TDA - fall 2025

Vineyards + time-varying data

Recap

- Final project proposals - due this week (slot coming soon)
- Office hours today, 2-3pm, if you have any questions
- Older assignments - please submit ASAP

Stability of persistence

Previously, we saw several notions of stability, ie:

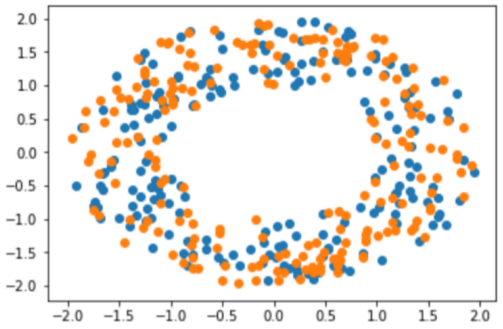
Fix a triangulable space X with 2 continuous, tame functions $f, g: X \to \mathbb{R}$, & let D_f & D_g be the resulting sublevel set persistence diagrams.

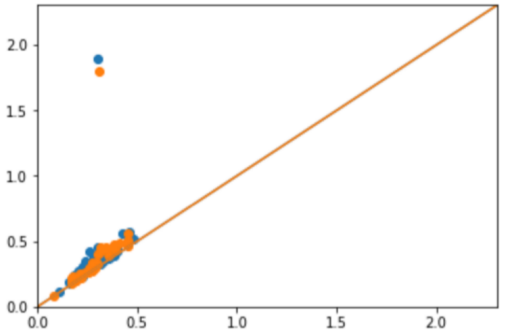
Then: $$B(D_f, D_g) \leq \|f - g\|_\infty$$

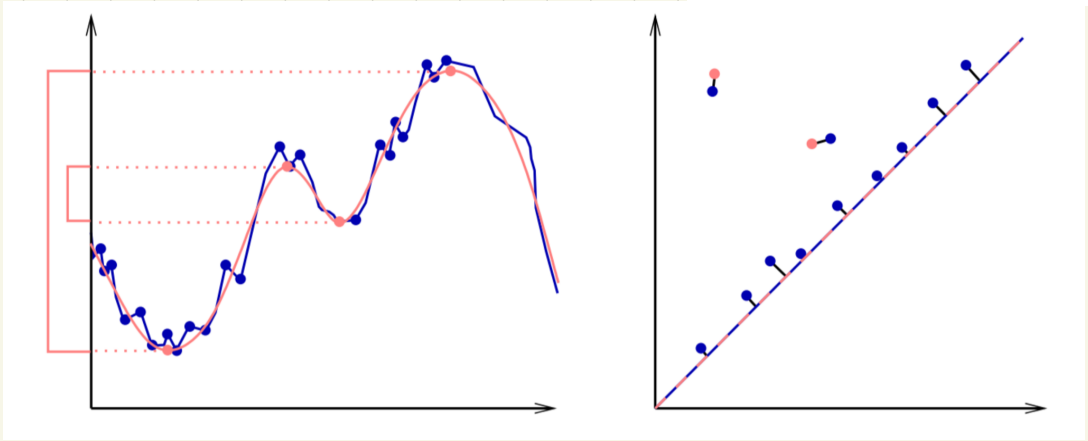
(similar statements for point clouds)

↳ Rips or Čech filtrations

Pictures







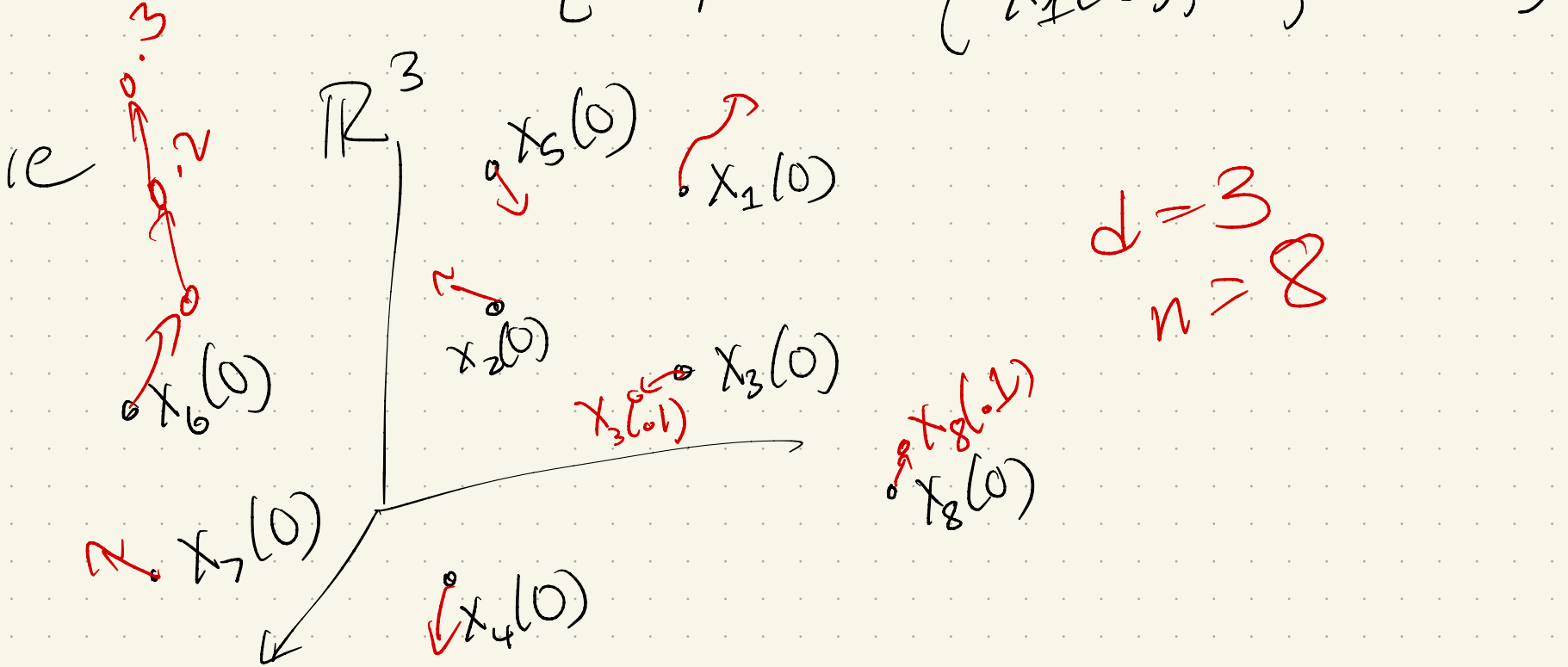
There are many notions of stability, but almost all result in an explicit map from D_g to D_f (where points on the diagonal are also used).

Time varying point clouds

A dynamic point cloud $X(t) = (x_1(t), \dots, x_n(t))$ is a point cloud which is moving continuously, for $t \in [0,1]$,

ie $[0,1] \longrightarrow (\mathbb{R}^d)^n$

$t \longmapsto (x_1(t), \dots, x_n(t))$



Vineyards

Cohen-Steiner, Edelsbrunner, Morozov 2006

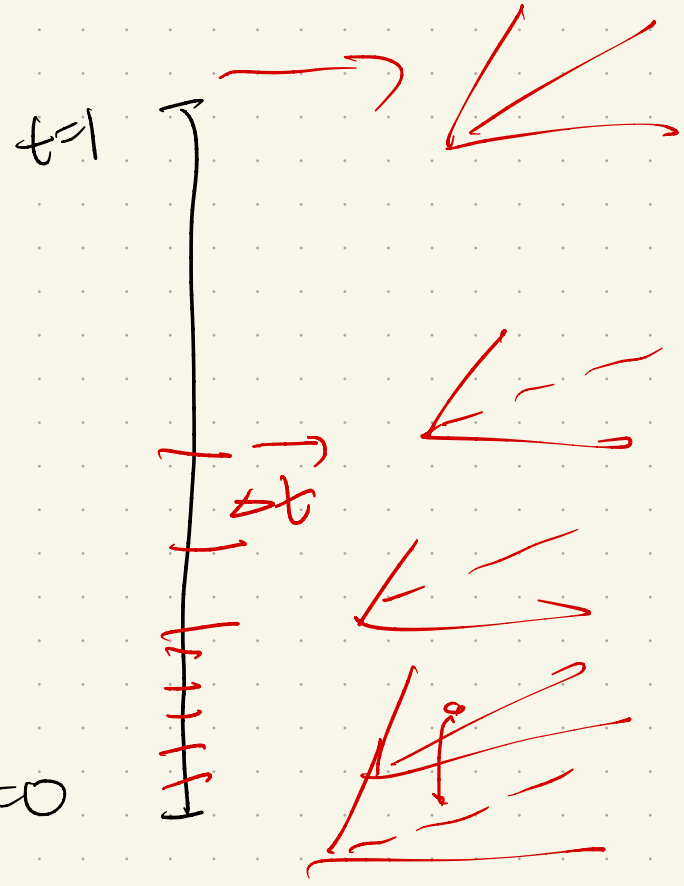
For each time t_i we have a persistence diagram $D(X(t_i))$.

This one parameter family is called a vineyard:

$$V(X) = \{D(X(t)) \mid t \in [0,1]\}$$

$$[0,1] \longrightarrow \mathbb{D} \quad \hookleftarrow \text{space of pers. diagrams}$$

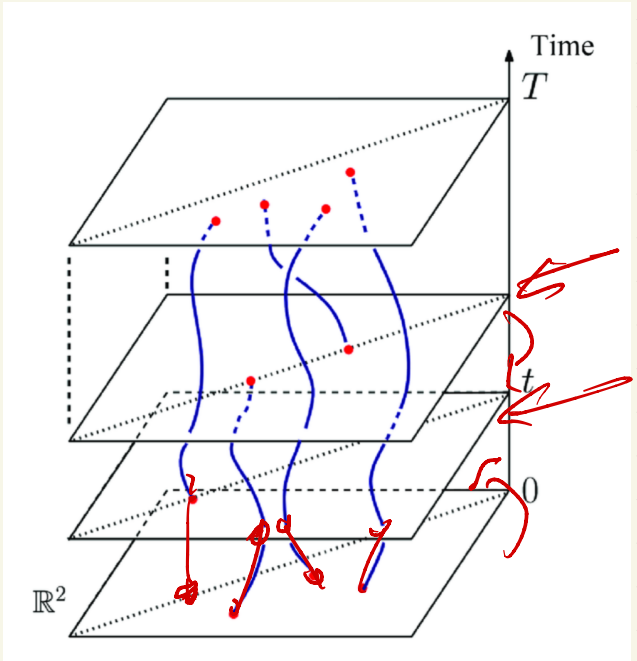
$$t \longmapsto D(X(t))$$



If the dynamic point set $X(t)$ is continuous with respect to Hausdorff distance, the Vineyard is continuous with respect to bottle neck distance.

Why? stability!

Vine: trace of some off-diagonal persistence point



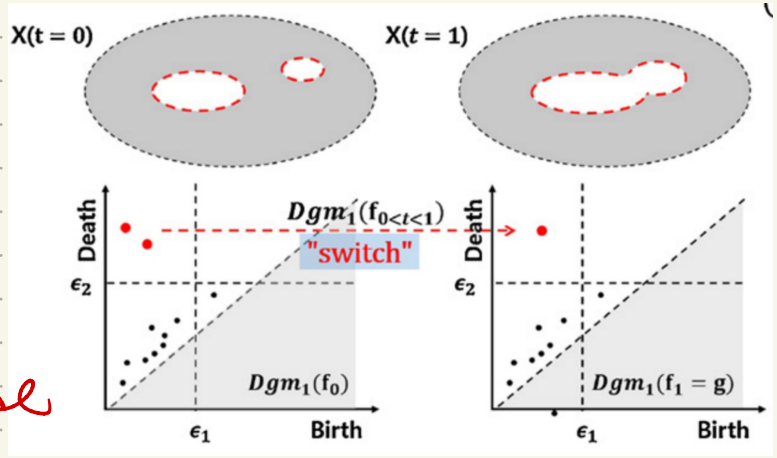
Note: things can appear from diagonal, disappear into diag, & collide

Similarly, consider a simplicial complex $|K|$ with 2 functions $f, g : |K| \to \mathbb{R}$ & any homotopy f_t interpolating from $f = f_0$ to $g = f_1$ (with each f_t tame).

Vines are smooth except where critical pairs change

↳ called knees.

How? places where birth/death times coincide



Aside on vines

Not clear if arbitrary vineyards can decompose nicely into vines.

Munch 2013 Turner 2023

(mostly because of diagonal trees)

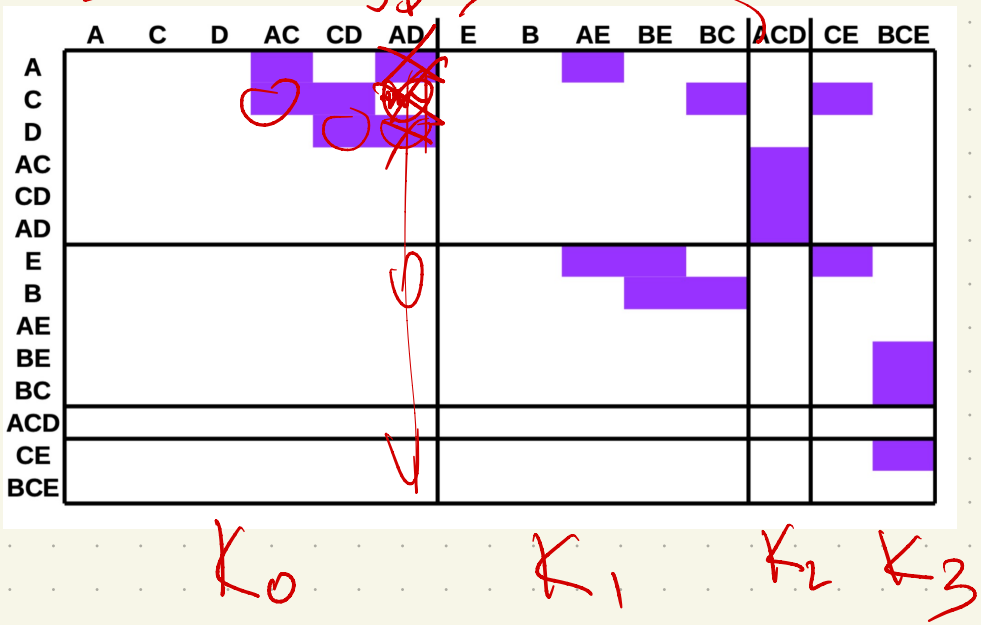
Nonetheless, computation + statistics for vineyards are well-studied.

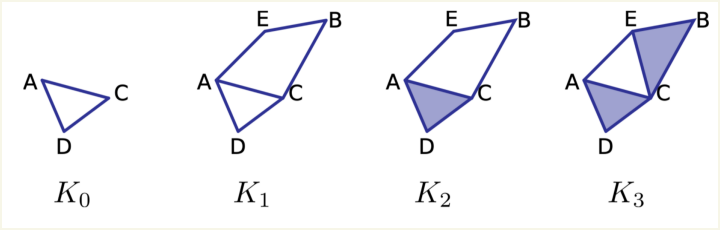
Computation

Cohen-Steiner et al 2006

For triangulation K of space X with monotone function f, recall our matrix algorithm:

$R = B$
for $j = 1 \cdots m$ **do**
  while $\exists\, j' < j$ with $low(j') = low(j)$ **do**
    add column j' to column j
  end while
end for





Result : pairs (σ_i, σ_j) with

$i = \text{low}_R(j)$

σ_i positive

σ_j negative

AC, C → CD, D

	A	C	D	AC	CD	AD	E	B	AE	BE	BC	ACD	CE	BCE
A														
C				*										
D					*									
AC														
CD														
AD												*		
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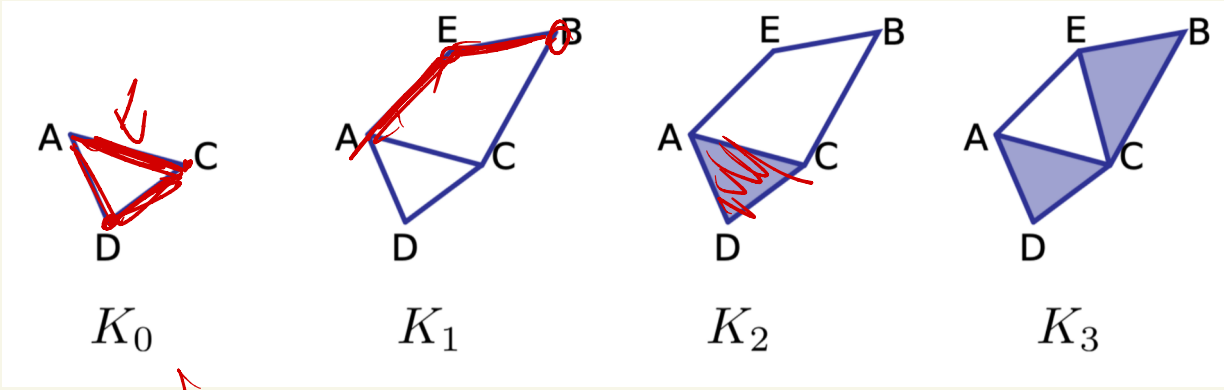
BCE														

R



Updating the pairing

Suppose order of 2 simplices flip: need to update persistence pairs (maybe).

Some linear algebra: can rewrite

$$R = DV, \quad V \text{ invertible + upper-triangular}$$

$$\Rightarrow D = R(V^{-1}) = RU$$

positive simplices → zero columns

negative → non-zero

Matrix cases

Swapping i & $i+1$ in filtration:
can cause change in birth/death pairs

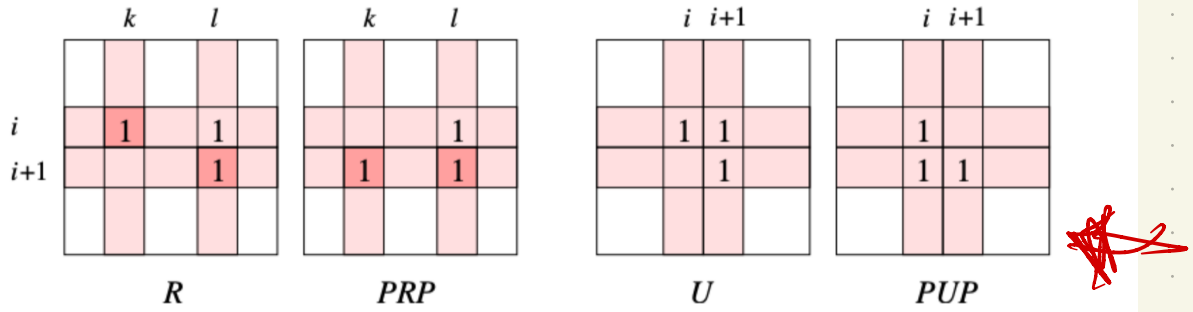


Figure 2: The transposition renders this particular R non-reduced and this particular U non-upper-triangular.

Worst case update cost:

$O(n)$ (at most the number of 1's in affected rows & columns)

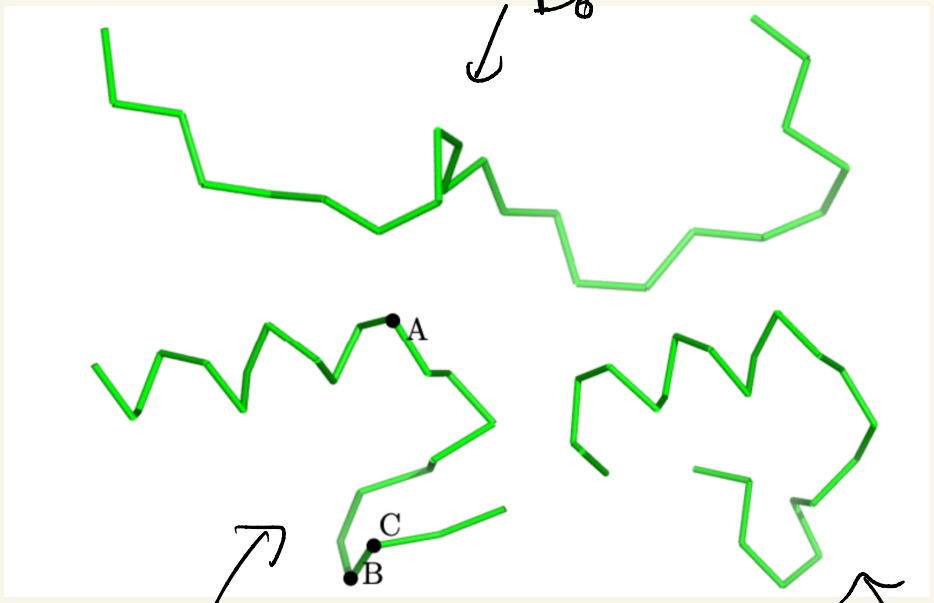
Initial application

Proteins : curve $b : [0,1] \to \mathbb{R}^3$

BBA5 : $N = 23$ amino acids

$m+1 = 201$ frames, where $\forall\, 0 \leq i \leq m$,

i^{th} snapshot is a curve b_i



They define a pairwise distance

$[0,1]^2 \to \mathbb{R}$ with

$(r,s) \longmapsto \|b(r) - b(s)\|$

on each b_i

↳ build filtration for b_i

Then, build vineyards:

Somewhat hard to parse, but gives evidence of stages

2nd stage
α-helix forms
& backbone is
an S-shape
[59 knees here]

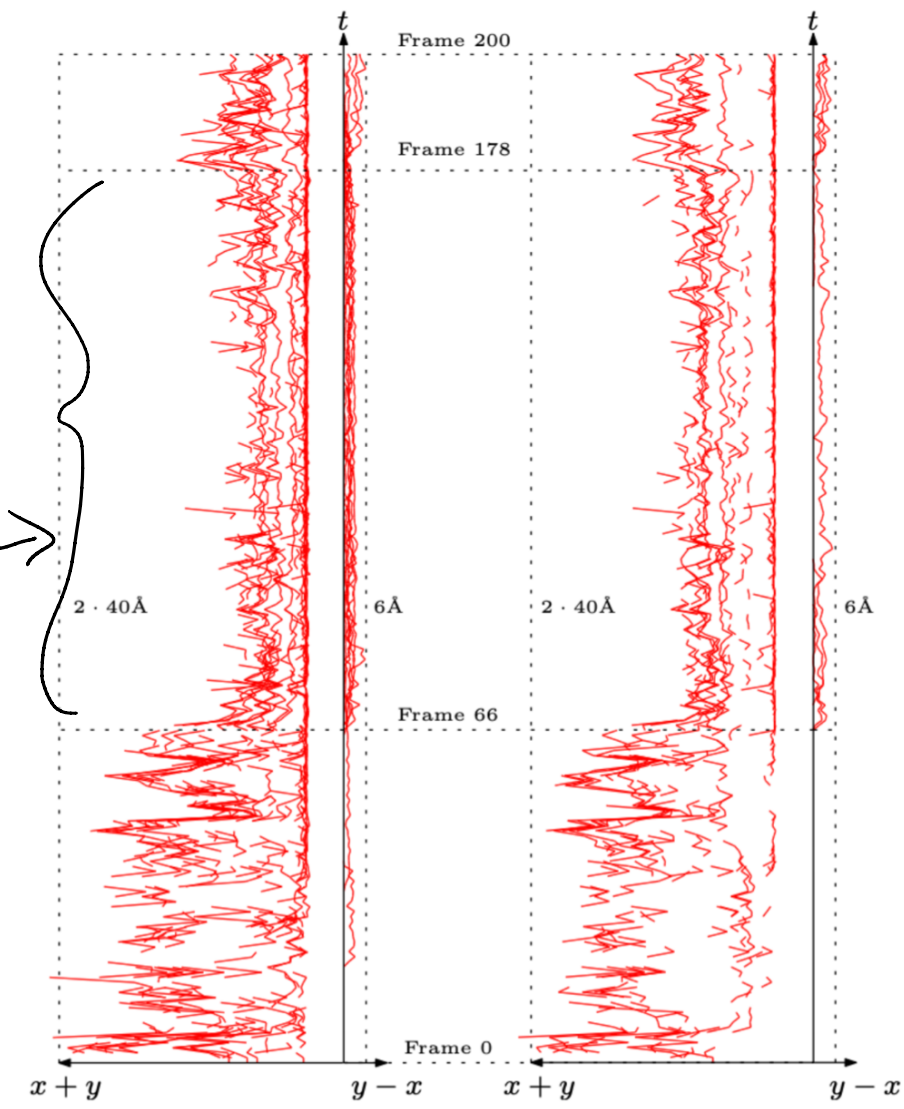


Figure 8: The front view $(x+y, t)$ and the side view $(y-x, t)$ of the dimension 0 vineyard on the left and the dimension 1 vineyard on the right. The side views are simplified by removing vines with lifetime less than 20 frames.

Another application

Brain connectivity

Yoo, Kim, Ahn, Ye 2016

Dynamic functional connectivity in resting and gaming stages

EEG data of 54 students

Using Dionysus tool

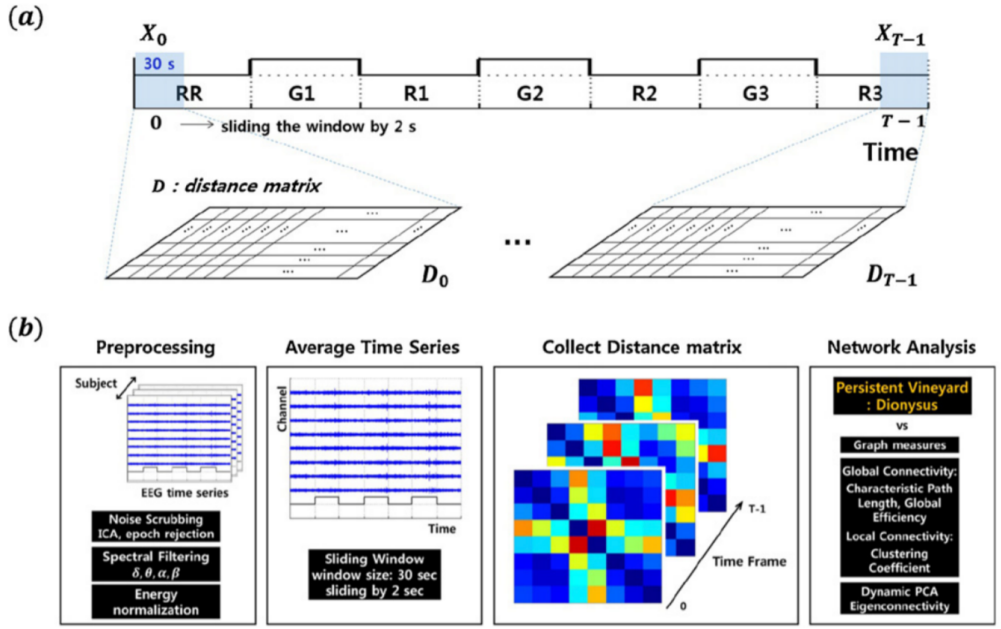
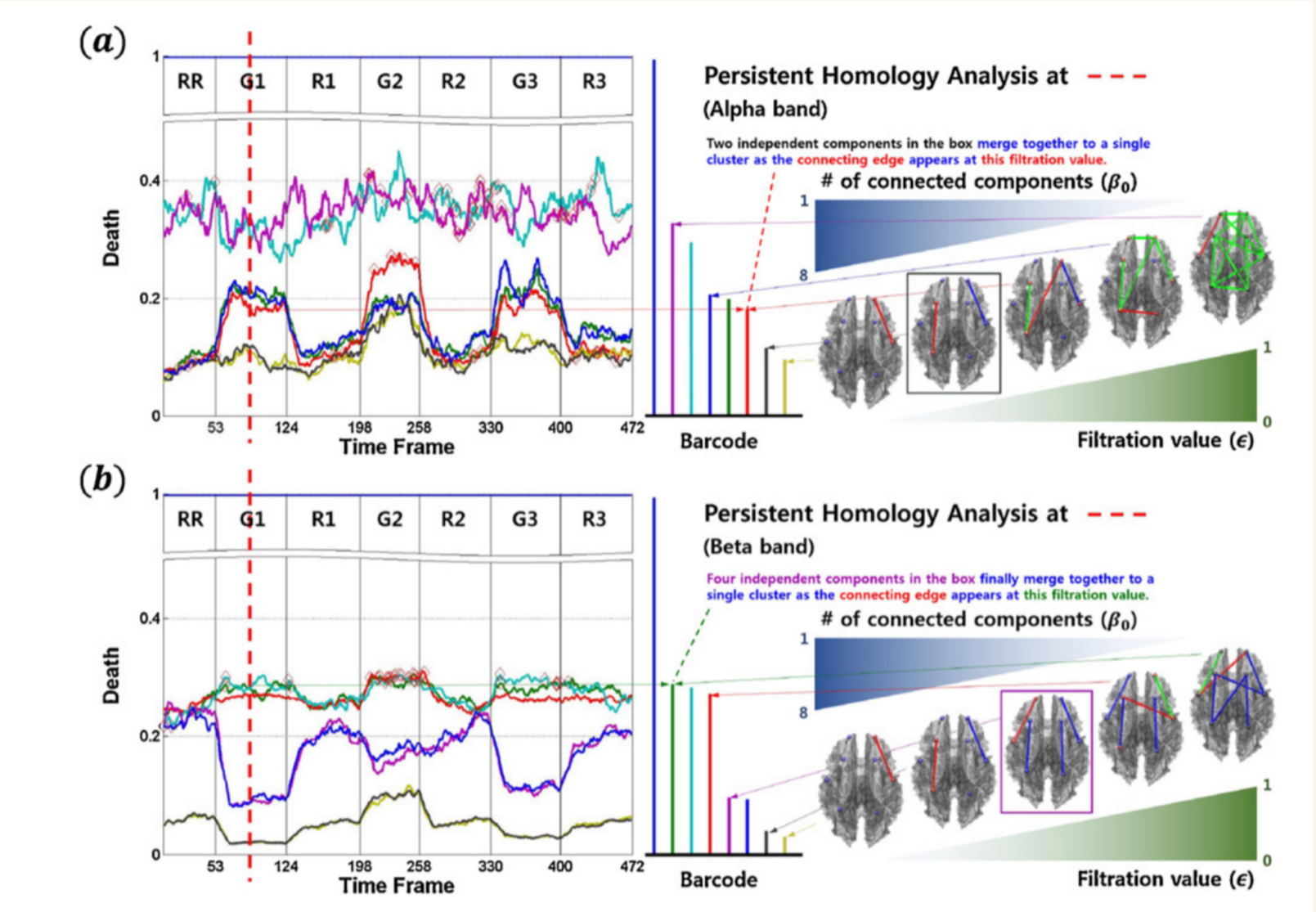


Fig. 3. The schematic illustration of the experiment and dynamic FC estimation using a sliding window analysis. (a) A block paradigm experiment is designed with the resting and gaming stages. The illustrative example of the sliding window analysis is shown with 30 s window length and 2 s step size. For the dynamic FC estimation, we calculated a distance matrix D_l for each $l \in \{0, \ldots, T-1\}$ window, where $T = 472$ in this case. (b) The entire flow chart of the experiment from the data preprocessing to the brain network analysis are shown.

Result: Worked better than PCA + eigenconnectivity



Crocker plots: combining scale & time

Consider k^{th} Betti number $\beta_k(\epsilon, t)$

as a function of both time & ϵ in filtration

bifiltration

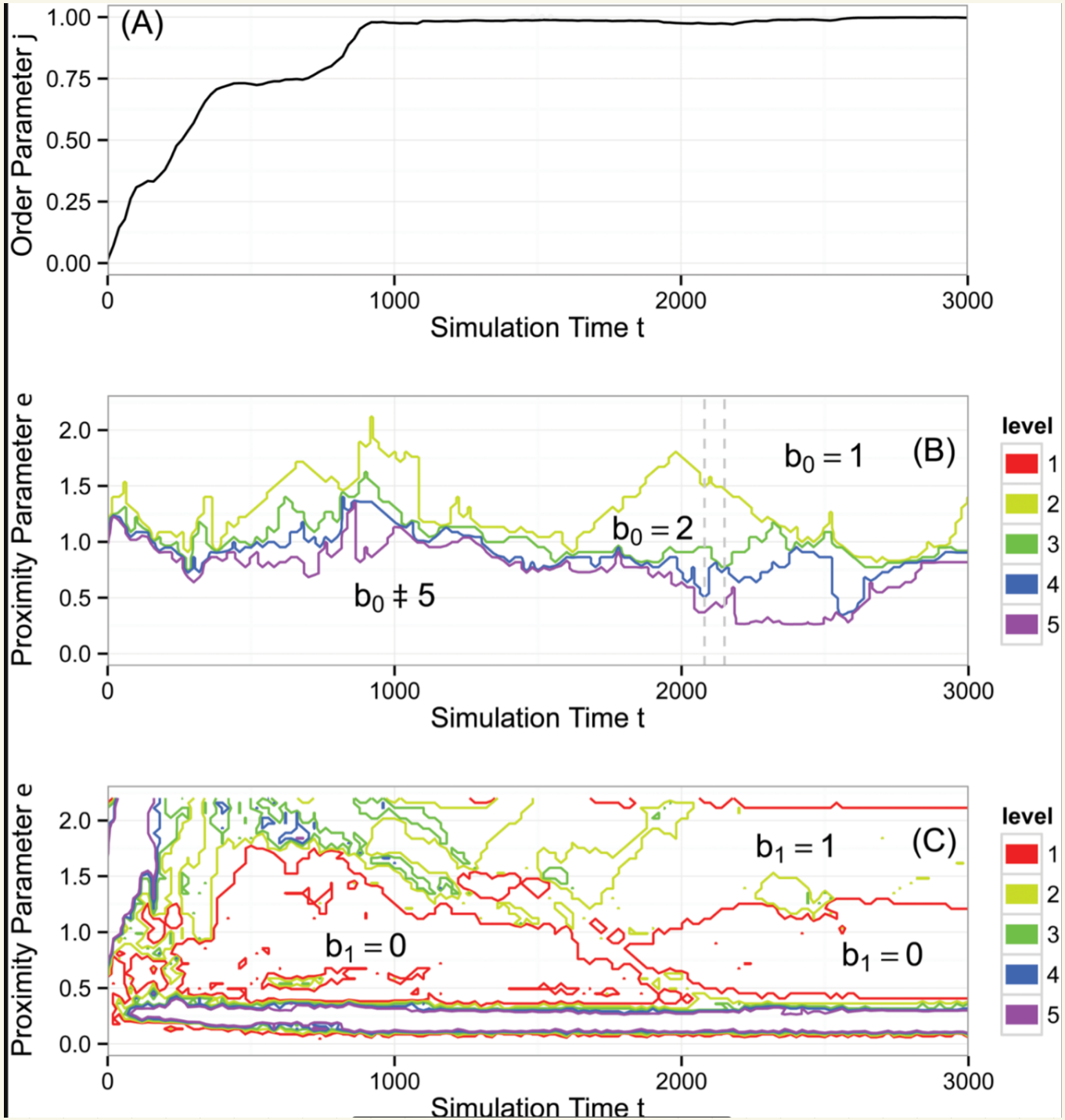
↳ build contour diagram

"Contour Realization of Computed k-dim hole Evolution in Rips complex"

Topaz, Ziegelmeier, Halverson 2015

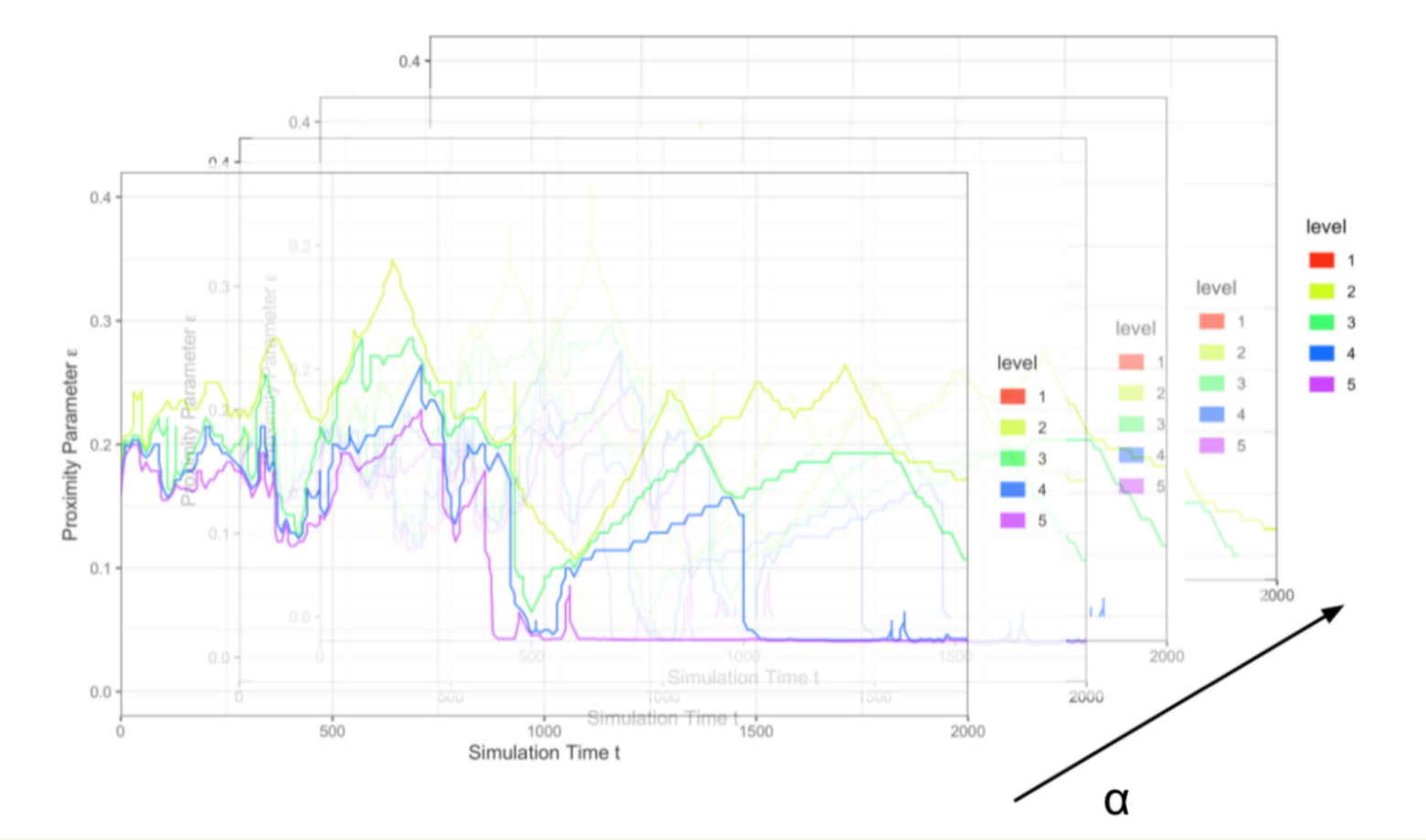
↳

Breaking this down..



Cracker stacks

Xian, Adams, Topaz, & Ziegelmeier 2020



α : Smoothing parameter

↳ can vectorize for ML models