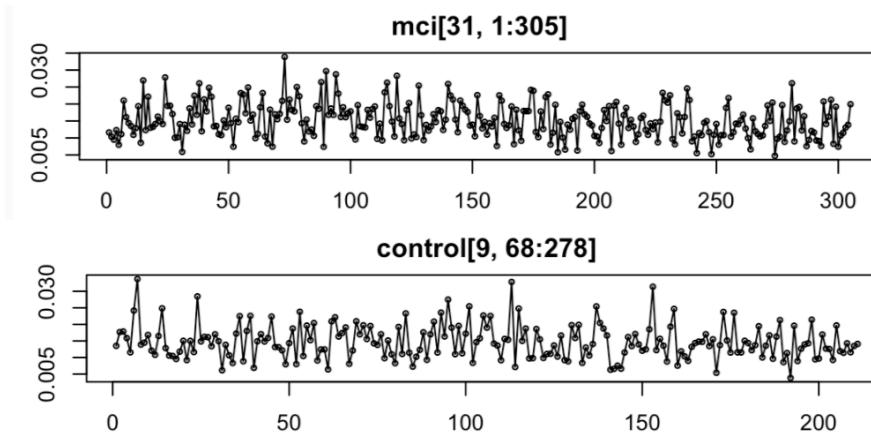
- Find linear transform to project the multi-channel data into low-dimensional spatial subspace with projection matrix P.
- Simultaneous diagonalization of the covariance matrices of both classes.
- After projection, the underlying variance of one subject will be separated.

Common Spatial Pattern

- 5-folds test on:
- A. the first 5s of the magnetic series after Fourier transformation: 84% .
- B. the



Transformed Train Sample
(5 seconds)



Transformed Test Sample
(5 seconds)

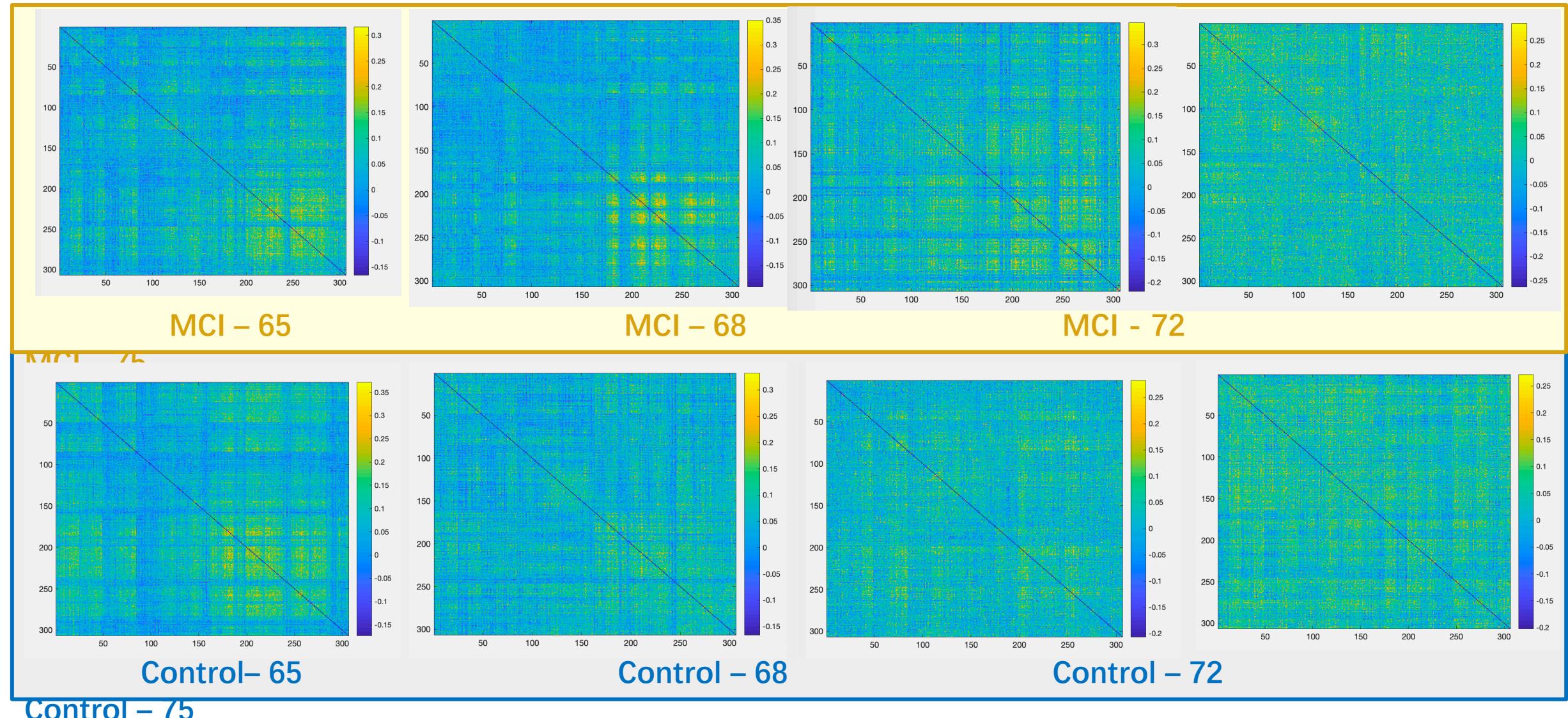
Performance of different connectivity measurements in distinguishing MCI groups from the control

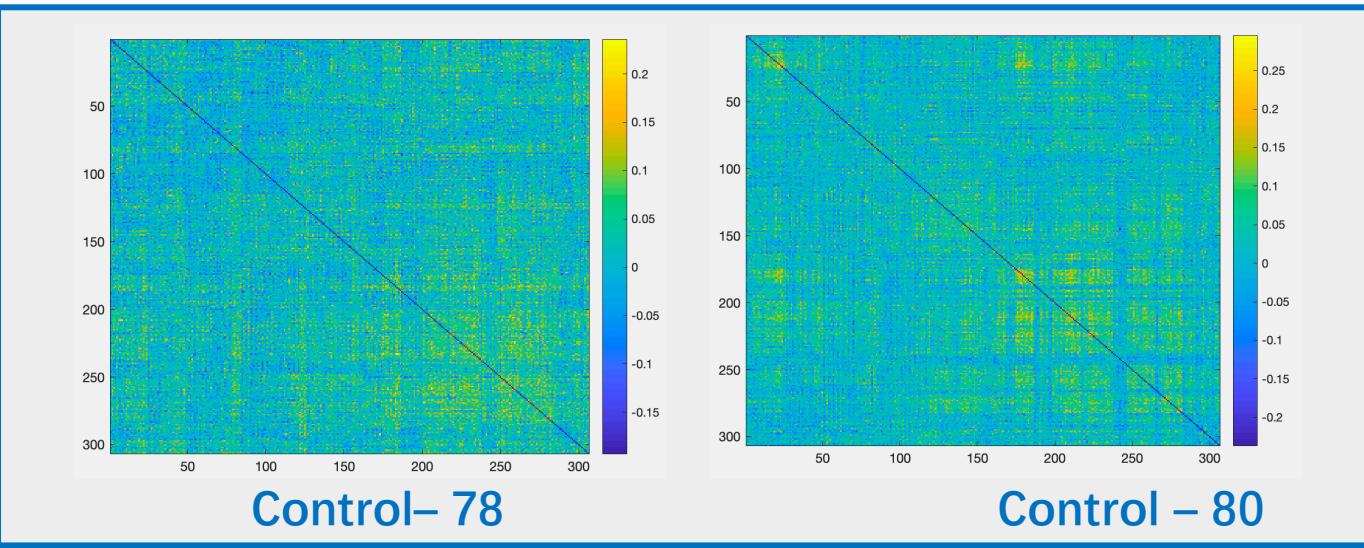
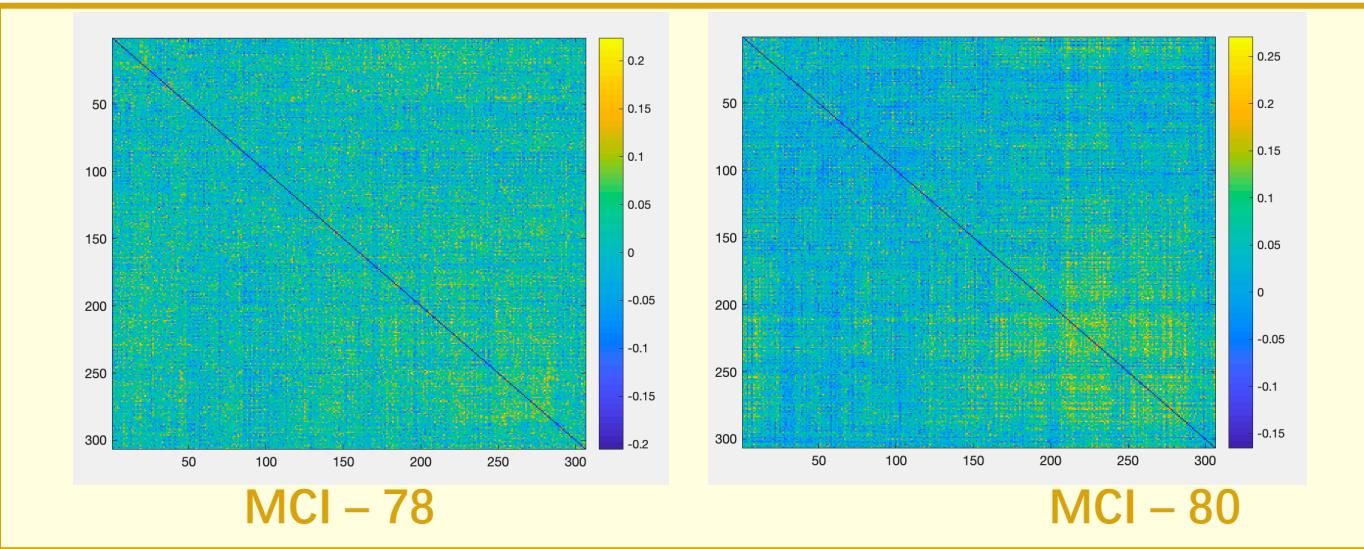
Classification Methods:
Chi-squared feature selection + ANN

| Summary of the classification results | | | | | | |
|---------------------------------------|---------------|---------------------|-------------------------------------|-------------------------------|---------------------------|--------------------|
| Overall Best Results: Red | | | | | | |
| Gender | Age Condition | Phase-Locking Value | Weighted Pairwise Phase Consistency | Cross Spectral Density Matrix | Orthogonal correation map | Mutual Information |
| Female | Age <=70 | 49% | 60% | 68% | 70% | 90% |
| | 70<Age<78 | 66% | 78% | 65% | 66% | 81% |
| | All | 58% | 67% | 67% | 55% | 86% |
| Male | Age <=70 | 72% | 67% | 65% | 70% | 92% |
| | 70<Age<78 | 87% | 84% | 87% | 85% | 94% |
| | All | 66% | 67% | 66% | 78% | 86% |
| All | Age <=70 | 53% | 58% | 50% | 64% | 89% |
| | 70<Age<78 | 70% | 68% | 65% | 71% | 79% |
| | All | 62% | 69% | 61% | 55% | 83% |

3. Discussion

A. Normal Aging and MCI (Individual orthogonal correlation map)





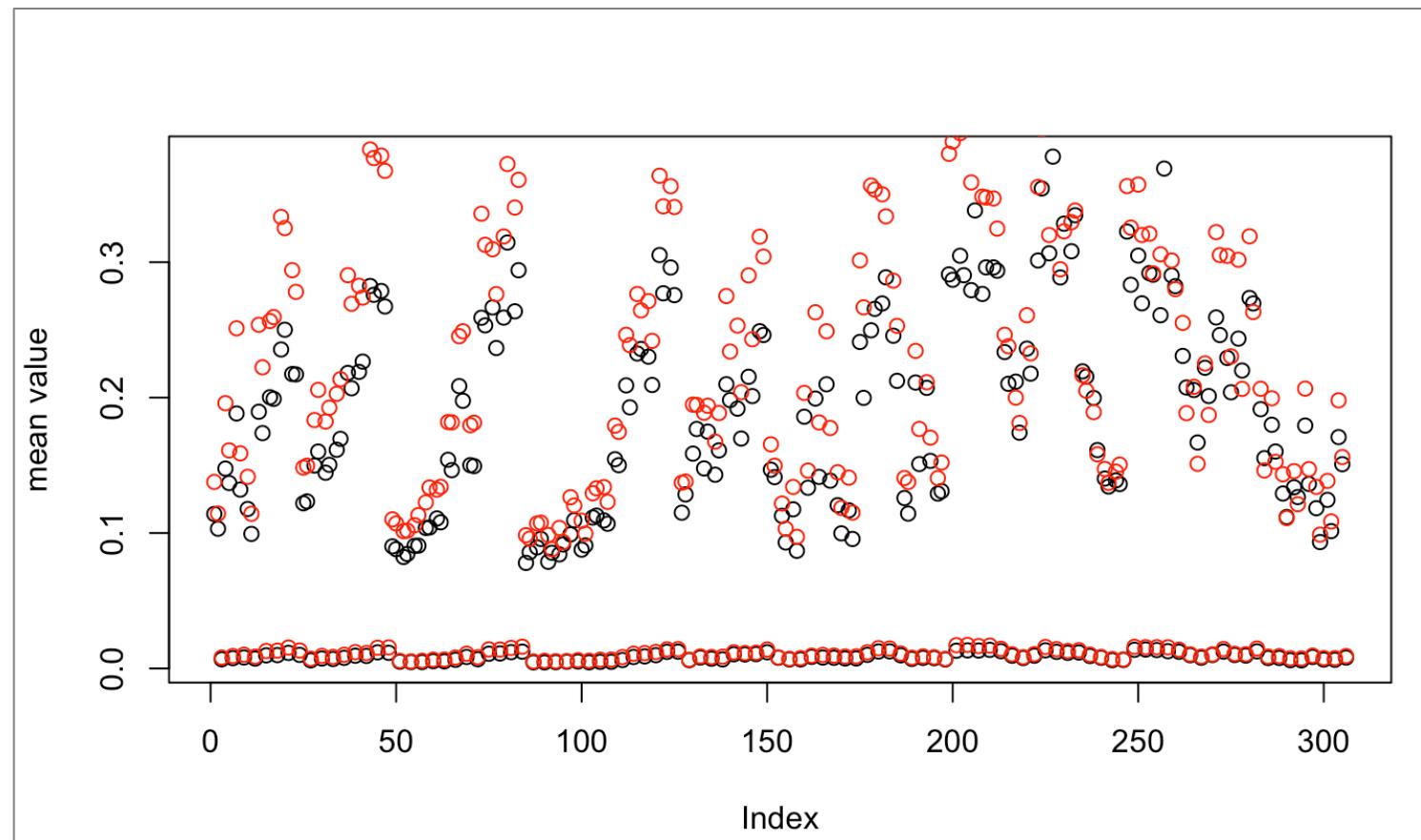
B. Gender and MCI Pattern

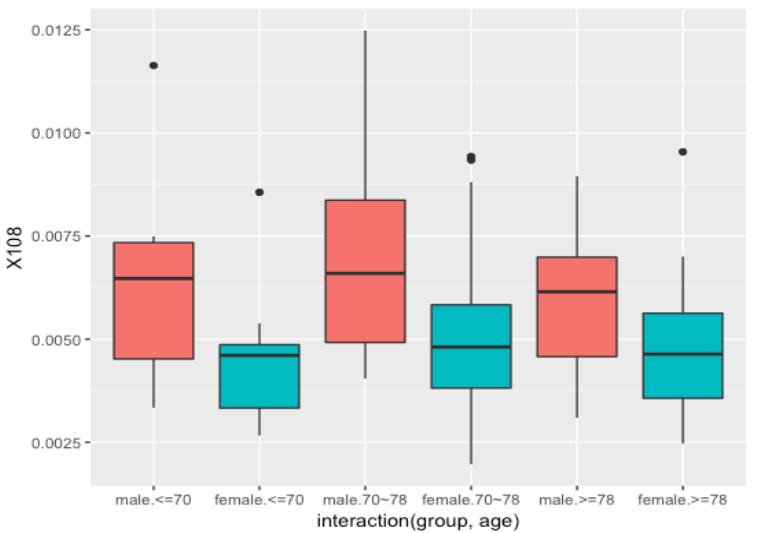
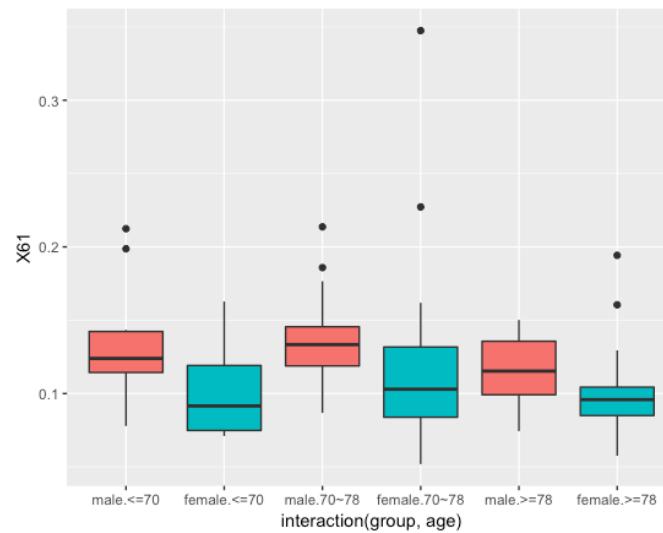
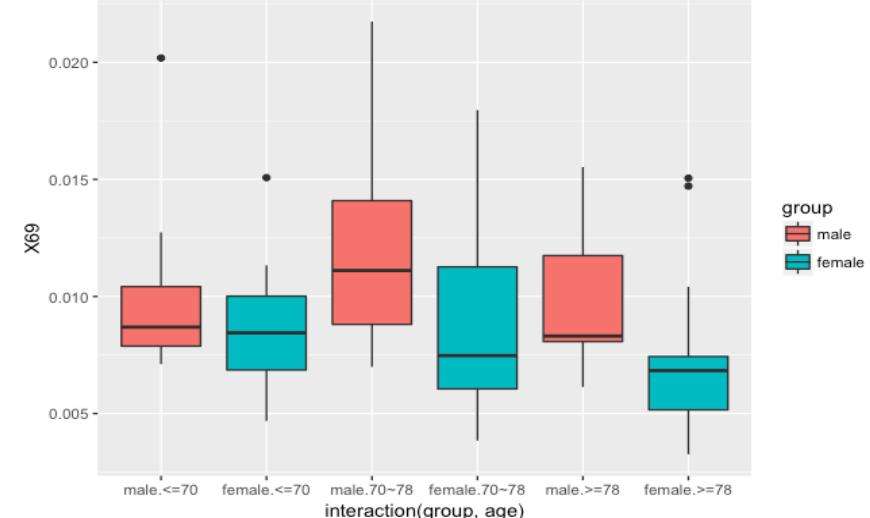
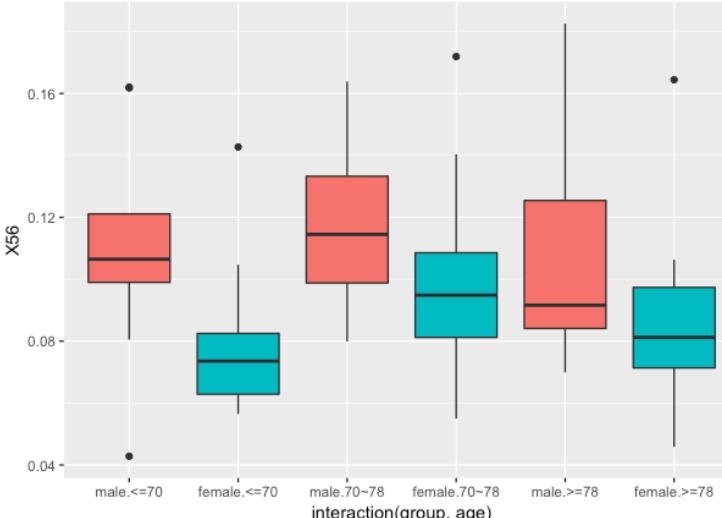
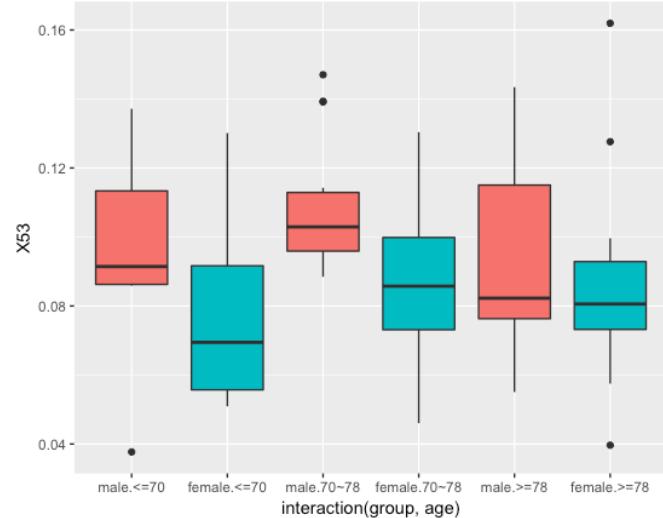
X: 306 channels

Y: group amplitude data on 306 channels.

Sample: MCI patients. (female: black, 47 cases, male: red, 31 cases)

Sample value: amplitude value of the first 5s on 306 channels, alpha band.





Channels that passed ks.test
($p < 0.001$):

53, 55, 56, 61, 64, 69, 72,
108, 111