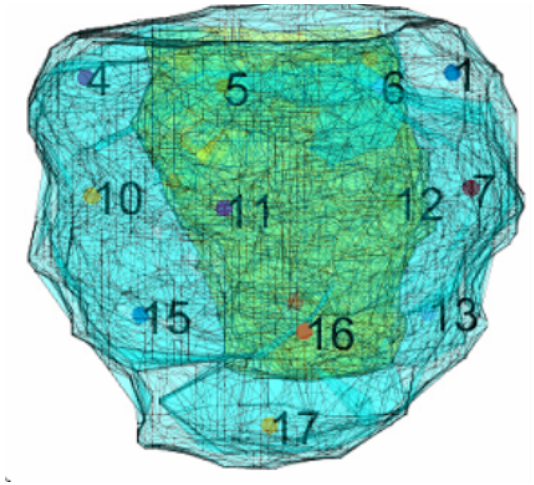
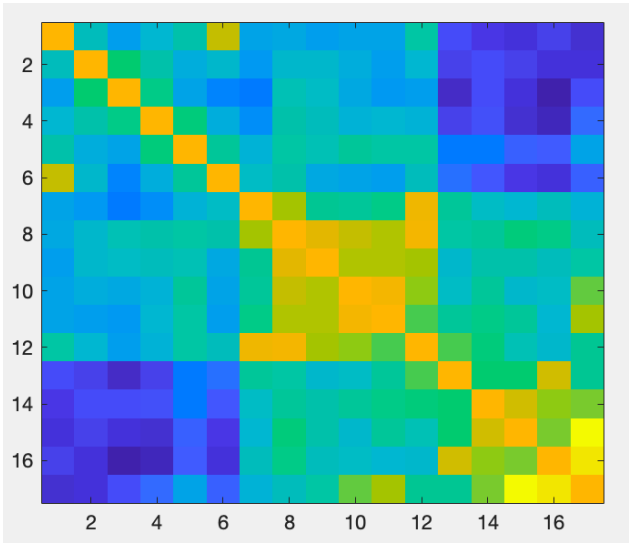
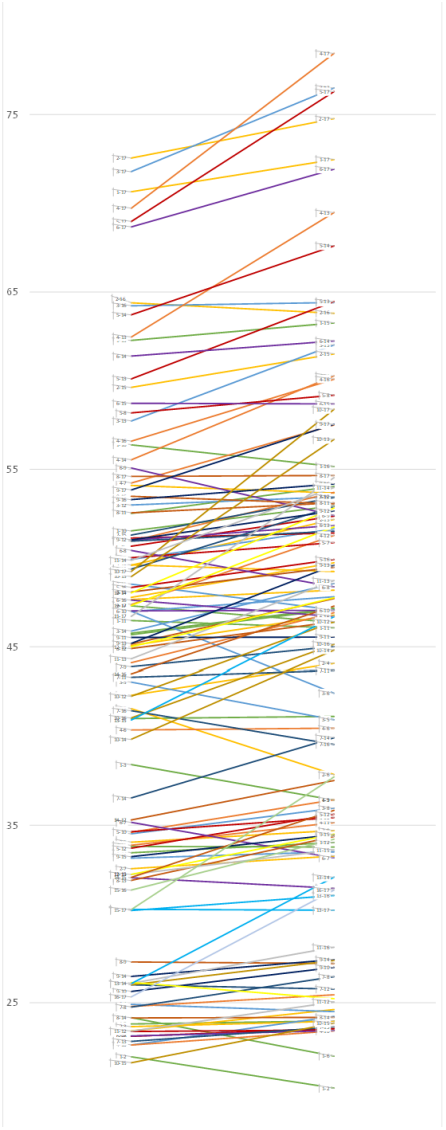
Graph Structure Inference on Cardiac Skeleton

Hypothesis: Heart Skeleton

the structural biomarker is associated with clinical outcomes– Worsen or Maintain function





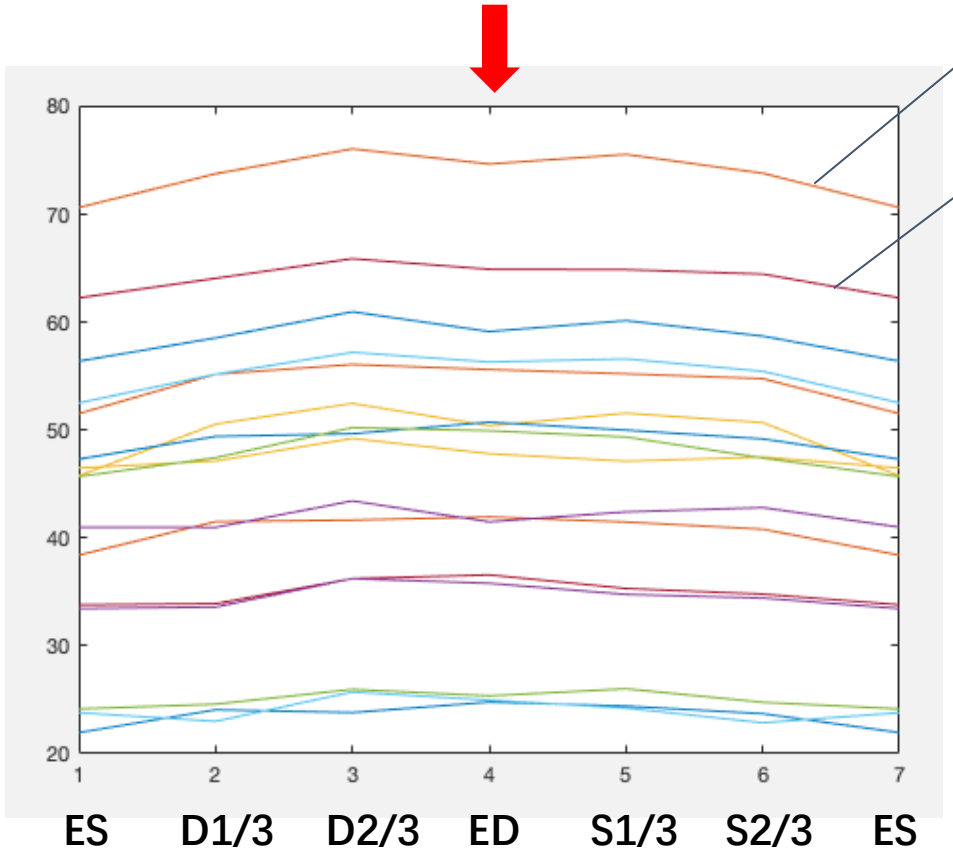


136 linkages

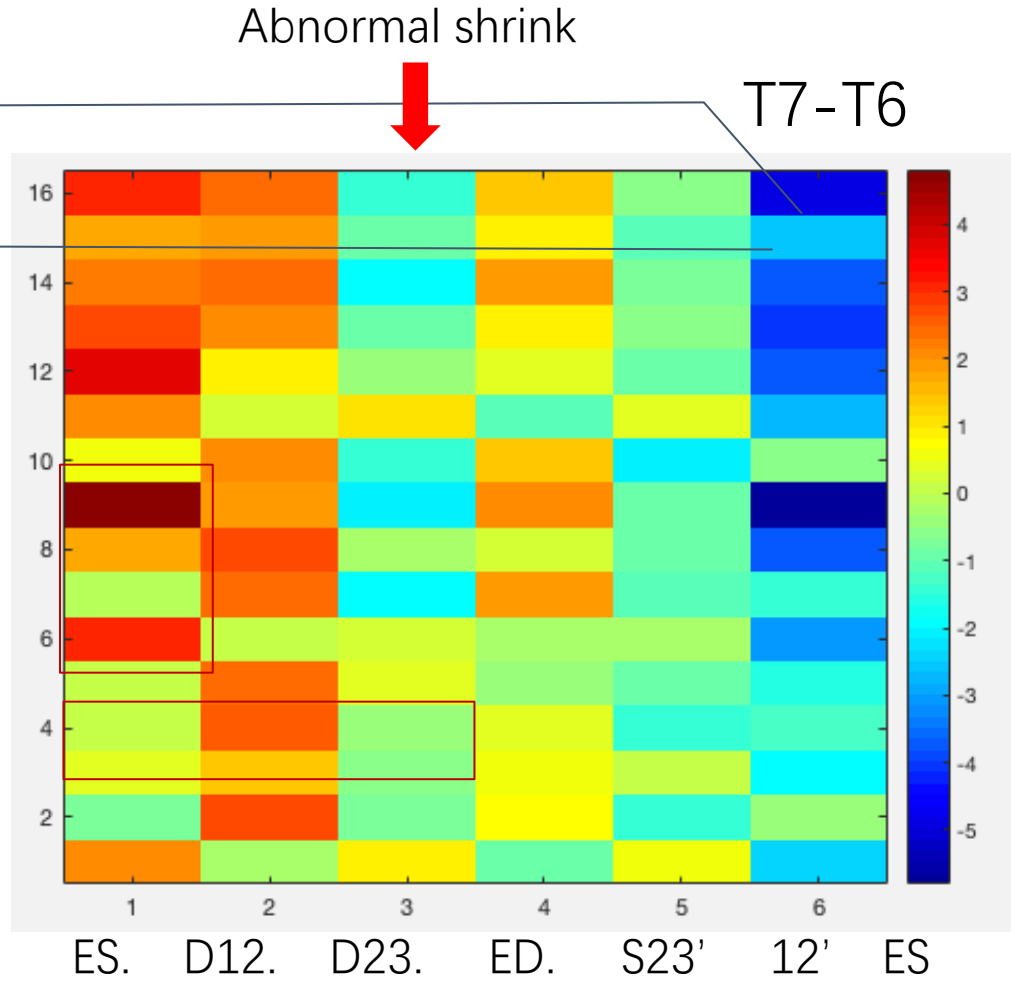
Skeleton was defined by linking the center points of 17 segments of the myocardium, which reflects the working relationship in between.

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

An Worsen case:

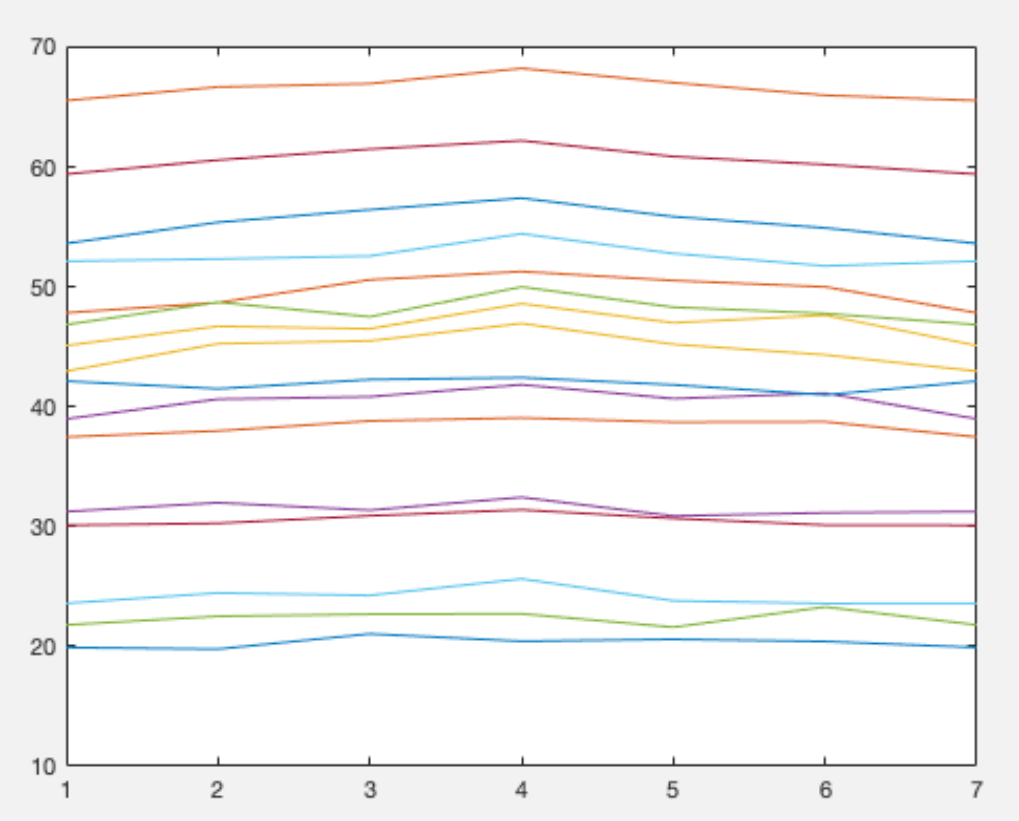


Segment 1 related edge values throughout the Cardiac Cycle



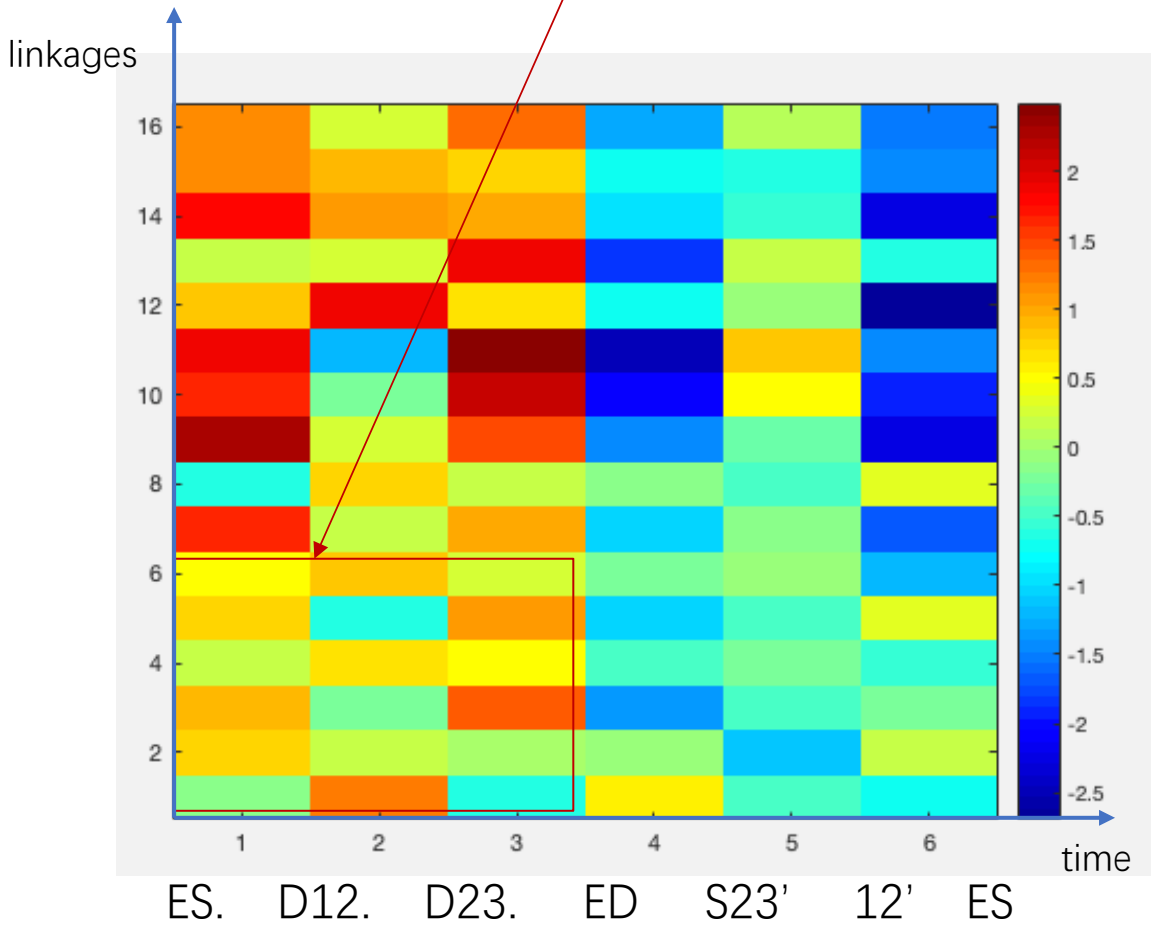
Δ Edge between neighbors on time frames

An Control Case



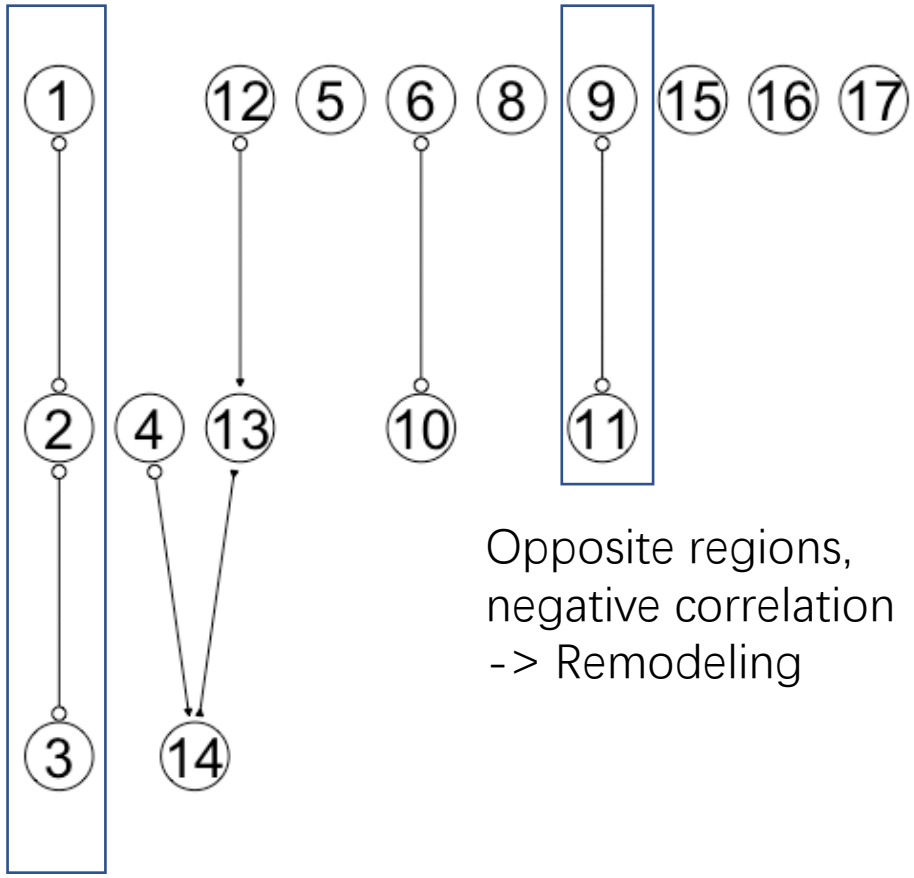
Segment 1 related edge values throughout the Cardiac Cycle

"Remodeling Compensation" : negative correlation between nearby regions throughout the cardiac cycle.



Δ Edge between neighbors on time frames

Causality Extraction



Opposite regions, negative correlation -> Remodeling

Nearby regions, positive correlation

The left figure showed the causality relationship between 16 linkages started from Region17 by using FCI algorithm. 25 time points were used. (“Causation, Prediction, and Search” , 1993, pp.140-145)

There are several problems about this model:

A. FCI performs badly on large scale dataset. It is not very practical to build causality on all the 136 edges on our dataset.

B. “Confounding” has no exact meanings in this cardiac system.

Fast Causal Inference Algorithm

A). Form the complete undirected graph Q on the vertex set **V**.
B). $n = 0$.
repeat
  repeat
    select an ordered pair of variables X and Y that are adjacent in Q such that **Adjacencies**(Q,X)\{Y} has cardinality greater than or equal to n, and a subset **S** of **Adjacencies**(Q,X)\{Y} of cardinality n, and if X and Y are d-separated given **S** delete the edge between X and Y from Q, and record **S** in **Sepset**(X,Y) and **Sepset**(Y,X)

  until all ordered variable pairs of adjacent variables X and Y such that **Adjacencies**(Q,X)\{Y} has cardinality greater than or equal to n and all subsets **S** of **Adjacencies**(Q,X)\{Y} of cardinality n have been tested for d-separation;
  $n = n + 1$;
until for each ordered pair of adjacent vertices X, Y, **Adjacencies**(Q,X)\{Y} is of cardinality less than n.
C). Let F' be the undirected graph resulting from step B). Orient each edge as o-o. For each triple of vertices A, B, C such that the pair A, B and the pair B, C are each adjacent in F' but the pair A, C are not adjacent in F', orient A *-* B *-* C as A *→ B ←* C if and only if B is not in **Sepset**(A,C).
D). For each pair of variables A and B adjacent in F', if A and B are d-separated given any subset **S** of **Possible-D-SEP**(A,B)\{A,B} or any subset **S** of **Possible-D-SEP**(B,A)\{A,B} in F remove the edge between A and B, and record **S** in **Sepset**(A,B) and **Sepset**(B,A).

(“from Causation, Prediction, and Search” , 1993, pp.144)

Graph Convolutional Network with Causality Inference

- A. Graph convolutional network:

$$H^{(l+1)} = \sigma\left(\widetilde{D}^{-\frac{1}{2}}\tilde{A}\widetilde{D}^{-\frac{1}{2}}H^{(l)}W^{(l)}\right)$$

Input: X- each row represents features of each subject.

H: Network layer.

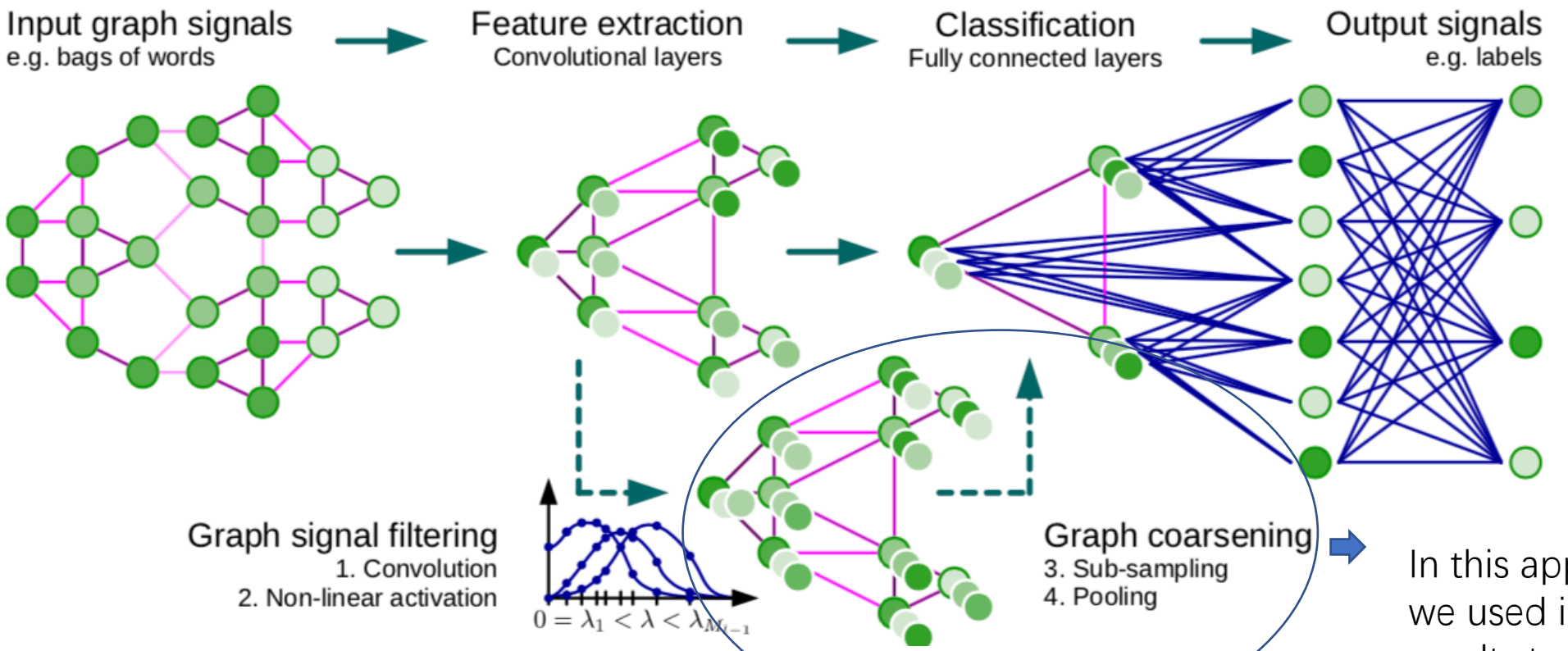
A: adjacent matrix of input X.

D: Diagonal(A).

W: Network weights.

σ: Relu function.

B. Spectral GCN structure



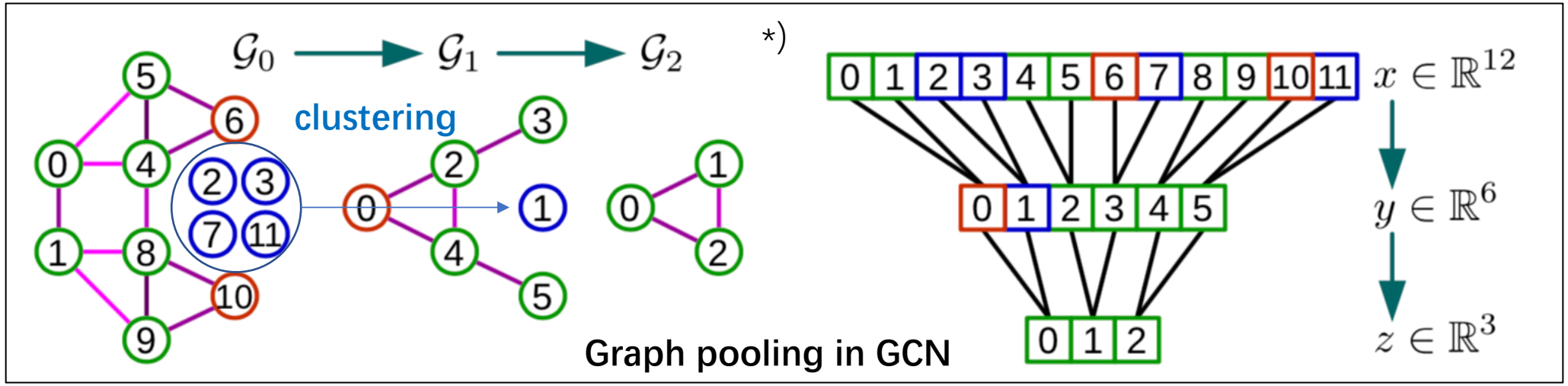
A. Cluster features together -> lower dimension.
B. 1D Pooling

In this application, we used inference results to replace coarsening algorithm.

arXiv:1606.09375

- C. Motivation behind:

arXiv:1606.09375



This graph pooling algorithm starts from the biggest edges, thus smaller/negative connections will be mixed together and biased. In biomedical signal processing, the useful information is contained in functional edges-the connectivity inference.

Three possible solutions to this problem:

A) In the pooling step, use causality results to select nodes, followed by fully connected layers.

B) Do graph pooling and A) step separately, concatenate the outputs to form network layers

- We are still processing the cardiac images to get enough samples for training.
- This work will be an important part of our AHA cardiac & ML proposal.