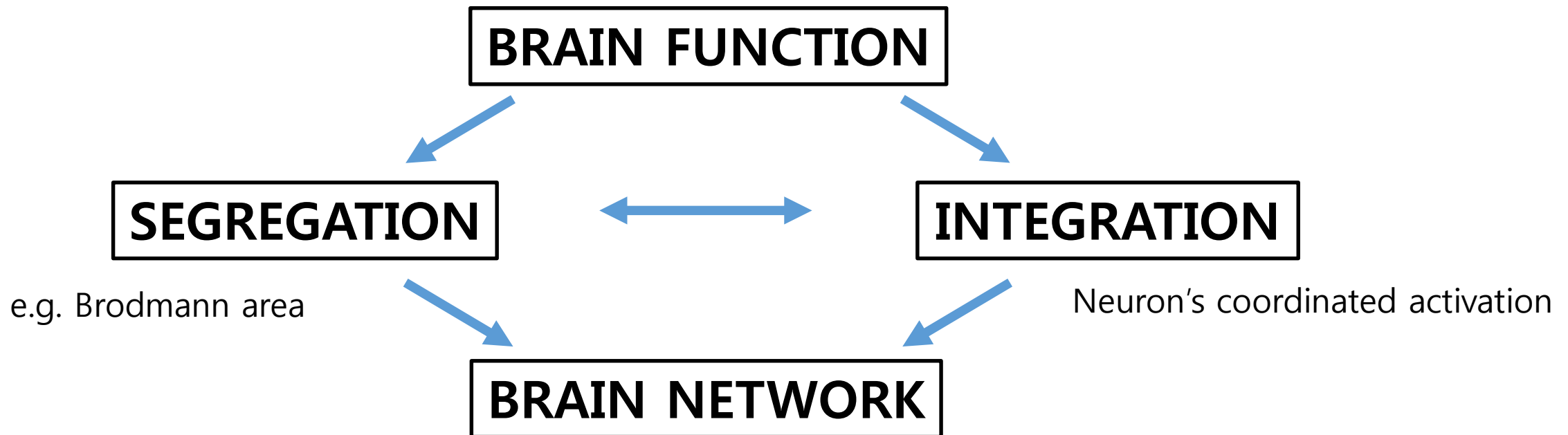


Topological data analysis(TDA) for functional connectivity: Persistence vineyard approach for brain dynamics

Presenter: Jaejun Yoo

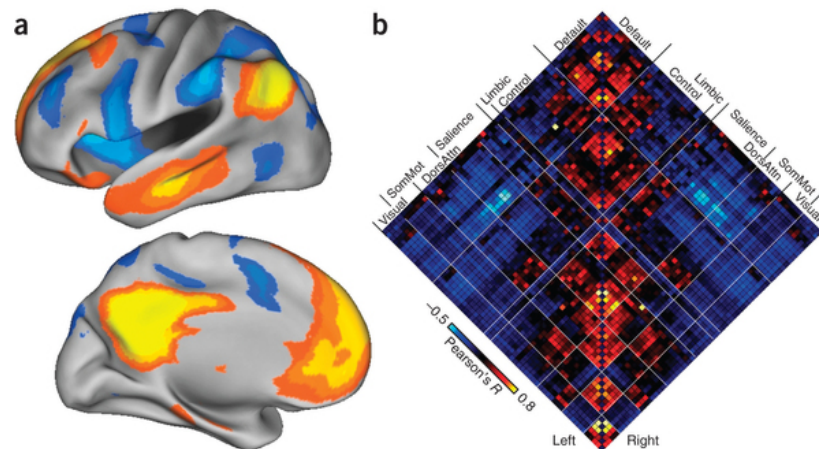
The Brain – A complex network

- Functional organization of the brain is characterized by **segregation** and **integration** of information being processed.



Functional Connectivity

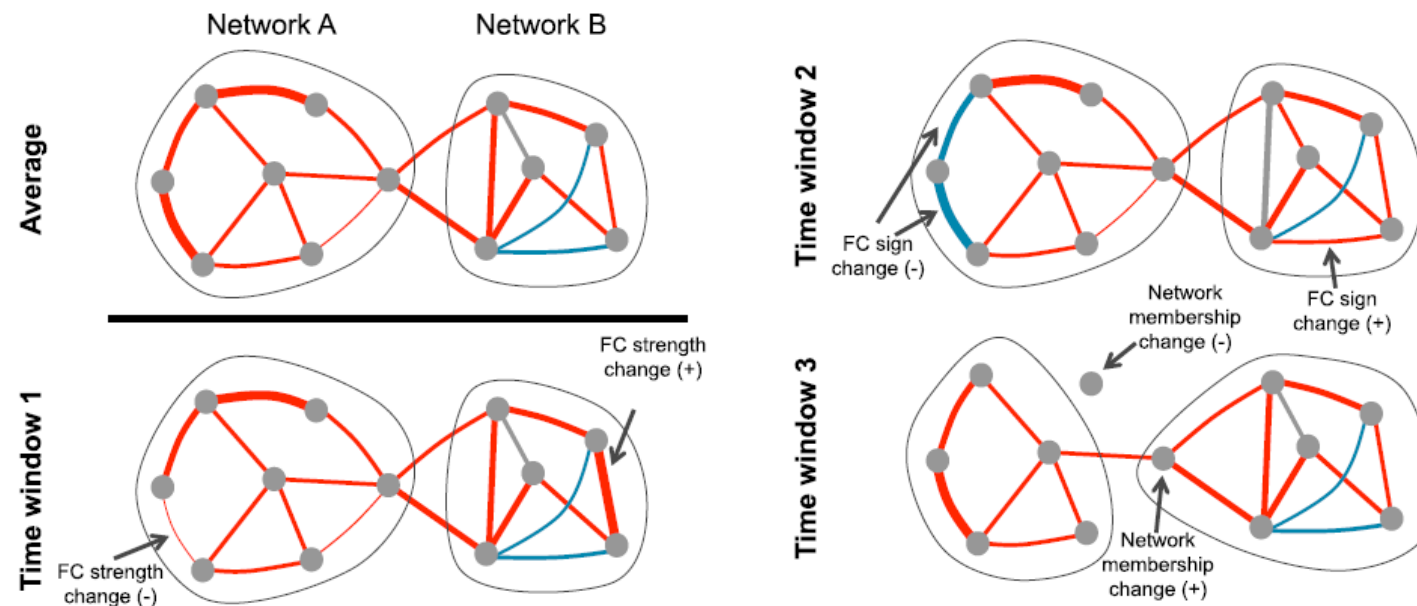
- **Temporal dependency of neural activation patterns** of anatomically separated brain regions.
- It reflects **statistical dependencies** between distinct and distant regions of information processing neuronal populations, e.g. correlation, covariance, spectral coherence, or phase locking.
- Deduced from neuroimaging modalities like fMRI, EEG, MEG, PET, and SPECT.



Buckner et al, 2013

Dynamic Functional Connectivity

- Unlike traditional analysis, recent studies reported that functional connectivity networks dynamically change on short time scales; sliding window analysis.



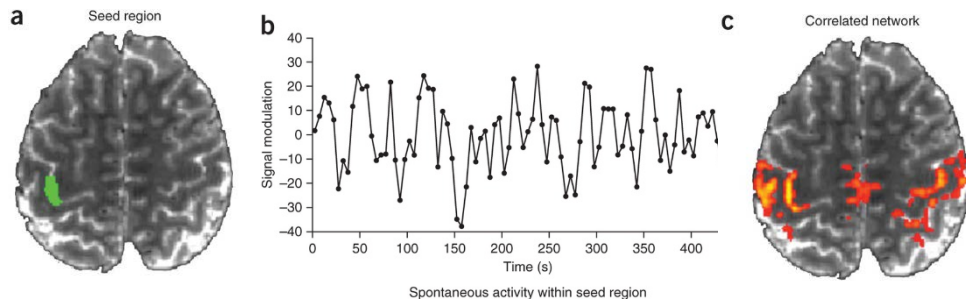
Limitation of traditional approach of averaging total time periods

Computational Methods to Quantify FC

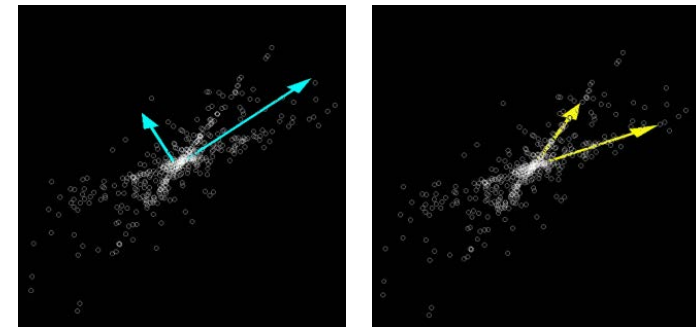
- Two broad classes of the computational methods

**Knowledge-based
Supervised**
(e.g SPM based on GLM and GRF)

**Data-driven
Explanatory
Unsupervised**
(e.g Decomposition, clustering)



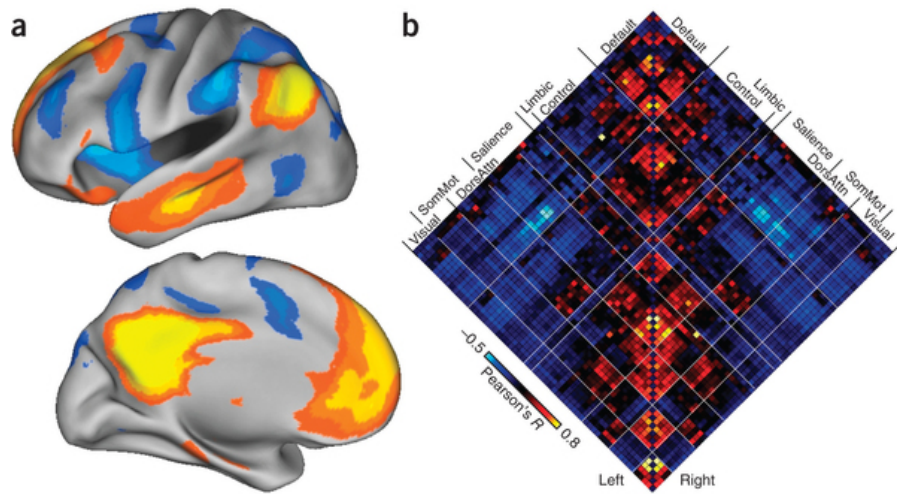
Buckner et al, 2013



Britz et al 2010 ICA

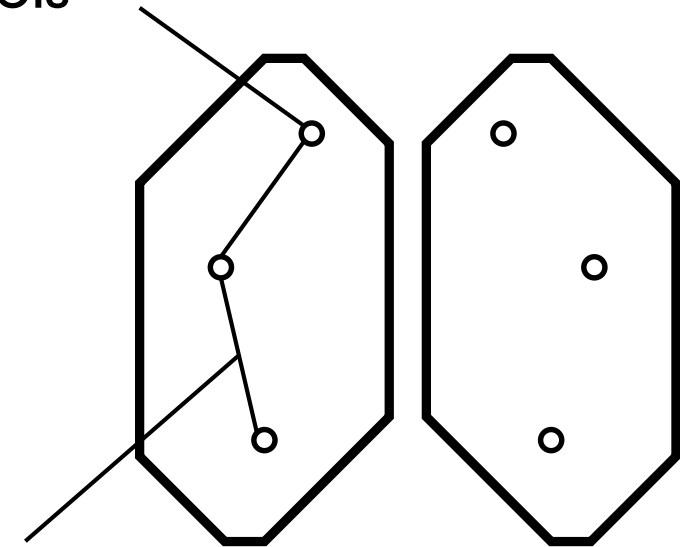
Computational Methods to Quantify FC

- Connectivity matrix can be mapped to a graphical model



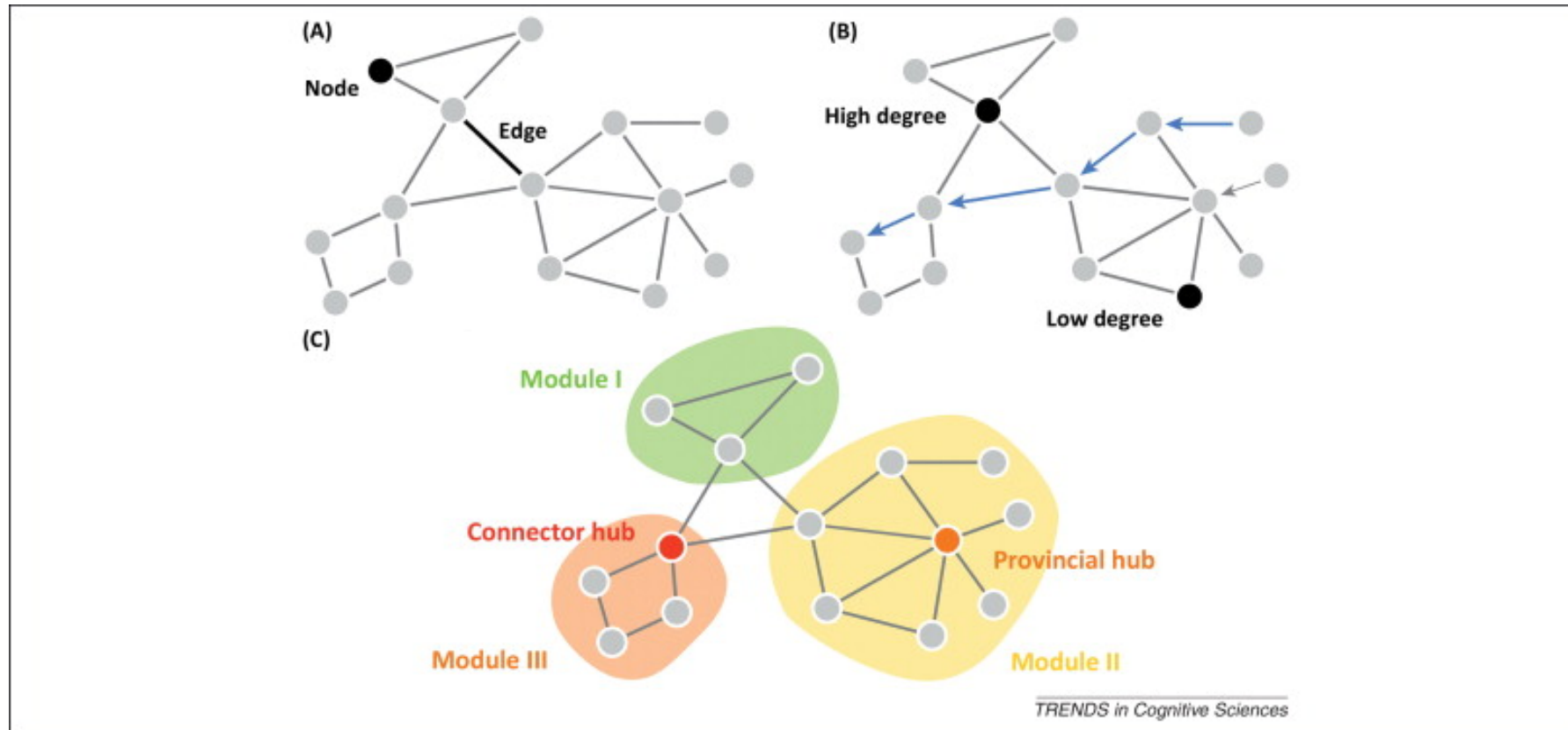
Buckner et al, 2013

Brain areas: ROIs
or Nodes



Relationships: Edges

Computational Methods to Quantify FC



Segregation
Clustering

Integration
Distance
Path Length

Influence
Degree
Centrality (Hubs)

Computational Methods to Quantify FC

- Shortcomings of standard methods

Knowledge-based Supervised

(e.g SPM based on GLM and GRF)

- Results depend on predefined seeds.
- It can only study what is already known.

Data-driven Explanatory Unsupervised

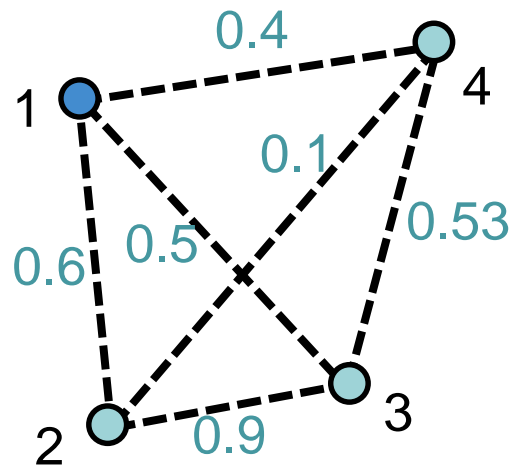
(e.g Decomposition, clustering)

- Intrinsic assumptions may fail.
e.g. orthogonality, independence, stationarity.
- Unknown number of components or clusters.
- Feature selection step

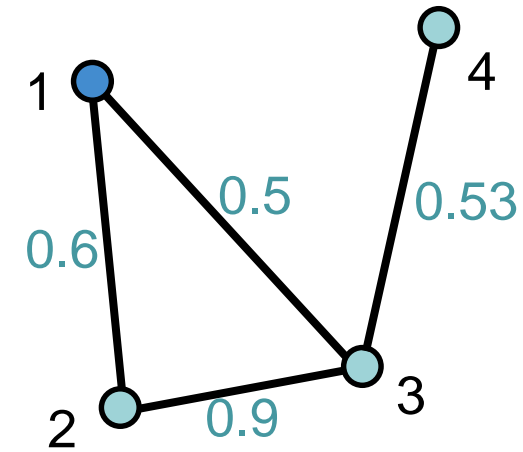
Computational Methods to Quantify FC

- Shortcomings of standard methods

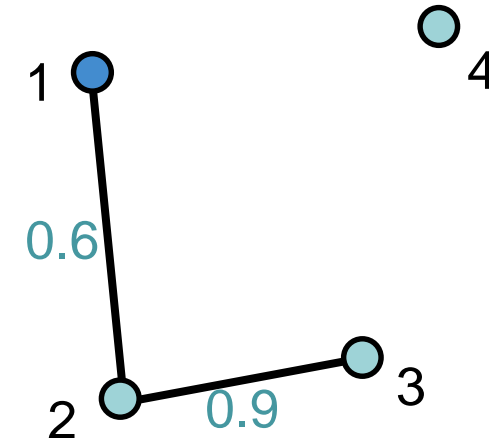
- **Thresholding issue**



Threshold at 0.5



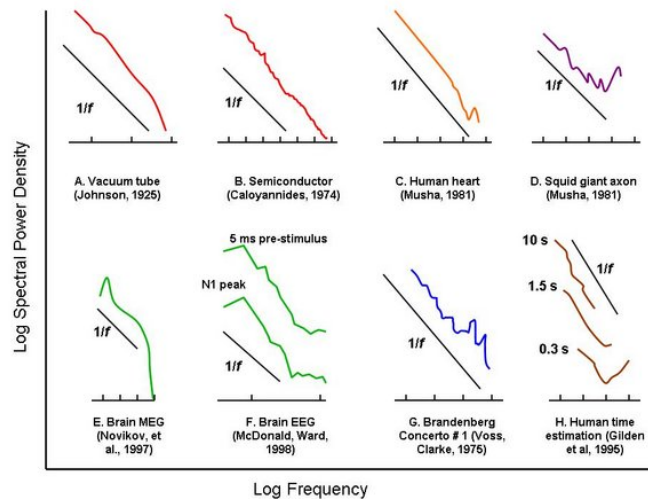
Threshold at 0.6



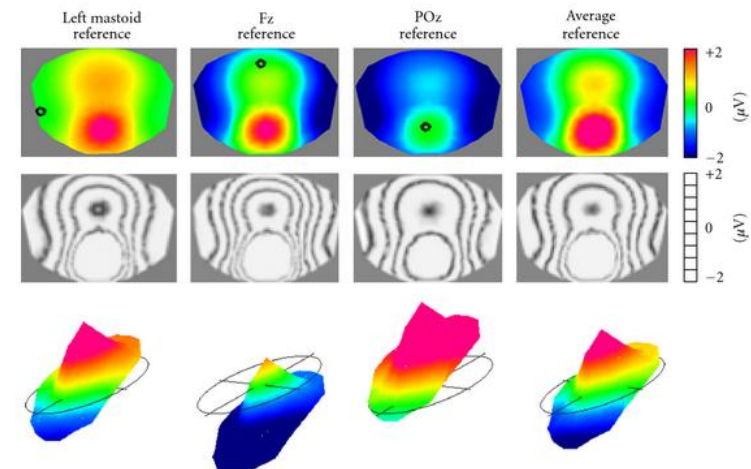
Computational Methods to Quantify FC

- Shortcomings of standard methods

- Thresholding issue
- Data perturbation across ...
1/f spectral distribution, subject by subject, condition to condition, ...



1/f noise – Scholarpedia,



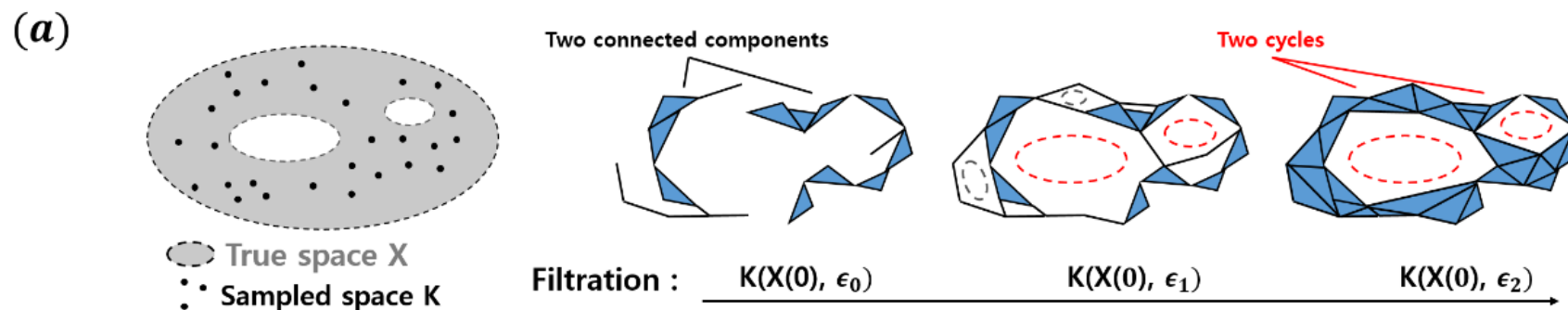
Brunet et al 2011

Topological Data Analysis

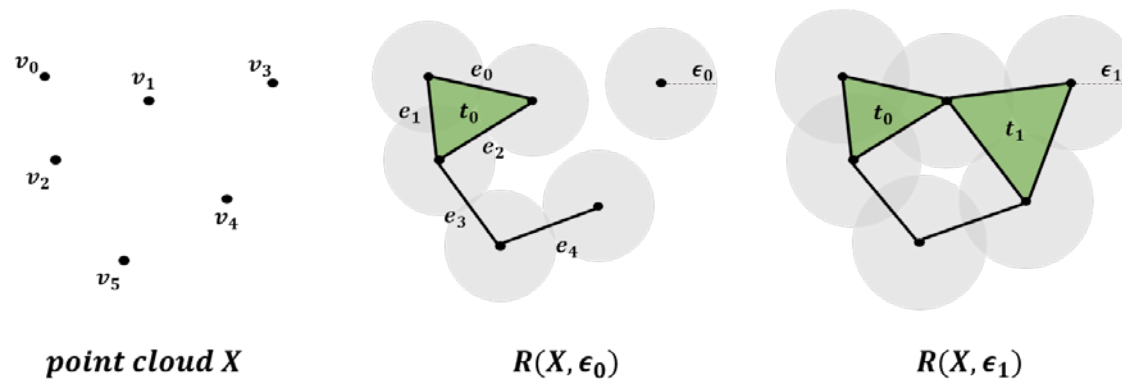
- **Data-Driven** Approach
- Studying complex high dimensional data **without any assumptions or feature selections**
- Shape has Meaning; **extracting shapes(patterns)** of data
- Qualitative and quantitative **summaries** of the data are provided.
- Especially, TDA using **PERSISTENT HOMOLOGY** provides *threshold-free* analysis.

Persistence Homology

- Examines **Topological Invariants**, e.g. **Homology** of the space

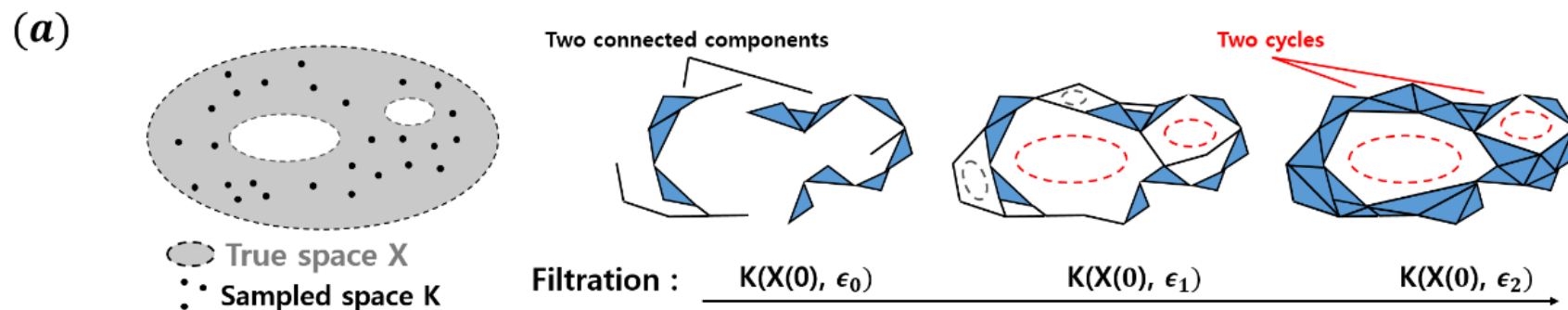


Watch the **evolution of simplicial complex K** increasing the radius, or threshold(ϵ)



Persistence Homology

- Examines **Topological Invariants**, e.g. **Homology** of the space



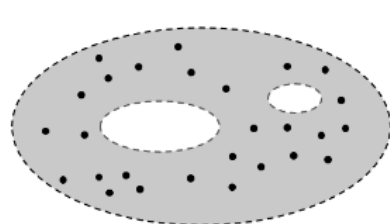
Values of simplex(nodes, edges, and faces) are determined by a height function $f: K \rightarrow \mathbb{R}$ and an order sequence of complexes is constructed,

$$O = K(X, \epsilon_0) \subseteq K(X, \epsilon_1) \subseteq \dots \subseteq K(X, \epsilon_n) = K$$

Persistence Homology

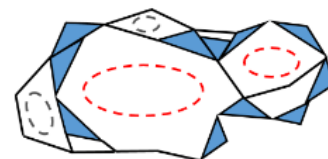
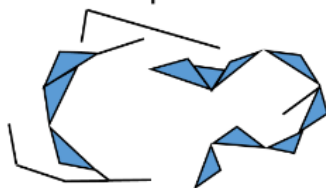
- Examines **Topological Invariants**, e.g. **Homology** of the space

(a)

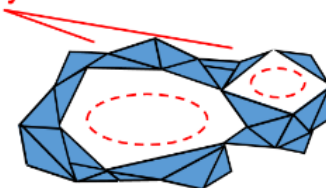


○ True space X
● Sampled space K

Two connected components

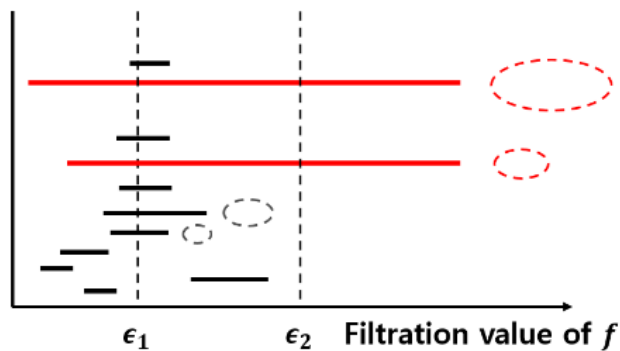


Two cycles

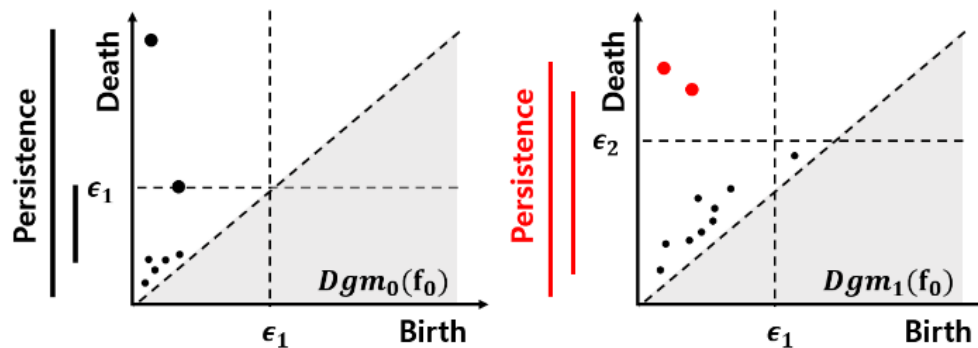


Filtration : $K(X(0), \epsilon_0)$ $K(X(0), \epsilon_1)$ $K(X(0), \epsilon_2)$

(b) Barcode (dim. 1)

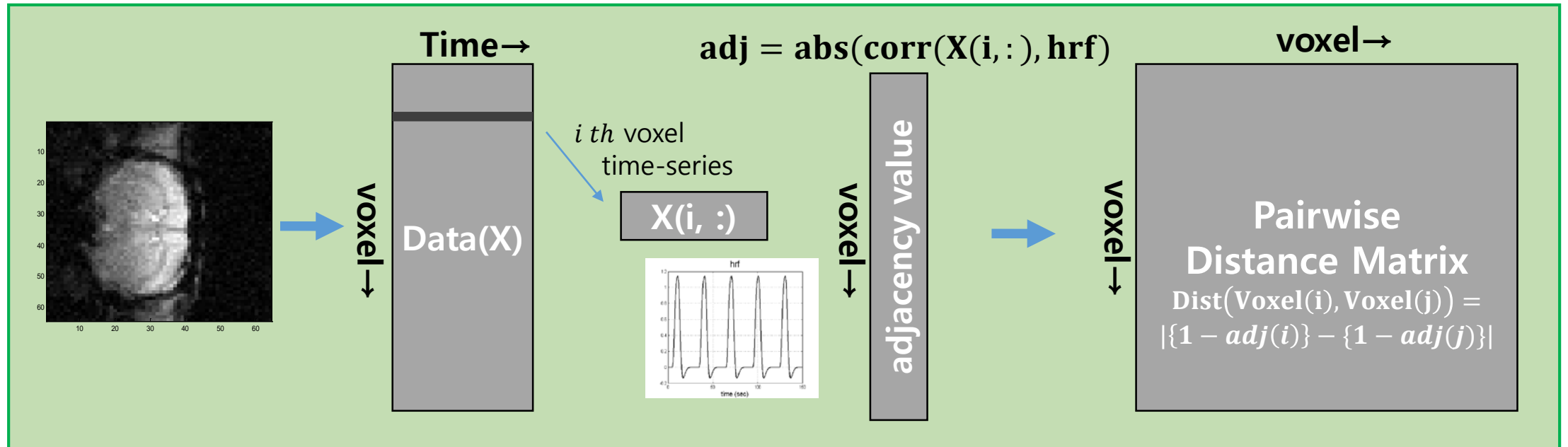


(c) Persistence Diagram (dim. 0 & 1)



Exemplary application: fMRI data

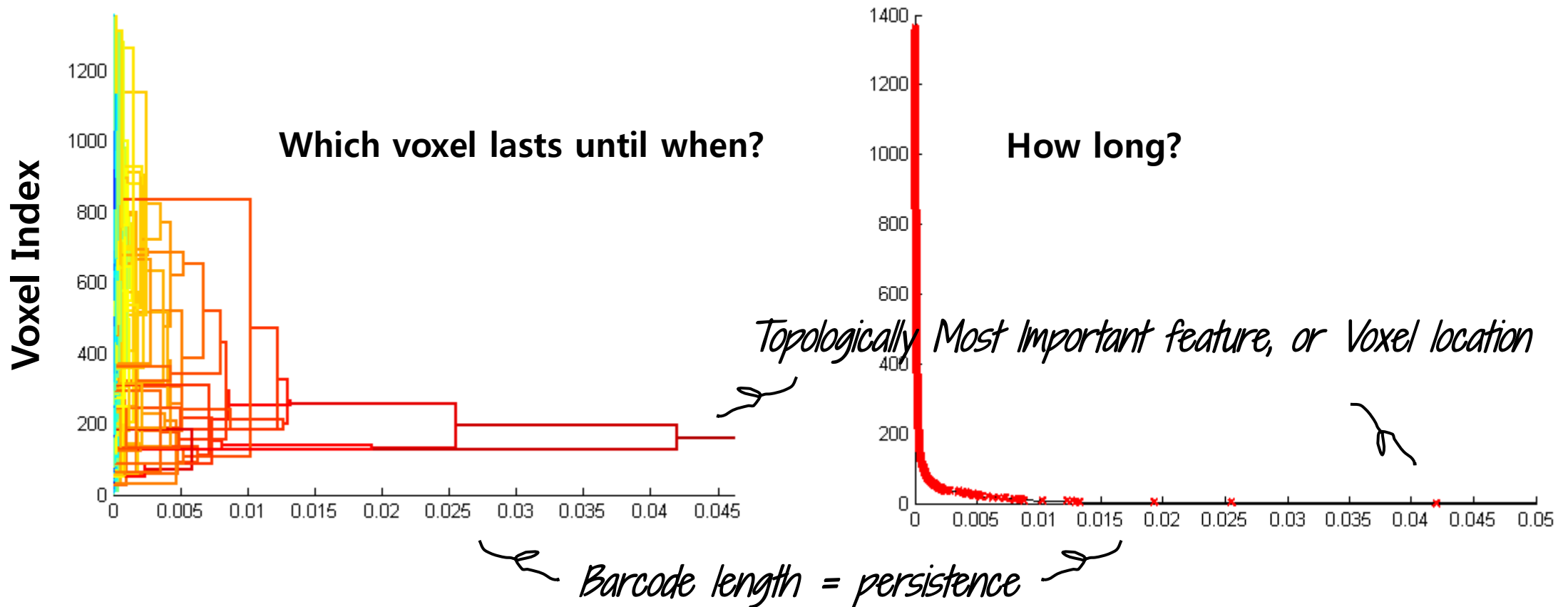
- Mouse forepaw stimulation, fMRI (full vs. 2X down sampled)
- Dimension: 64 by 64 by 150 (time)
- Distance was calculated by the correlation with their hemodynamic response function



Schematic flow of distance matrix calculation

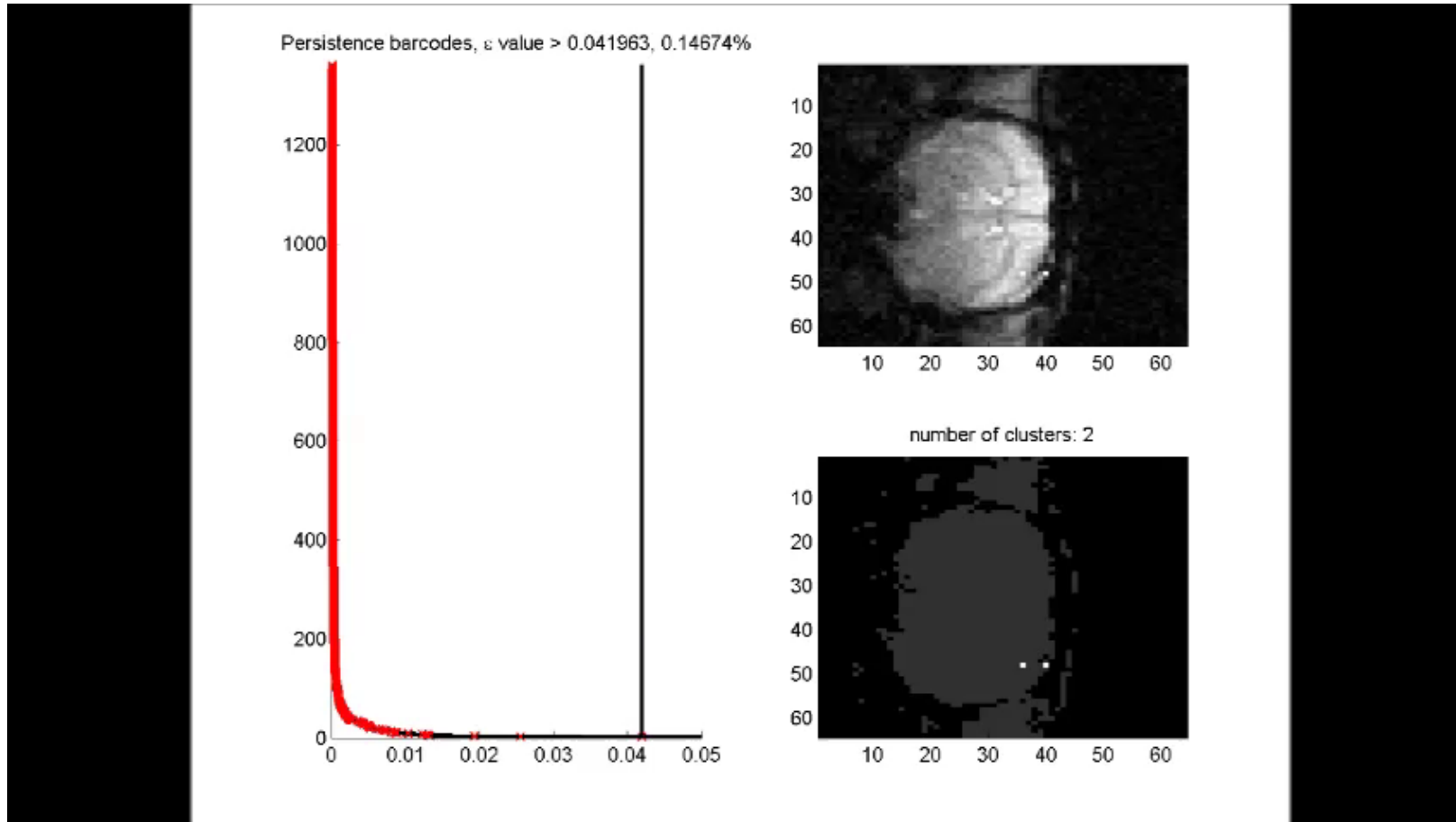
Result

- Dendrogram and barcodes merging



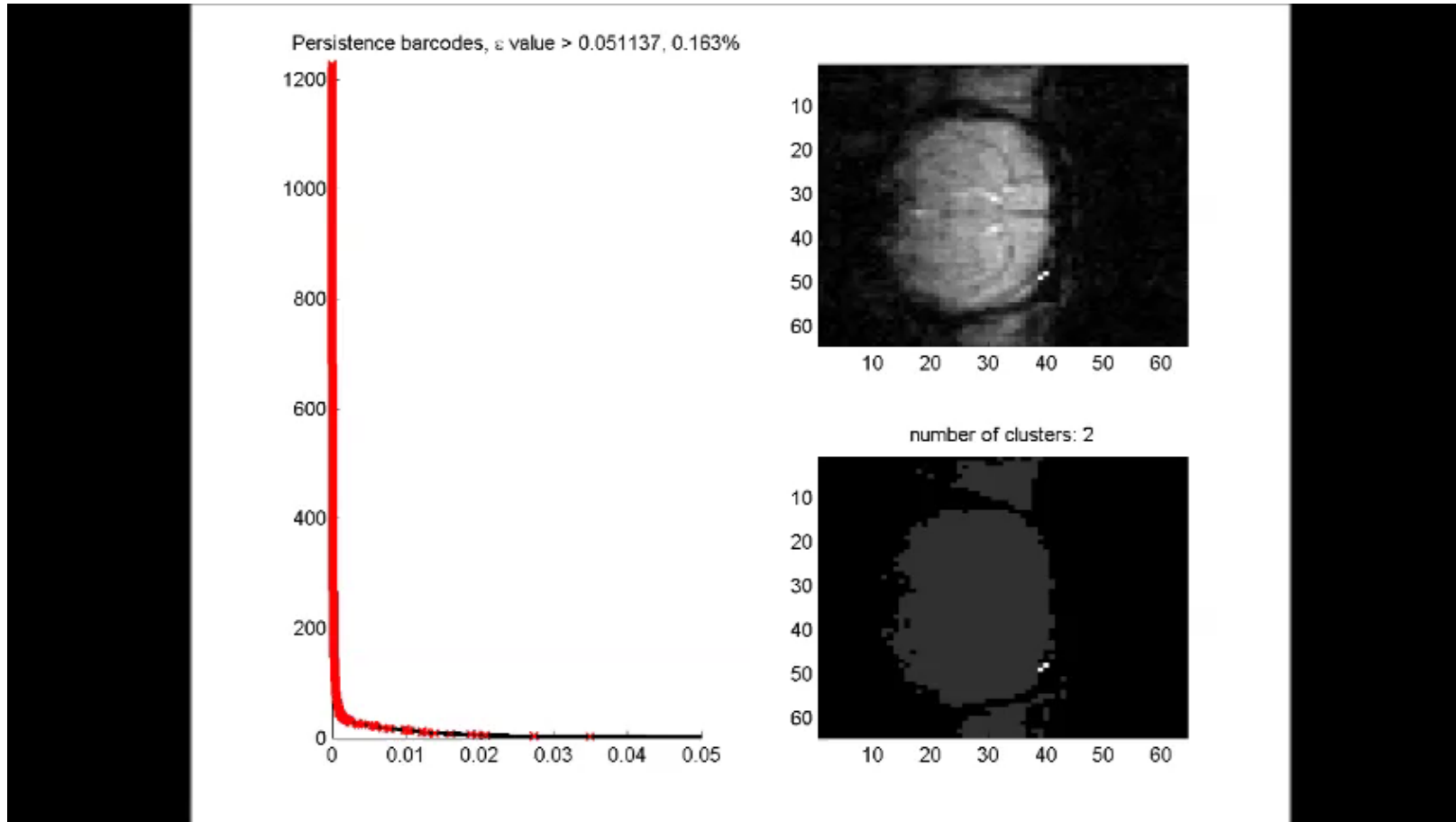
Result

fMRI **full** data



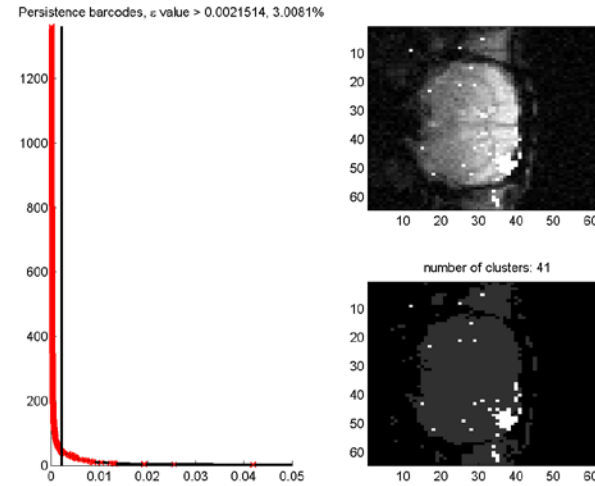
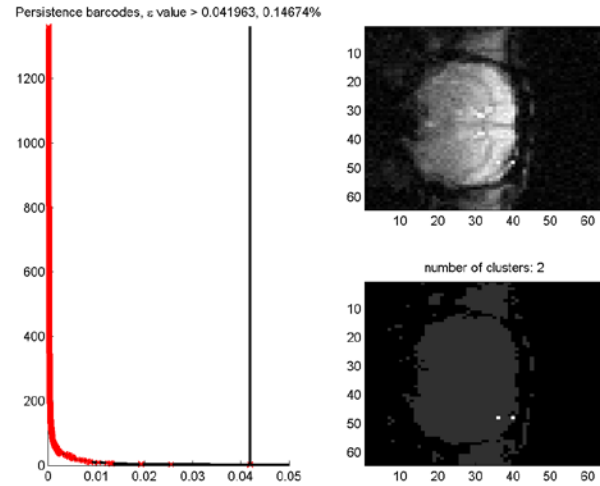
Result

fMRI Down sampled 2X data

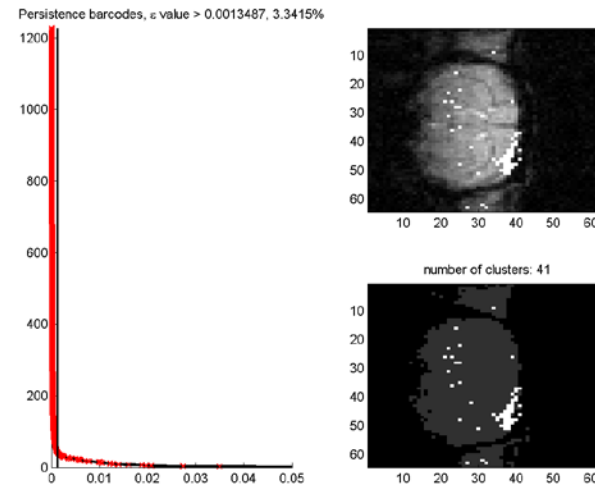
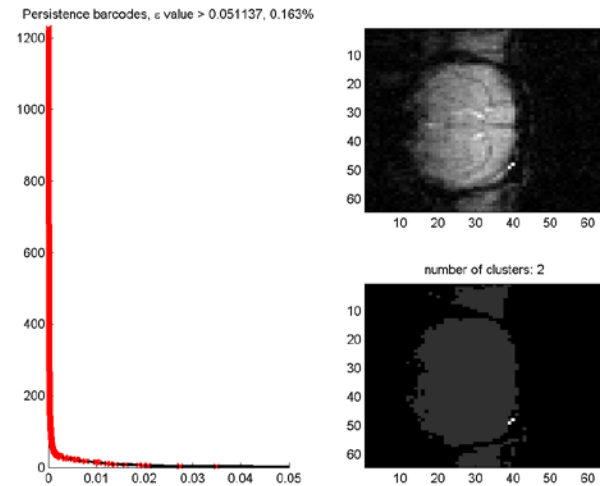


Result

fMRI full



fMRI down 2X



NOTE THAT...

- No t-test relying on p-value selection was performed.
- Quantified criteria of topological importance of the features are provided.

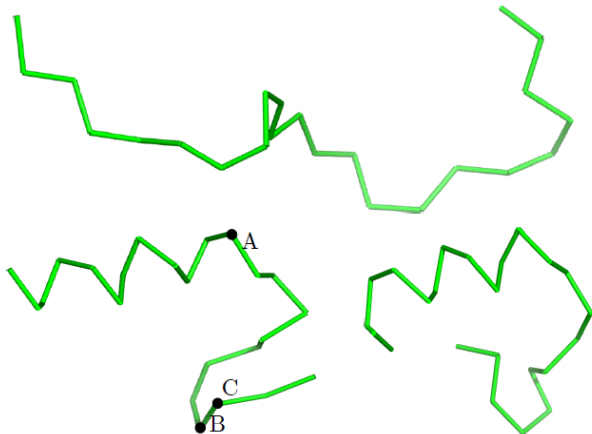
**TO FURTHER ASSESS DYNAMICS
OF FUNCTIONAL CONNECTIVITY...**

Persistence Vineyard

- Stability of persistence diagram (Cohen et al 2006)
"Persistence diagram remains stable unless there exists a distinctive change in the space."
- By exploiting stability theorem, the authors introduced a computational algorithm to efficiently update persistence diagrams over data perturbations, which is called "*persistence vineyard*".

Persistence vineyard follows

how the continuous changes of data affect characteristics of the space.

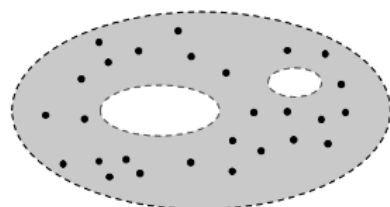


Protein folding varies over time, Cohen et al (2006)

Persistence Homology

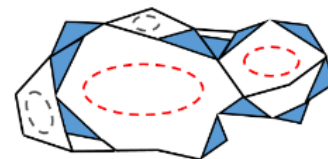
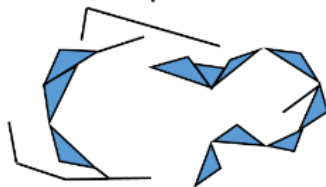
- Examines Topological characteristics of the space at *single time frame*.

(a)

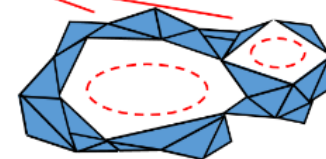


● True space X
● Sampled space K

Two connected components



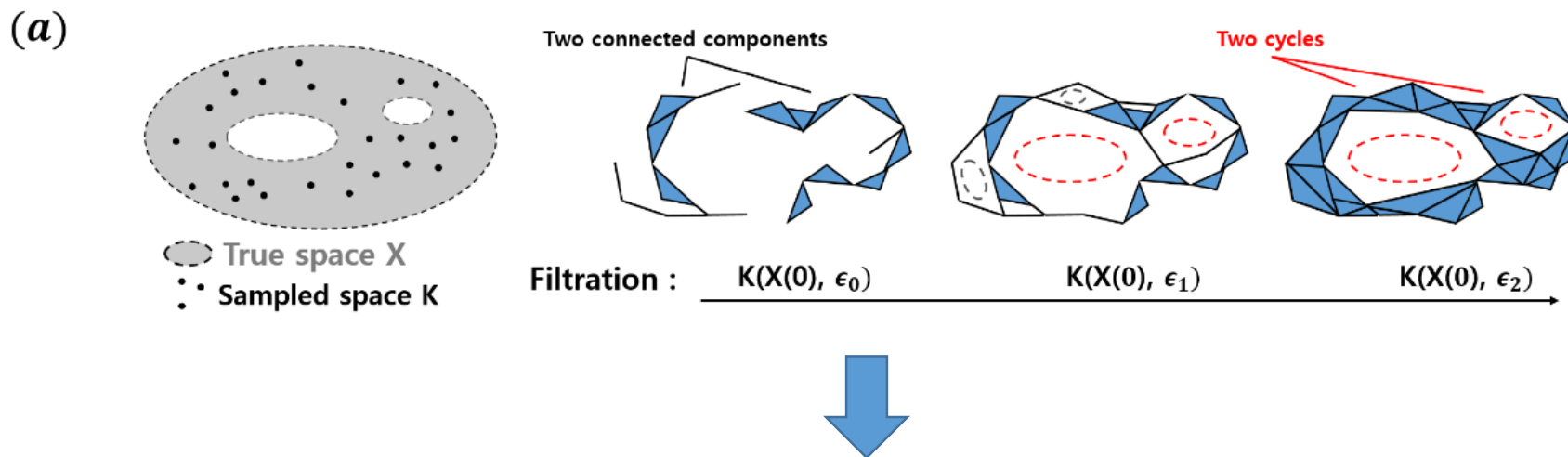
Two cycles



Filtration : $K(X(0), \epsilon_0)$ $K(X(0), \epsilon_1)$ $K(X(0), \epsilon_2)$

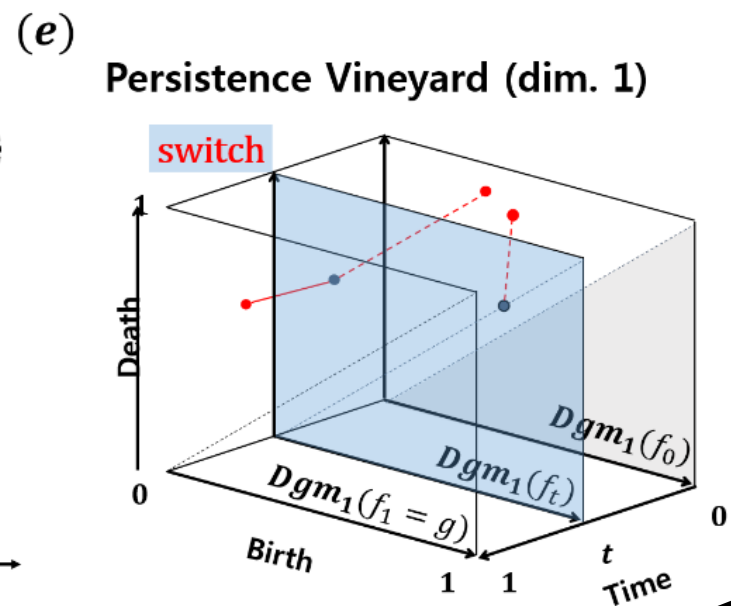
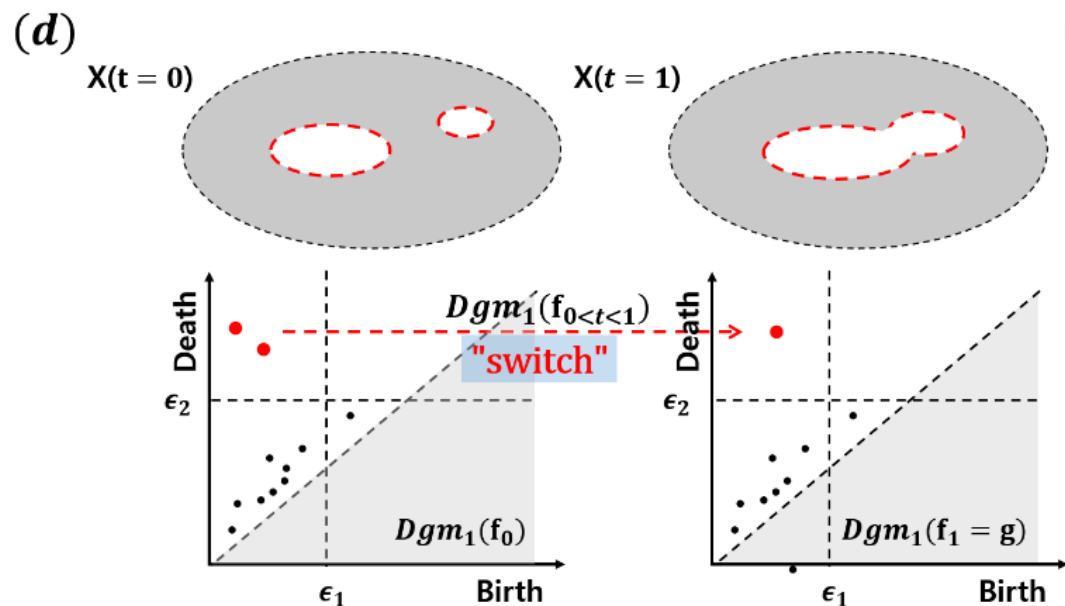
Persistence Homology

- Examines Topological characteristics of the space at *single time frame*.



Extend the *persistent homology* analysis toward the 3rd dimension:
“temporal domain”, “Examine the variation over multiple time frame”

Persistence Vineyard



$$f_t = (1 - t)f(\sigma) + tg(\sigma), \text{ for } t \in [0, 1]$$

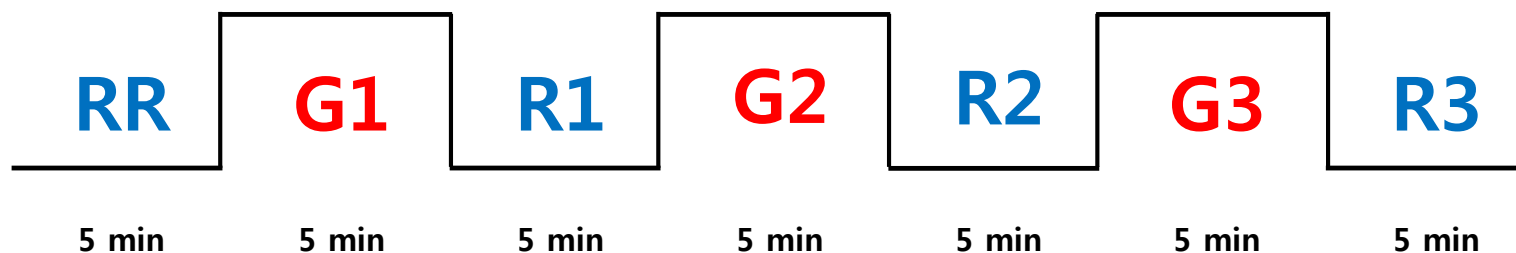
Tracks the change of height function

Stacking the persistent diagrams along time direction

Application: EEG data

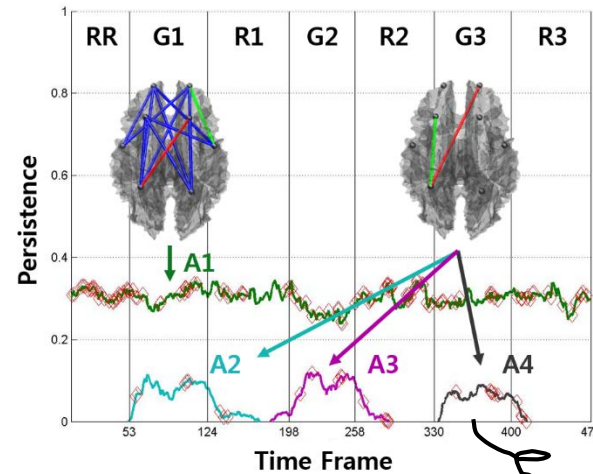
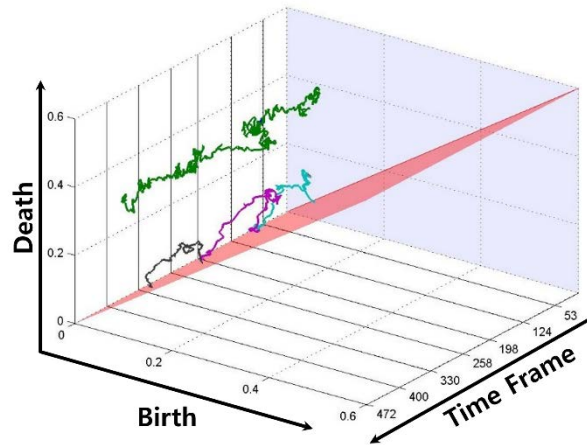
Normal Subjects, resting and gaming alternatively

- EEG, 8 channel,
- Sampling rate: 512 Hz
- Sliding window analysis
- window length: 30 s / shifting length : 2 s (2m 30 s = 31 frame)
- Delta (0.3-4 Hz), Theta (4-8 Hz), Alpha (8-13 Hz), Beta (13-30 Hz)
- ICA, Epoch rejection performed

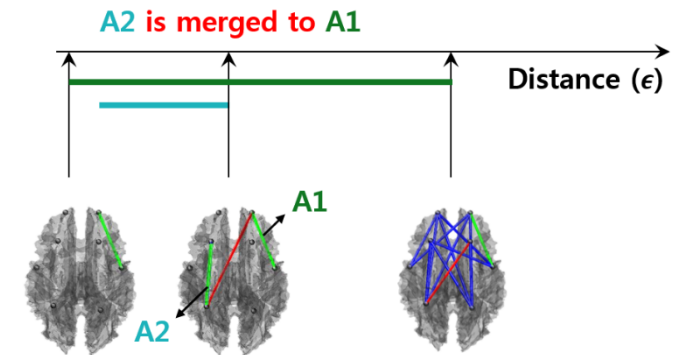


Persistence Vineyard

Alpha band



Barcode at an arbitrary time frame of G1

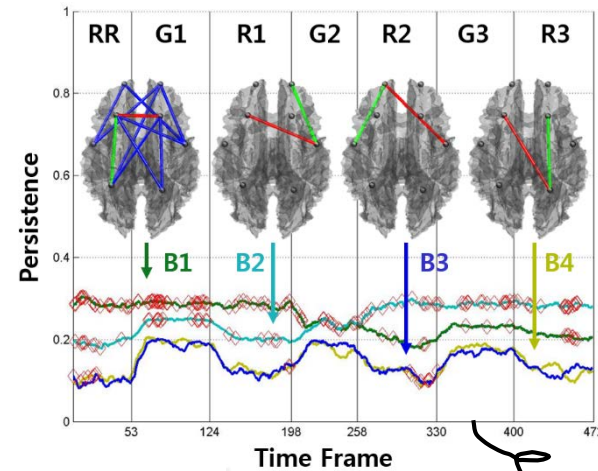
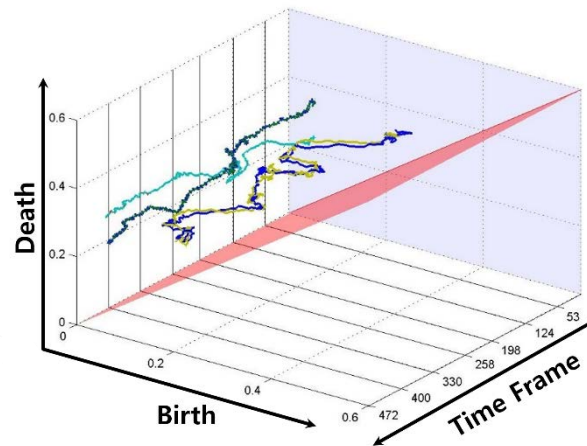


◇'s are "Switch" locations

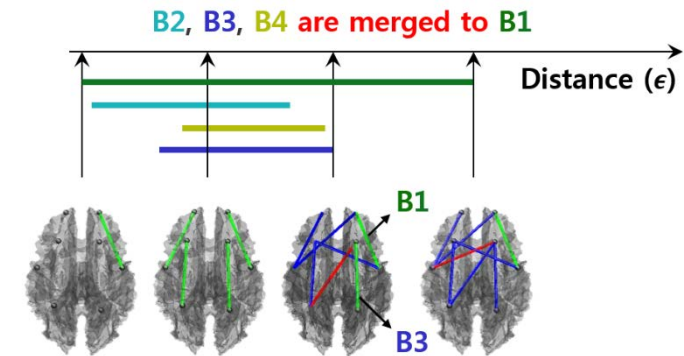
- **Two** components are extracted.
- Whole network **breaks down to two component** during the gaming stages **only**.
- Components' connectivity was **reduced** during gaming.

Persistence Vineyard

Beta band



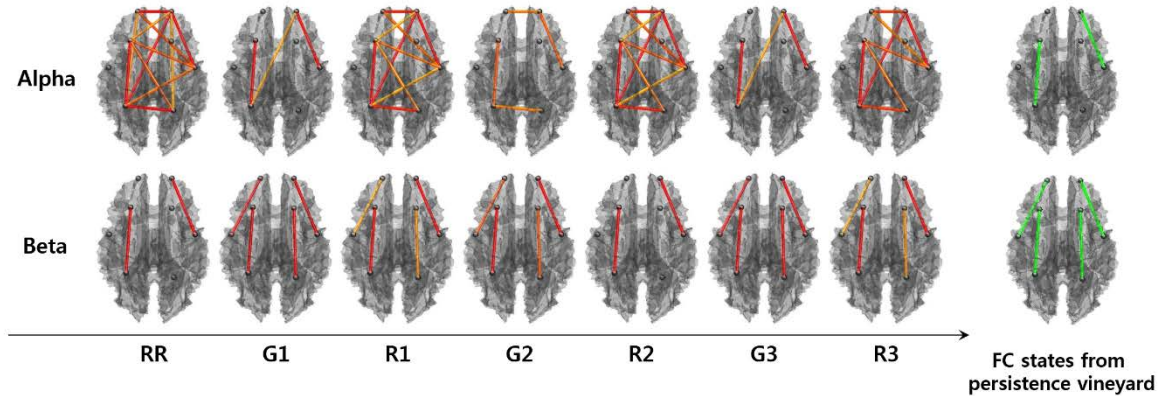
Barcode at an arbitrary time frame of G1



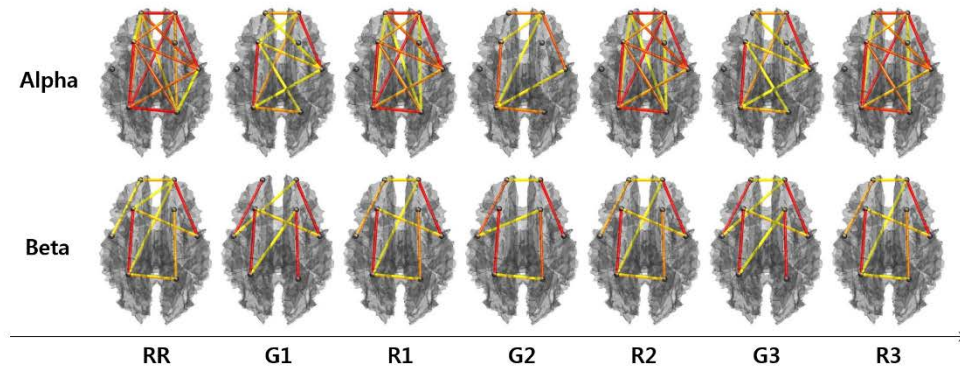
- **Four** components are extracted.
- Components exist in hierarchical way residing in different strengths.
- Components' connectivity was **enhanced** during gaming.

Standard Graphical Methods

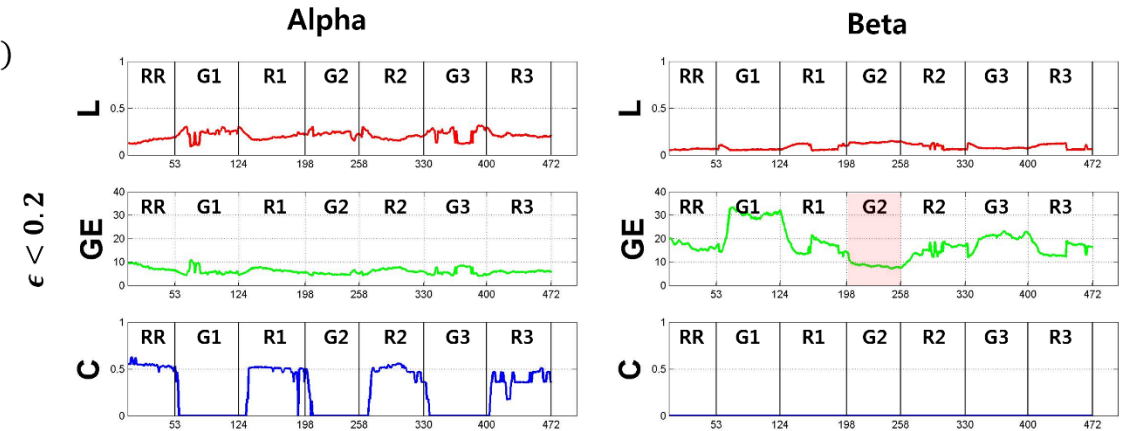
(a) Connectivity distance (ϵ , linear) < 0.2



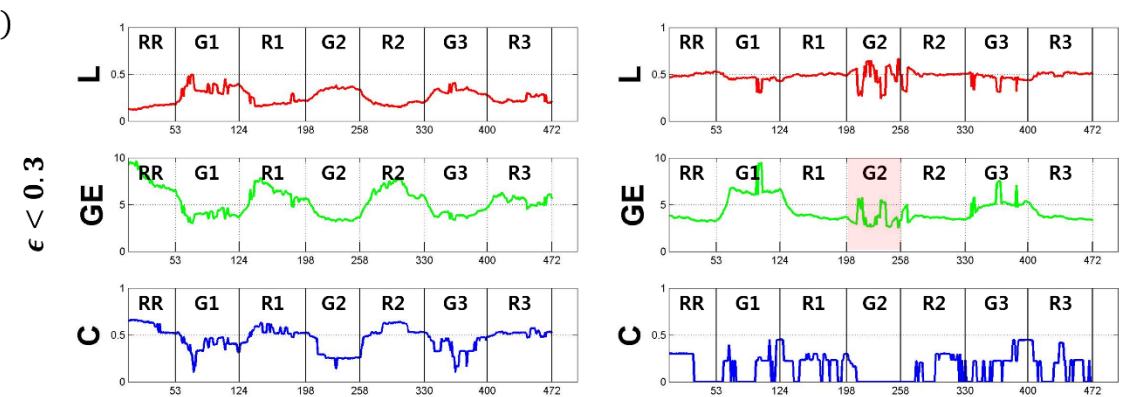
(b) Connectivity distance (ϵ , linear) < 0.3



(a)

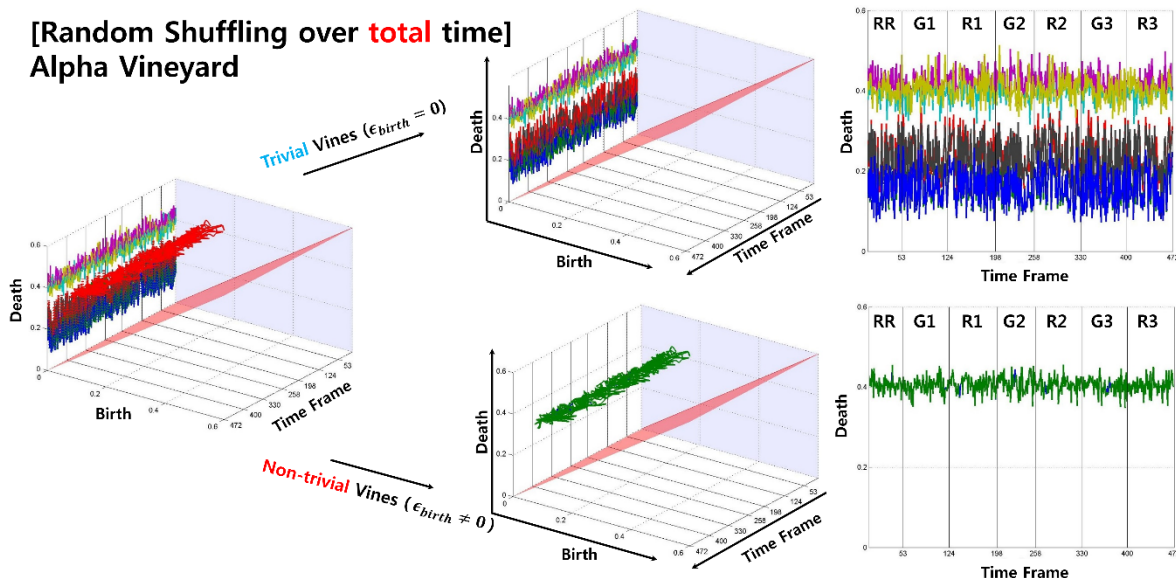


(b)

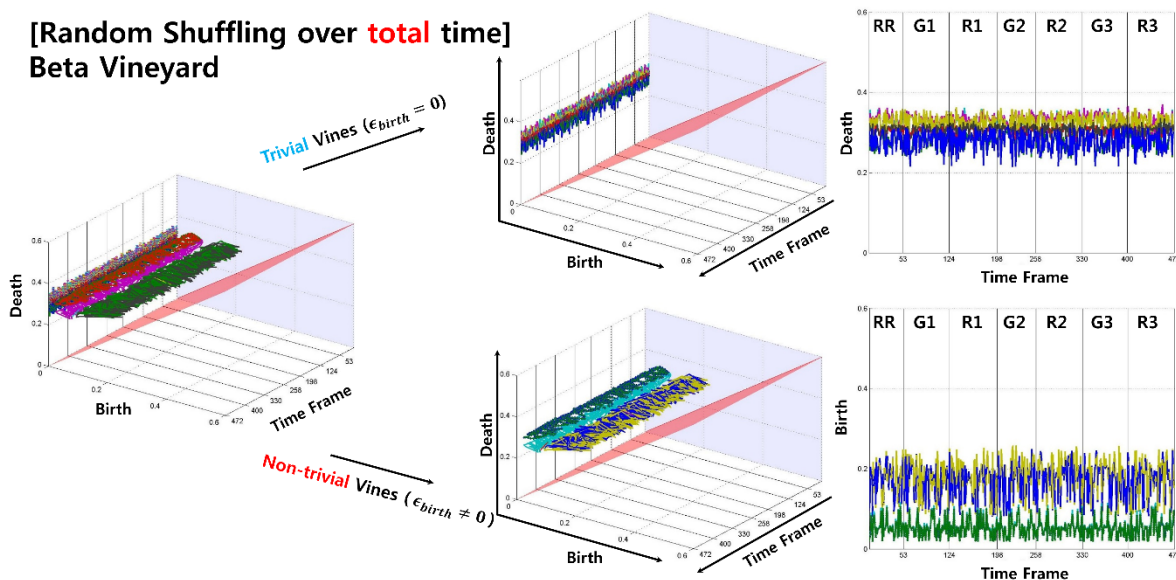


Results are **fluctuating** across thresholds and spectral bands.

[Random Shuffling over **total time**]
Alpha Vineyard

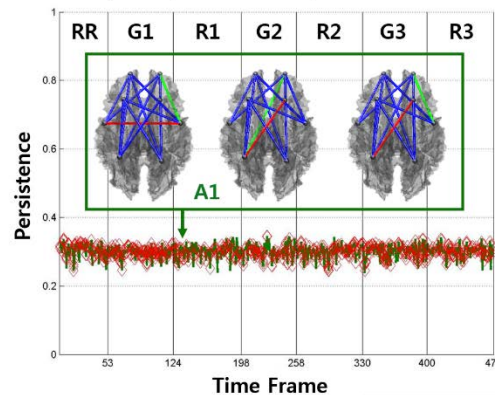


[Random Shuffling over **total time**]
Beta Vineyard

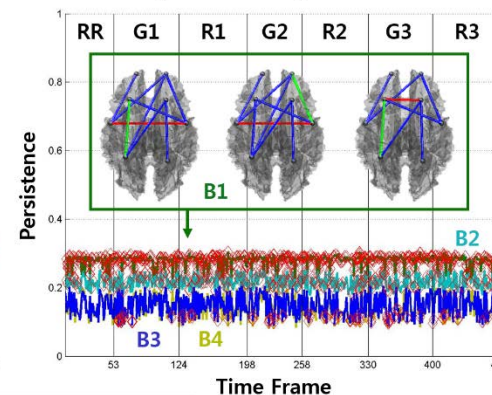


- Comparison with the vineyard generated under **null hypothesis** (randomly shuffled in time order)
- **No** significant structure or consistent pattern was found

R/S-Alpha (**non-trivial**)



R/S-Beta (**non-trivial**)



◇'s on vines: switch locations

- **Number of SWITCH** soared

Vineyards \ Vines		Vines							
		A1	A2	A3	A4	B1	B2	B3	B4
Original	vine length	471	119	107.25	79.626	471	471	471	471
	# of switches	124	8	10	10	98	88	4	13
R/S	vine length	471	-	-	-	471	471	471	471
	# of switches	611	-	-	-	611	221	48	62

[SUMMARY]

Advantages of Persistence Vineyard

- Retain the advantages of TDA and persistent homology;
e.g. Data-driven, threshold-free, assumption-free approach. Do not require feature selection (features and their are determined by the data).
- Good properties with mathematical background.
- Provide quantified summaries of network variation
- Displayed consistent results with the previous EEG studies.
Alpha : resting
Beta : attention, task-related