Application of topological data analysis in biomechanics

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Introduction

- What is the topological data analysis (TDA):
 - The recently proposed data analysis method in computational topology.
 - It requires algebraic topology and programming skills

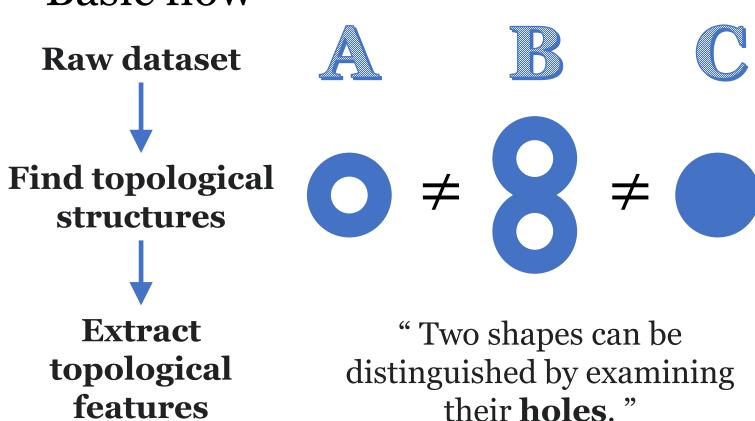
• Why we use this:

- This method **finds topological structure** and extracts some topological features.
- It can be **effective in finding hidden features of raw data** that cannot be found with conventional data analysis methods.

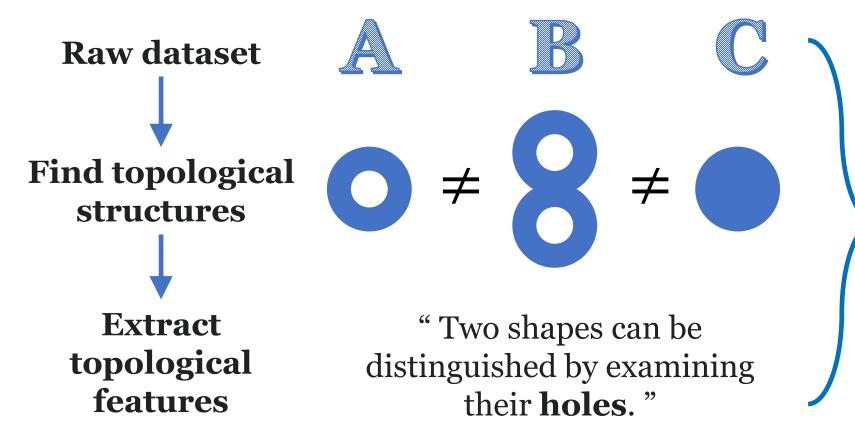
• Purpose:

- To obtain topological features of biomechanical data **using TDA**.
- To quantify similarities or dissimilarities between subjects.

Basic flow



Basic flow



"The number of k-dimensional holes in the space."

Betti Number β_k

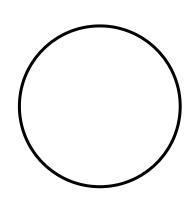
• Betti Number β_k : (intuitively)

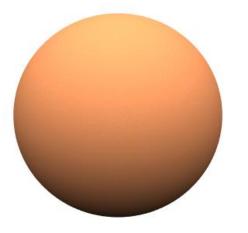
 β_0 : the number of **connected components** (connectivity)

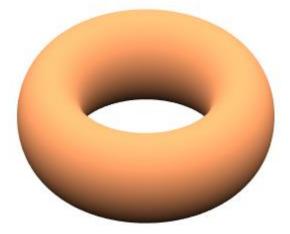
 β_1 : the number of 1-dimensional **holes** or **loops**

 β_2 : the number of enclosed solid **voids** (2-dimensional voids)









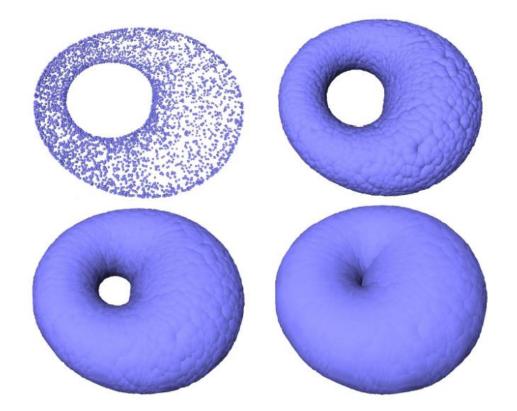
$$(\beta_0, \beta_1, \beta_2) = (1, 0, 0)$$
 $(\beta_0, \beta_1, \beta_2) = (1, 1, 0)$ $(\beta_0, \beta_1, \beta_2) = (1, 1, 1)$ $(\beta_0, \beta_1, \beta_2) = (1, 2, 1)$

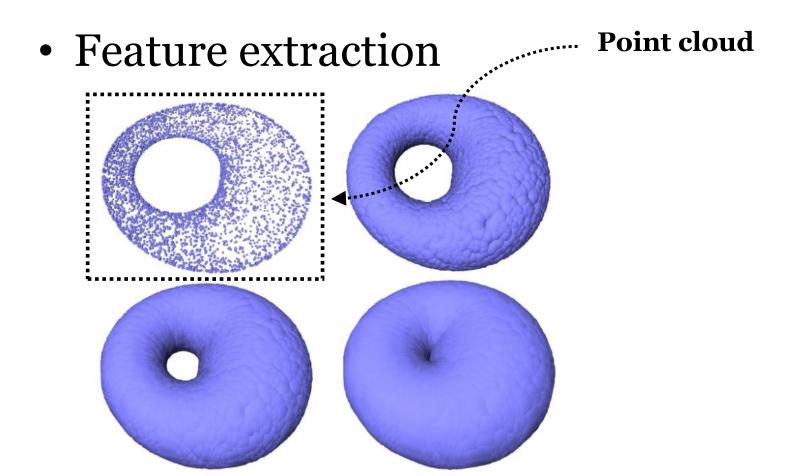
$$(\beta_0, \beta_1, \beta_2) = (1, 1, 0)$$

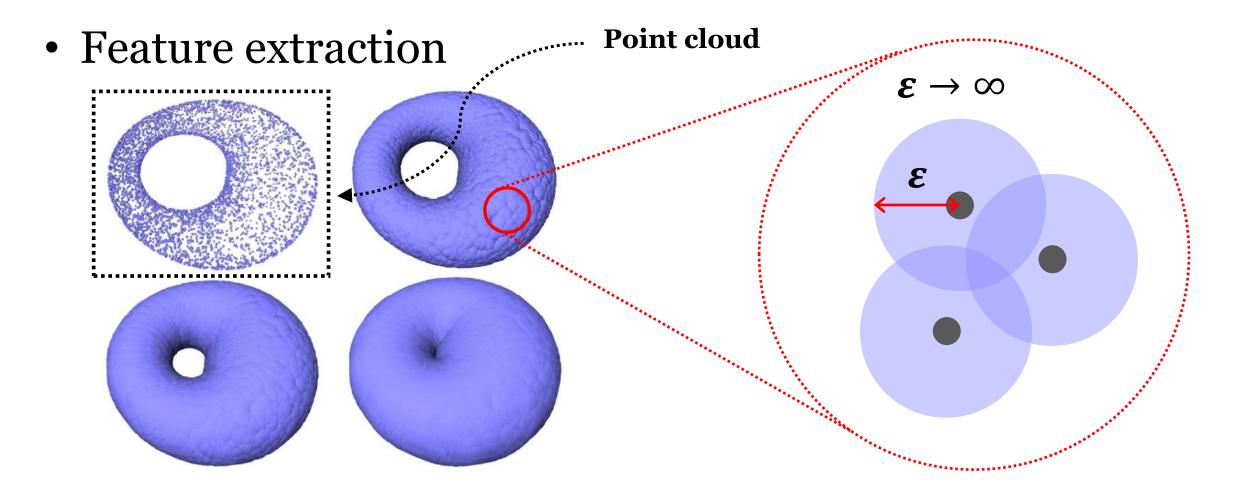
$$(\beta_0, \beta_1, \beta_2) = (1, 1, 1)$$

$$(\beta_0, \beta_1, \beta_2) = (1, 2, 1)$$

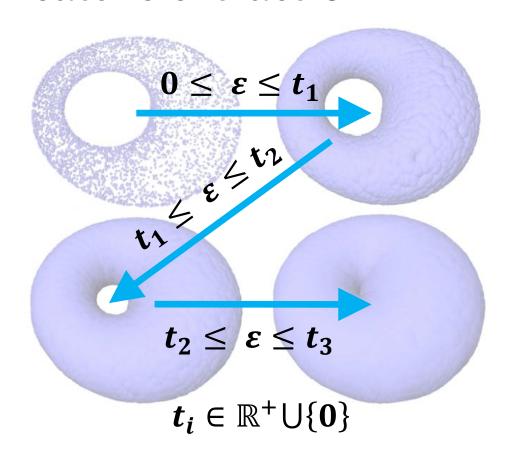
Feature extraction





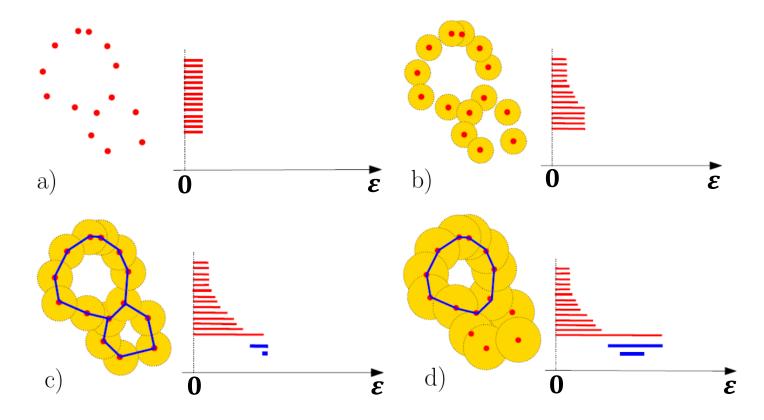


Feature extraction

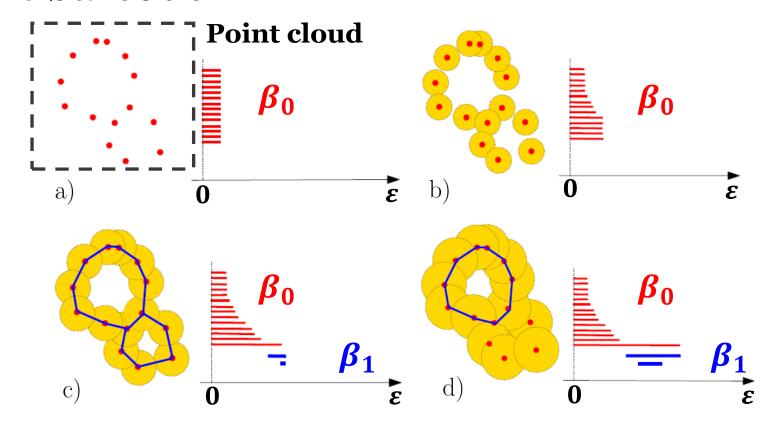


$$m{arepsilon} = m{0}$$
 $m{arepsilon} = m{t}_1$ $(m{eta}_0, m{eta}_1, m{eta}_2) = (m{n}, m{0}, m{0}) \; (m{eta}_0, m{eta}_1, m{eta}_2) = (m{1}, m{2}, m{1})$ $m{arepsilon} = m{t}_2$ $m{arepsilon} = m{t}_3$ $(m{eta}_0, m{eta}_1, m{eta}_2) = (m{1}, m{2}, m{1}) \; (m{eta}_0, m{eta}_1, m{eta}_2) = (m{1}, m{1}, m{1})$

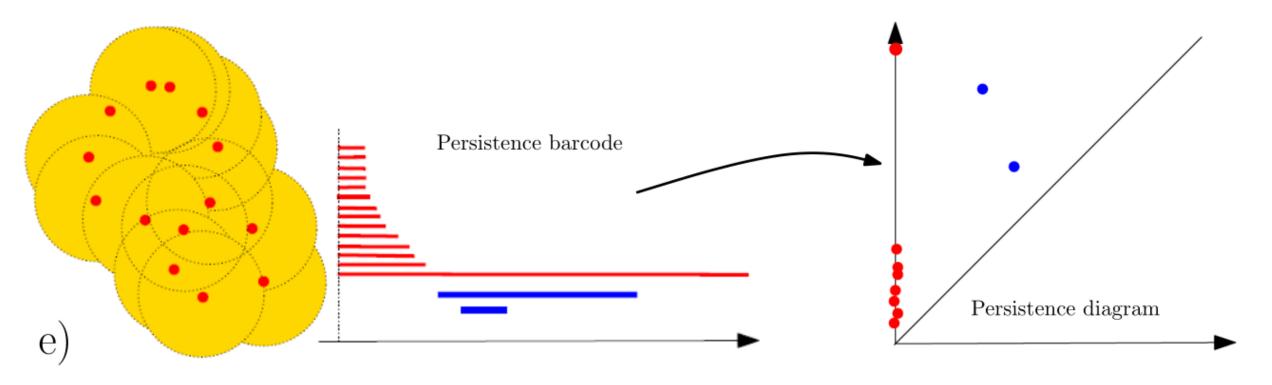
Persistent barcode



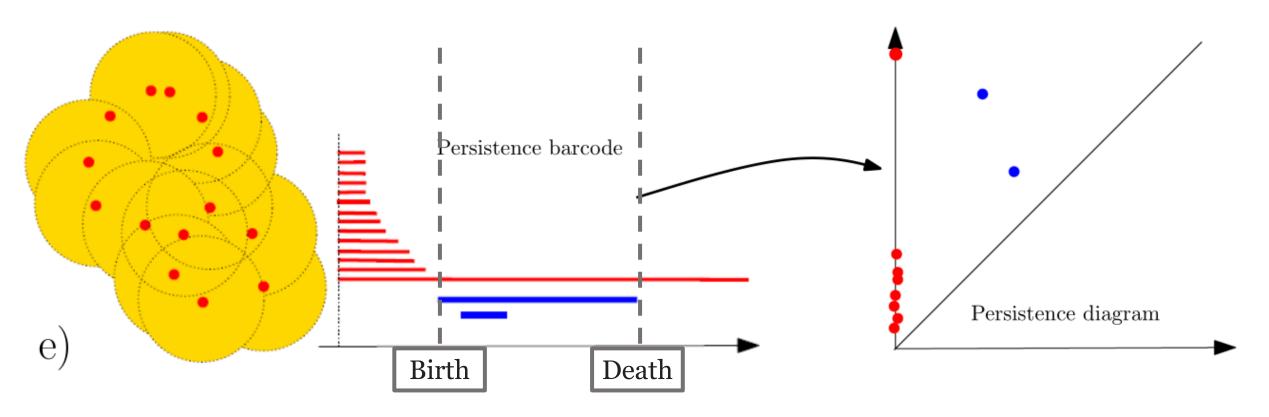
Persistent barcode

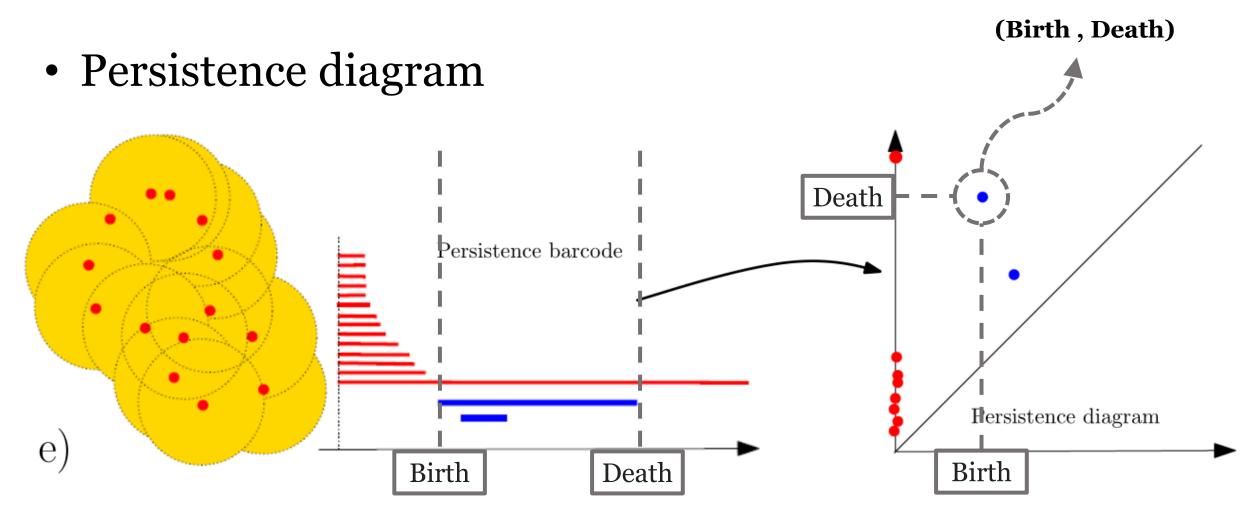


Persistence diagram



• Persistence diagram





Method: point cloud

Given a dataset
$$X = \begin{pmatrix} x_{11} & \cdots & x_{1n} \\ \vdots & \ddots & \vdots \\ x_{p1} & \cdots & x_{pn} \end{pmatrix} \in \mathbb{R}^{p \times n}$$
, let $\mathbf{x}_j = \begin{pmatrix} x_{1j} \\ \vdots \\ x_{pj} \end{pmatrix}$, $j = 1, \cdots, n$.

Assume that x_i are centered and normalized:

$$\sum_{i=1}^{p} x_{ij} = 0 \qquad \qquad \left\| x_{j} \right\|^{2} = 1$$

$$c_X(\mathbf{x_i}, \mathbf{x_j}) = \sqrt{1 - |corr(\mathbf{x_i}, \mathbf{x_j})|} \in \mathbb{R}^{n \times n}$$
 where

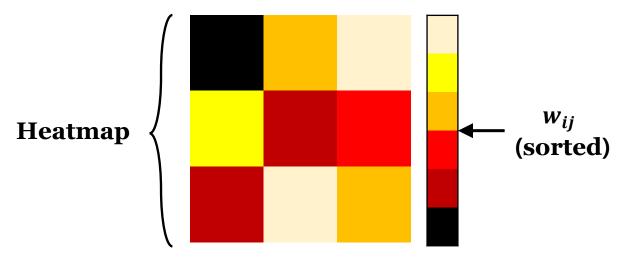
 $corr(\cdot, \cdot)$ is the Pearson correlation coefficient between x_i and x_i

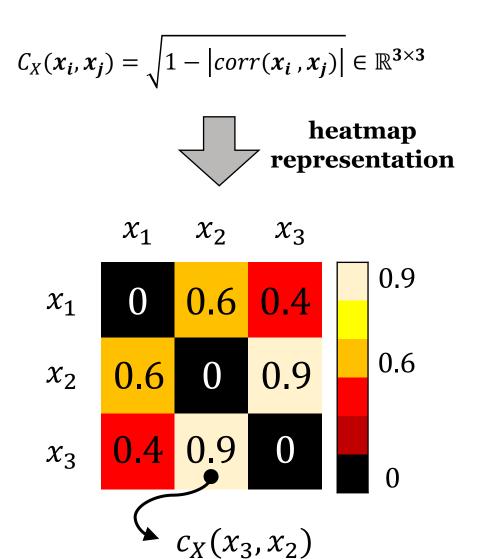
Method: point cloud

Heatmap:

Data visualization technique with colored representation based on matrix element value.

$$M = \begin{pmatrix} w_{11} & \cdots & w_{1n} \\ \vdots & \ddots & \vdots \\ w_{p1} & \cdots & w_{pn} \end{pmatrix} \in \mathbb{R}^{p \times n}$$





Method: barcode

- Features in β_0 are always shown but features in β_1 or β_2 are not.

- The result of barcode for β_0 does not generate a noise in the process
 - → accurate topological information can be obtained.
- Thus, we only consider the zeroth betti number β_0 in this study.

Method: barcode

- In order to obtain the more accurate results for β_0 , we consider geometric information of β_0 , with a topological information.

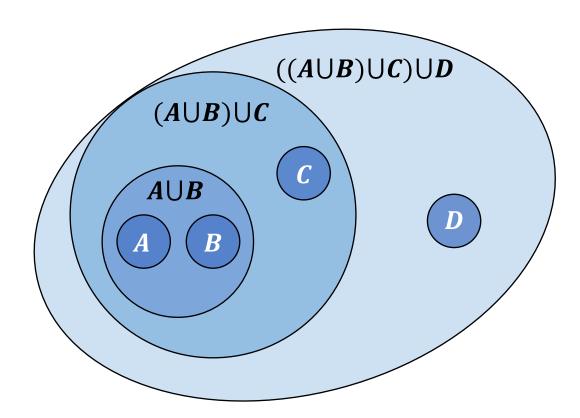
- We use the dendrogram in this study as geometric information of β_0 as

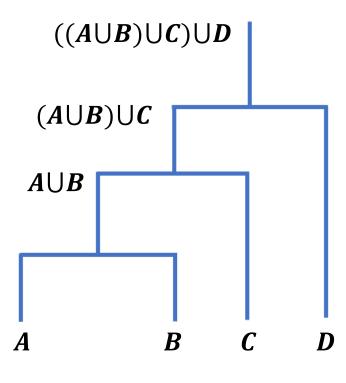
Lee et al., Persistent brain network homology from the perspective of dendrogram, IEEE transactions on medical imaging, 2012.

Method: dendrogram

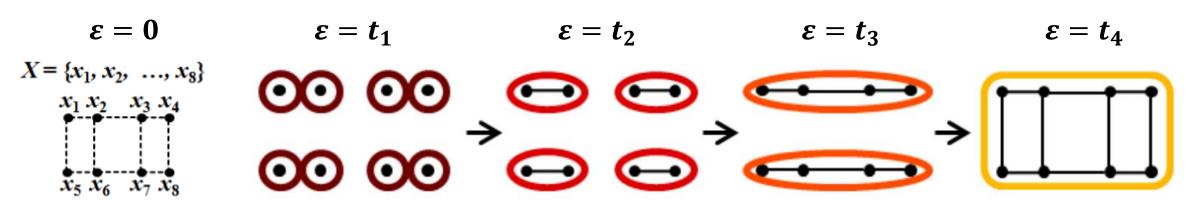
${\bf Dendrogram:}$

The diagram that shows the hierarchical relationship between objects such as stem of a tree.

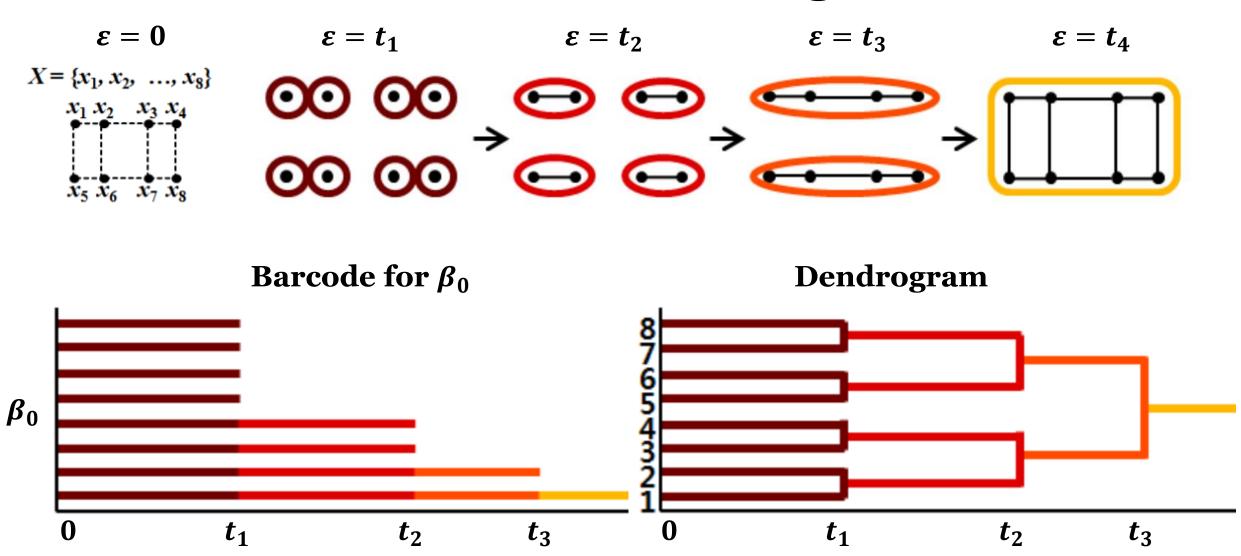




Method: barcode and dendrogram

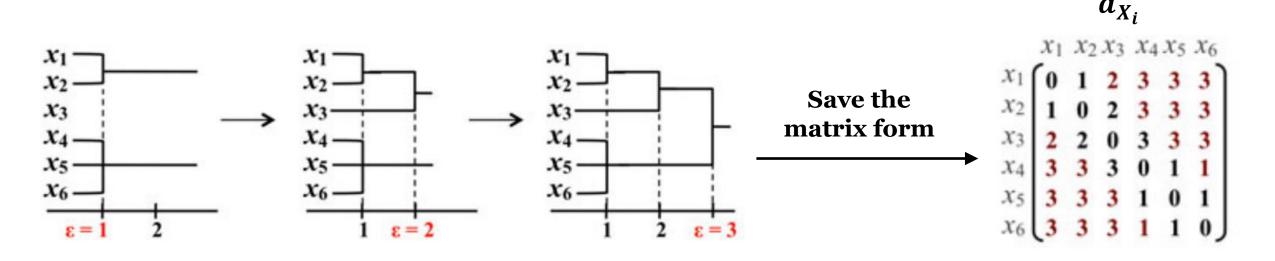


Method: barcode and dendrogram



Method: comparison between subjects

For each dataset of subject X_i , $i = 1, \dots n$, we obtain d_{X_i} as follows.



Method: comparison between subjects

We want to compute the distance between two subjects $X_i, X_j \in \mathbb{R}^{p \times n}$.

Gromov-Hausdorff distance (GH distance)

$$d_{GH}(X_i, X_j) = \frac{1}{2} \max_{\forall i, j} \left| d_{X_i} - d_{X_j} \right|$$

 d_{X_i} , $d_{X_j} \in \mathbb{R}^{n \times n}$: the matrices which are converted subjects for X_i, X_j .

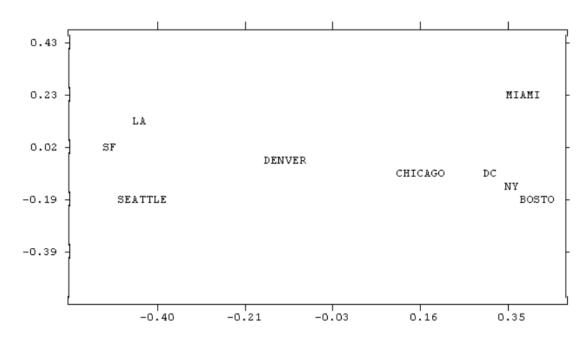
Method: multidimensional scaling (MDS)

• A technique that represents proximities among objects as distances among points in a low-dimensional space (with given dimensionality).

Input as the distance matrix:

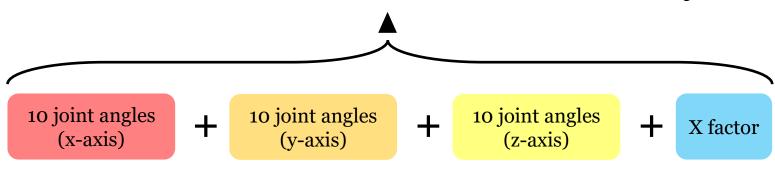
1 2 3 4 5 6 7 8 9 BOST NY DC MIAM CHIC SEAT SF LA DENV BOSTON 0 206 429 1504 963 2976 3095 2979 1949 NY 206 0 233 1308 802 2815 2934 2786 1771 DC 429 233 0 1075 671 2684 2799 2631 1616 MIAMI 1504 1308 1075 0 1329 3273 3053 2687 2037 CHICAGO 963 802 671 1329 0 2013 2142 2054 996 SEATTLE 2976 2815 2684 3273 2013 0 808 1131 1307 SF 3095 2934 2799 3053 2142 808 0 379 1235 LA 2979 2786 2631 2687 2054 1131 379 0 1059 DENVER 1949 1771 1616 2037 996 1307 1235 1059 0

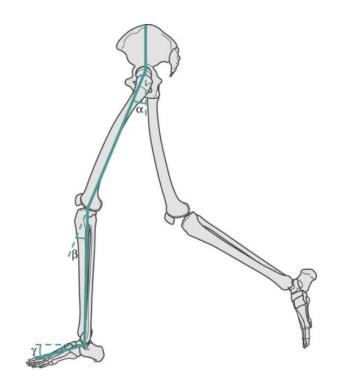
Output as proximities:



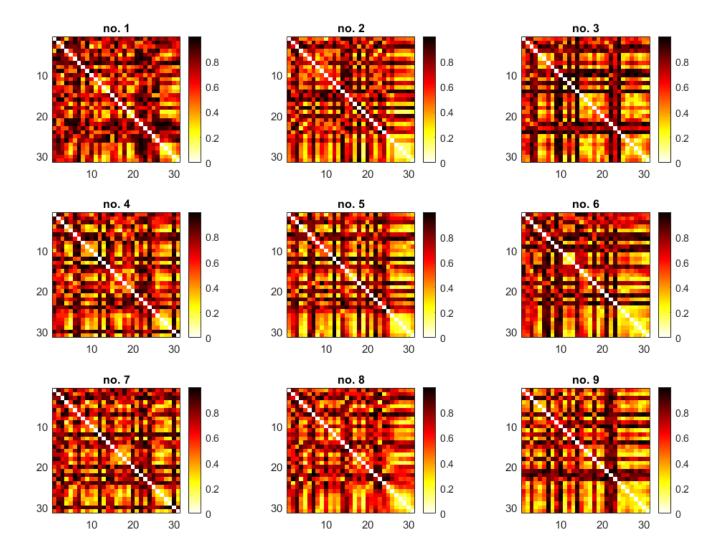
Application

- Dataset: biomechanical data (kinematics)
 - Joint angle measurement dataset
 - Data size : (100 times) \times (31 variables) \times (9 subjects)





Point cloud

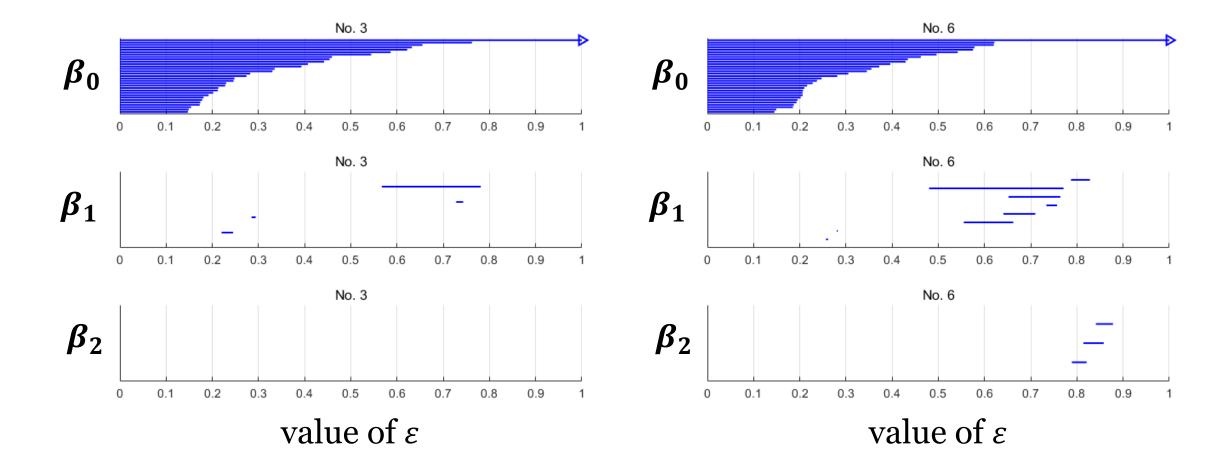


Define a point cloud.

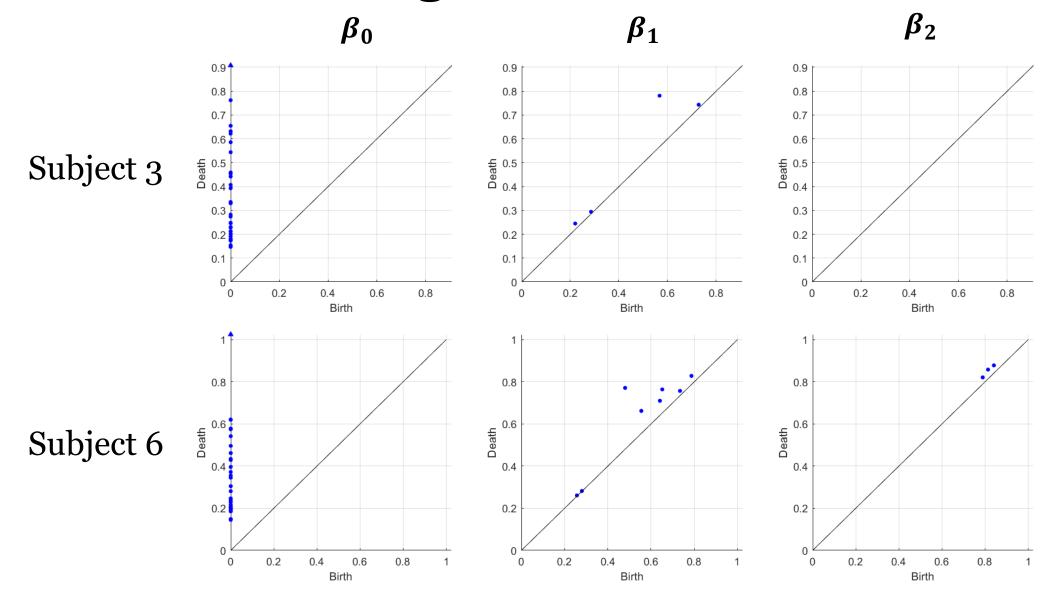
For the subject X_i , $i = 1, \dots 9$,

$$c_{X_i} = \sqrt{1 - |corr(X_i)|} \in \mathbb{R}^{31 \times 31}$$

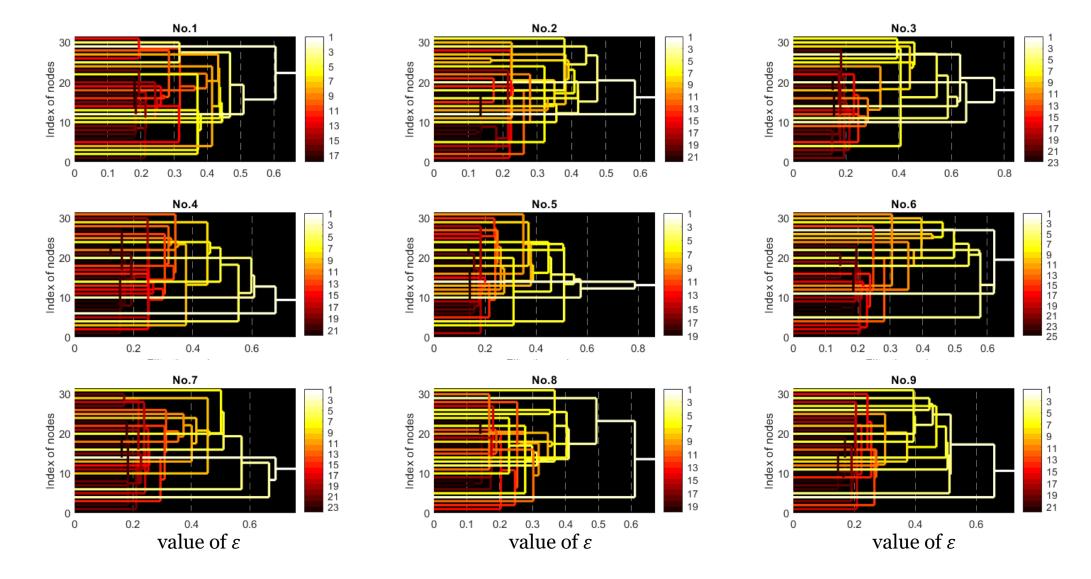
Barcode



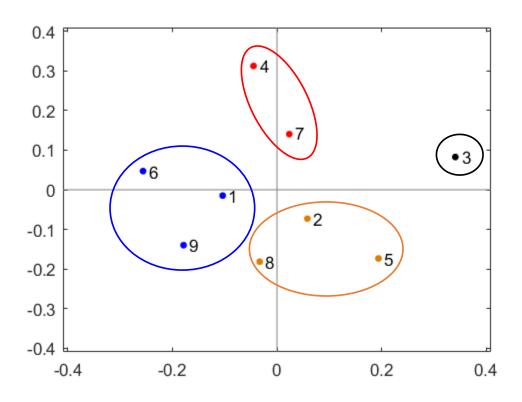
Persistence diagram



Dendrogram



Multidimensional scaling



Multidimensional scaling result

The indices $1 \sim 9 = \text{subject number } 1 \sim 9$

Input distance matrix:

Gromov_Hausdorff_distance =

0	0.3018	0.5194	0.4992	0.4728	0.2639	0.3911	0.3000	0.2788
0.3018	0	0.4062	0.5444	0.4371	0.3945	0.4484	0.3936	0.4408
0.5194	0.4062	0	0.5255	0.4502	0.5555	0.4630	0.5336	0.5980
0.4992	0.5444	0.5255	0	0.5229	0.4942	0.2629	0.5074	0.5333
0.4728	0.4371	0.4502	0.5229	0	0.5708	0.4148	0.3840	0.4108
0.2639	0.3945	0.5555	0.4942	0.5708	0	0.4717	0.4525	0.3769
0.3911	0.4484	0.4630	0.2629	0.4148	0.4717	0	0.3993	0.4252
0.3000	0.3936	0.5336	0.5074	0.3840	0.4525	0.3993	0	0.3374
0.2788	0.4408	0.5980	0.5333	0.4108	0.3769	0.4252	0.3374	0

Output:

MDS_2D_coordinates =

-0.0147
-0.0729
0.0826
0.3121
-0.1732
0.0471
0.1402
-0.1813
-0.1399

Summary

- Overall, there is a distinct difference in β_0 between subject.
- Especially in β_0 , the connectivity of subject 3,6, and 9 is slower than others.
- As a result of the MDS, all the subjects were separated by 3 partial groups.
- The subject 3 had the largest dissimilarity than others.

• It is necessary to find the key variables representing difference among subjects

Thank you!

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