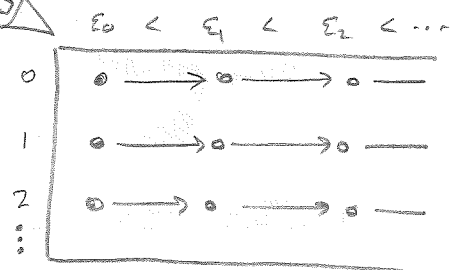
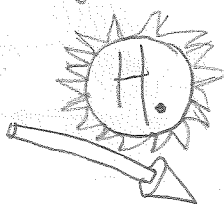
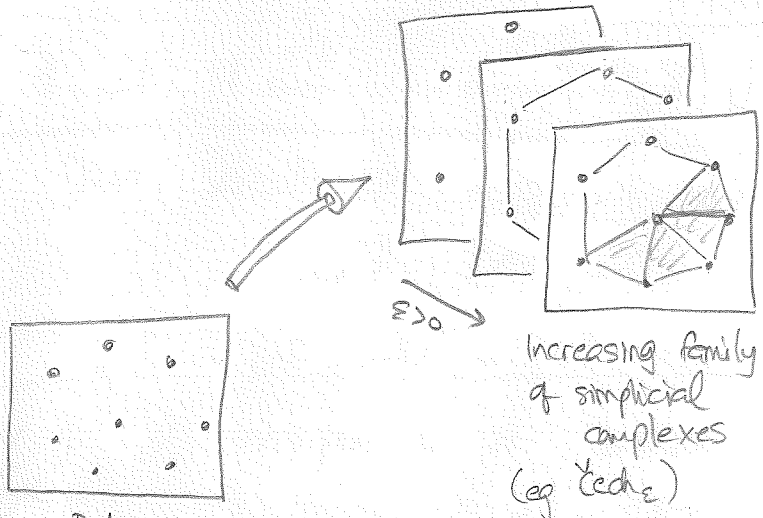


# CAT 6 Persistence

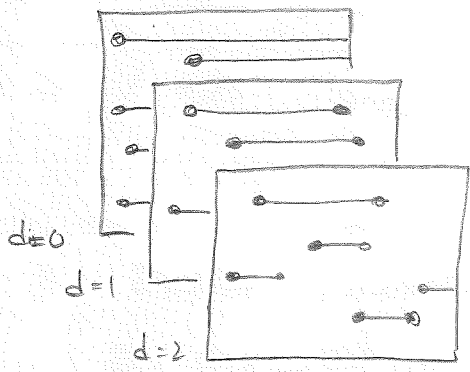
The BIG picture. homological data analysis. (persistent homology)



In each dimension  $d$ , an  $\epsilon$ -indexed sequence of vector spaces.

Data  
(Points in  $\mathbb{R}^n$ ,  
or a finite  
metric space)

Increasing family  
of simplicial  
complexes  
(eg  $\check{C}ech_\epsilon$ )



"Barcodes",  
one for  
each  $d \geq 0$ .

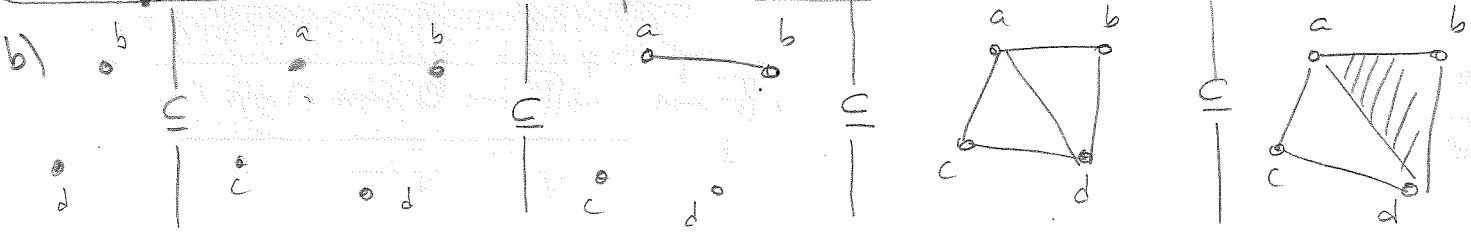
Today's  
focus

Def 1  
a) A FILTRATION of a simplicial complex  $K$  is a sequence of subcomplexes of the form

$$K_0 \subseteq K_1 \subseteq \dots \subseteq K_n.$$

[We have already seen at least one example: for a finite set  $P \subseteq \mathbb{R}^n$ , consider  $\check{C}ech_\epsilon(P)$ , the Čech complex whose homology coincides (by the Nerve Theorem) with that of  $\bigcup_{p \in P} \text{Ball}(p; \epsilon)$ , i.e., union of  $\epsilon$ -balls around  $p \in P$ .]

Here's another example:



Note 2

Applying  $d$ -dimensional homology with coefficients in a field  $F$ , i.e.,  $H_d(\cdot; F)$ , to a filtration gives a sequence of vector spaces & linear maps:

$$\boxed{H_d(K_0; F) \xrightarrow{H_d f_0} H_d(K_1; F) \xrightarrow{H_d f_1} \dots \xrightarrow{H_d f_{n-1}} H_d(K_n; F)}$$

where  $f_0$  is the inclusion simplicial map sending  $K_0$  to the next  $K_{0+1}$ .

(Note that this need NOT be a chain complex!)

Def 3

a)

A PERSISTENCE MODULE is a sequence  $V_0$  of vector spaces and linear maps, i.e.,

$$\boxed{V_0 \xrightarrow{\varphi_0} V_1 \xrightarrow{\varphi_1} V_2 \xrightarrow{\varphi_2} \dots \xrightarrow{\varphi_{n-1}} V_n}$$

In our hearts, these are the homology of some filtration.

[We usually assume  $\dim V_i < \infty$  for all  $i$ ]

b)

The PERSISTENT HOMOLOGY GROUPS of  $V_0$  are

$$H_i^j(V_0) = \text{im} [\varphi_{j-1} \circ \dots \circ \varphi_{i+1} \circ \varphi_i], \quad [i \leq j]$$

note that this composite goes from  $V_i$  to  $V_j$ .

For convenience, let's write it as  $\varphi_i^j: V_i \rightarrow V_j$

c)

An element  $\alpha \in V_i$

- is BORN at  $i$  if  $\alpha \notin \text{im } \varphi_{i-1}$ .

- DIES at  $j > i$  if  $\varphi_i^j(\alpha) = 0$  but  $\varphi_i^{j-1}(\alpha) \neq 0$

say "dies at  $\infty$ " if  $\exists$  no such  $j$ .

Q4

How to organize all this information?

Def 5

Given  $i < j$ , the INTERVAL MODULE  $\mathbb{I}_0^{[i,j]}$  is:

$$\begin{array}{ccccccc} \rightarrow & 0 & \rightarrow & \dots & 0 & \rightarrow & \mathbb{F} & \xrightarrow{1} & \mathbb{F} & \xrightarrow{1} & \dots & \xrightarrow{1} & \mathbb{F} & \rightarrow & 0 & \rightarrow & 0 & \rightarrow & \dots \\ & & & & & & \parallel & & \parallel & & & & \parallel & & \parallel & & & & & \\ & & & & & & V_i & & V_{i+1} & & & & V_{j-1} & & V_j & & & & & \end{array}$$

Nicest possible persistence modules.

Thm 6  
STRUCTURE  
THEOREM!

To each persistence module  $V_\bullet$  of vector spaces over  $F$ , one can associate a multi-set of intervals

$$\text{Bar}(V_\bullet) = \{ [i, j) \mid 0 \leq i < j \leq \infty \} \leftarrow \text{"Barcode" of } V_\bullet$$

so that  $V_\bullet$  is isomorphic to a direct sum of interval modules,

$$V_\bullet \cong \bigoplus_{[i,j) \in \text{Bar}(V_\bullet)} \mathbb{I}_\bullet^{[i,j)}$$

Every persistence module is an "honest module" in the sense of abstract algebra over the polynomial ring  $F[t]$ , where  $t$  acts on  $x \in V_i$  by pushing it to  $\varphi_i(x) \in V_{i+1}$ . These "finitely generated modules" over  $F[t]$ , a principal ideal domain, decompose as follows.  $\exists \{ \alpha_i, i \in \mathbb{Z} \}$  and  $\{ \beta_j < \delta_j, j \in J \}$  so that

$$V_\bullet \cong \bigoplus_{\alpha_i} t^{\alpha_i} \cdot F[t] \oplus \bigoplus_{\beta_j < \delta_j} t^{\beta_j} \cdot F[t] / (t^{\delta_j})$$

"free part"

"torsion part",  
quotient by ideal.

and in this case

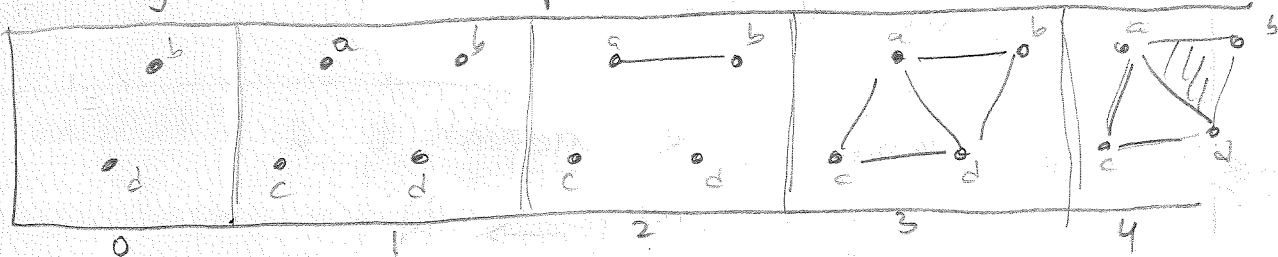
$$\text{Bar}(V_\bullet) = \bigsqcup_i \{ [\alpha_i, \infty) \} \sqcup \bigsqcup_j \{ [\beta_j, \delta_j) \}$$

infinite bars                      finite bars

Ex 7

ELDER  
Rule

Returning to our example: (see Def 1b)



$0_d$  barcode:  $[0, \infty)$ ,  $[0, 3)$ ,  $[1, 2)$ ,  $[1, 3)$

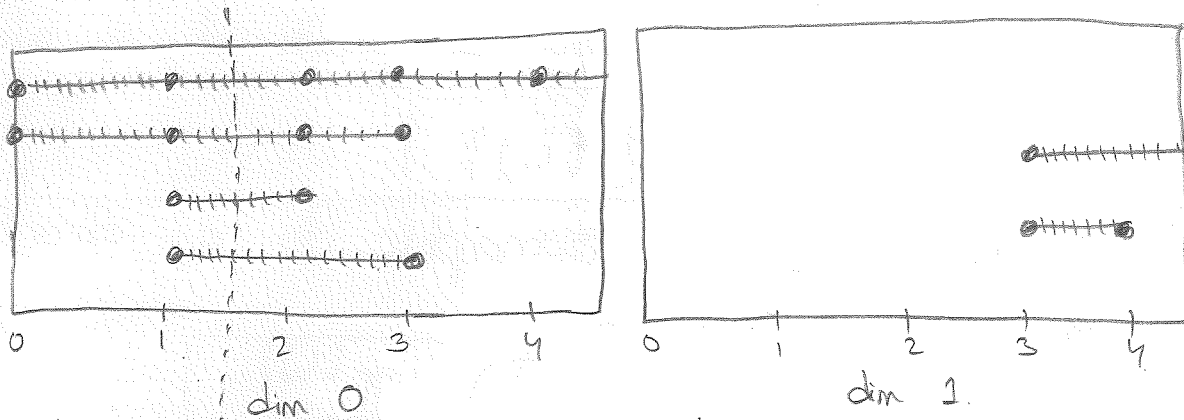
$1_d$  barcode:  $[3, \infty)$ ,  $[3, 4)$

all other barcodes:  $\emptyset$

Eg. every abelian group  $A$  is  $A \cong \mathbb{Z}^n \oplus T$  where  $T = \bigoplus_{\alpha_i} \mathbb{Z}/\alpha_i \mathbb{Z}$  with  $\alpha_i | \alpha_{i+1}$

Fig 8

Let's draw these:



# intersections gives  
Betti number!  $\beta_0 = 4$   
between "1" and "2"

# ALGORITHM

Note 9  
a)

For a one-step filtration  $K_0 = K$ , computing persistent homology is the same as computing ordinary homology  $H_d(K; \mathbb{F})$ : all barcode-intervals are of the form  $[0, \infty)$ , and their number is just  $\dim H_d(K; \mathbb{F})$ . So, we will need the usual row- and -column operations on boundary matrices.

b) BUT for a general filtration

$$K_0 \subseteq K_1 \subseteq \dots \subseteq K_{n-1} \subseteq K_n = K,$$

there is a nice & simple ordering of the simplices which allows us to compute the barcode all at once using ONLY COLUMN OPERATIONS.

Note 10 Every filtration of  $K$  corresponds to a "FILTERING FUNCTION"

$$\underline{c}: \left\{ \begin{array}{l} \text{simplices} \\ \text{of } K \end{array} \right\} \rightarrow \mathbb{N}$$

where  $\underline{c}(\alpha) \leq \underline{c}(\tau)$  whenever  $\alpha$  is a face of  $\tau$ , as follows.

$$K_i = \{ \alpha \in K \mid \underline{c}(\alpha) \leq i \}, \text{ or (to go back)} \\ \underline{c}(\alpha) = \min \{ i \in \mathbb{N} \mid \alpha \in K_i \}$$

# Algo 11

Assume that simplices of  $K$  have been totally ordered into  $(\alpha_1, \alpha_2, \dots, \alpha_N)$  so that

- a) • if  $\underline{c}(\alpha) \leq \underline{c}(\tau)$  then  $\alpha$  precedes  $\tau$ , and
  - if  $\underline{c}(\alpha) = \underline{c}(\tau)$  and  $\dim \alpha < \dim \tau$ , then  $\alpha$  precedes  $\tau$ .
- i.e., order first by  $\underline{c}$ -value, then by dimension. [You can break ties arbitrarily.]

b) The input is the ENTIRE boundary matrix, which will be block-upper triangular.

$$\Delta = \begin{matrix} & \alpha_1 & \alpha_2 & \dots & \alpha_i & \dots & \alpha_N \\ \begin{matrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_j \\ \vdots \\ \alpha_N \end{matrix} & \left[ \begin{array}{ccccccc} & & & & & & \\ & & & & & & \\ & & & & & & \\ & & & & & & \\ & & & & m_{ij} & & \\ & & & & & & \\ & & & & & & \end{array} \right] \end{matrix}$$

Here,  

$$m_{ij} = \begin{cases} \pm 1 & \text{if } \alpha_j \leq \alpha_i \text{ with } \dim \alpha_i - \dim \alpha_j = 1 \\ 0 & \text{else} \end{cases}$$
 The sign depends on orientation as usual.

c) For each  $i \in \{1, \dots, N\}$ , let  $\text{low}(i)$  be the largest row-index  $j$  so that  $m_{ij} \neq 0$  [i.e., index of the last-born codimension-one face of  $\alpha_i$ ]

## PSEUDO-CODE 1

Set  $P =$  empty list of simplex-pairs

1. For  $i = 1$  to  $N$
2.     Set  $k = \text{low}(i)$      [= 0 if  $\text{col}(i)$  is zero].
3.     While  $\exists j < i$  with  $\text{low}(j) = k \neq 0$ ,
4.         add  $[-m_{ik}/m_{jk}] \cdot \text{col}(j)$  to  $\text{col}(i)$
5.     end while
6. end for

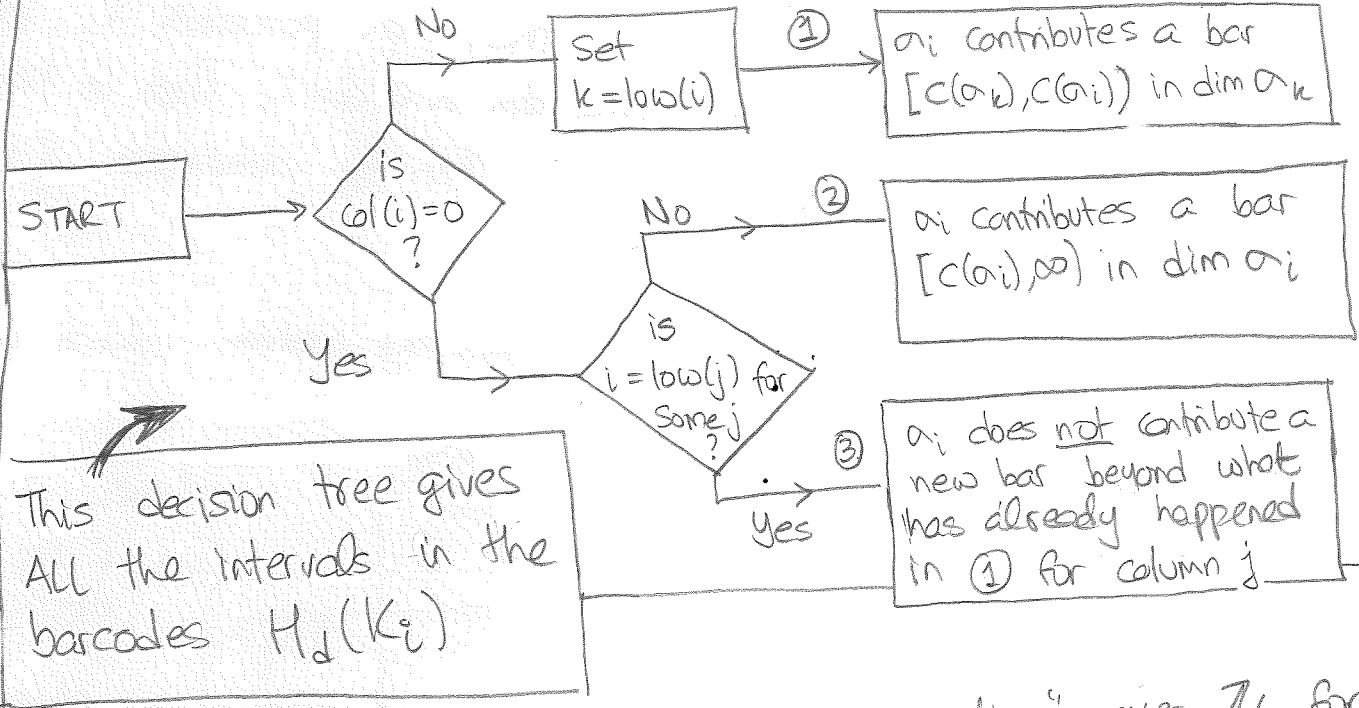
This uses the previous lows to clear out the current low.

Namely, IF two columns have their lowest nonzero entry in the same row, THEN add a multiple of the left one to zero out the lowest entry of the right one.

$$k \begin{bmatrix} & d_i & d_j \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \end{bmatrix} \Rightarrow \text{col}_i \leftarrow \text{col}_i + \alpha \text{col}_j$$

Prop 12  
The trinity

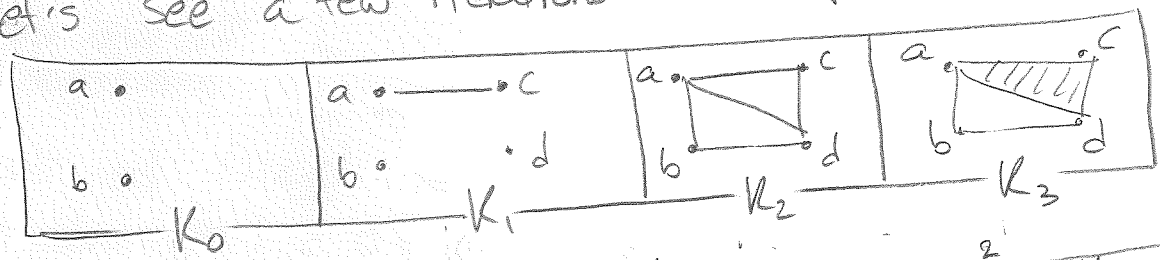
When the above algorithm terminates, there are three possibilities in each column  $i$ , labelled ①, ②, ③:



This decision tree gives ALL the intervals in the barcodes  $H_d(K_i)$

Note 13

Let's see a few iterations "in practice" over  $\mathbb{Z}/2$  for



$$\Delta = \begin{matrix} & \overset{0}{a} & & \overset{1}{c} & & \overset{2}{ab} & & \overset{3}{acd} \\ \begin{matrix} a \\ b \\ c \\ d \\ ac \\ ab \\ ad \\ bd \\ cd \\ acd \end{matrix} & | & & | & & | & & | & & | \end{matrix}$$

[All unwritten entries are zero. In general this matrix is VERY sparse!]

The first nontrivial step is  $col(bd) \leftarrow col(bd) + col(ad)$ , which gives  $col(bd) = [1, 1, 0, \dots]^T$ . The next step is  $col(bd) \leftarrow col(bd) + col(ab)$ , which clears it out completely!

Can you keep going?

So far, the "main theorem" of persistent homology appears to be the STRUCTURE THEOREM (Thm 6). But there is a NEWER, DEEPER result which justifies the use of homology in data analysis

# STABILITY

Def 15 a) Let  $B$  and  $B'$  be two barcodes. An  $\epsilon$ -MATCHING between them is a bijection  $\mu: B_0 \xrightarrow{\cong} B'_0$  where  $B_0 \subseteq B$  and  $B'_0 \subseteq B'$  satisfying:

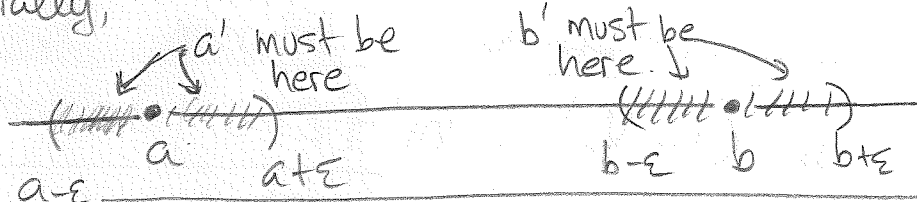
(A) All intervals in  $(B - B_0)$  and  $(B' - B'_0)$  have length  $\leq 2\epsilon$ .

(B) IF  $\mu([a, b]) = [a', b']$  for some  $[a, b] \in B_0$ , then:

$$|a - a'| < \epsilon > |b - b'|$$

Note: for infinite bars  $[a, \infty)$ ,  $[a', \infty)$  we don't have any constraint on the "b". Just k-alter.

Pictorially,



b) The BOTTLENECK DISTANCE between barcodes  $B$  and  $B'$  is given by

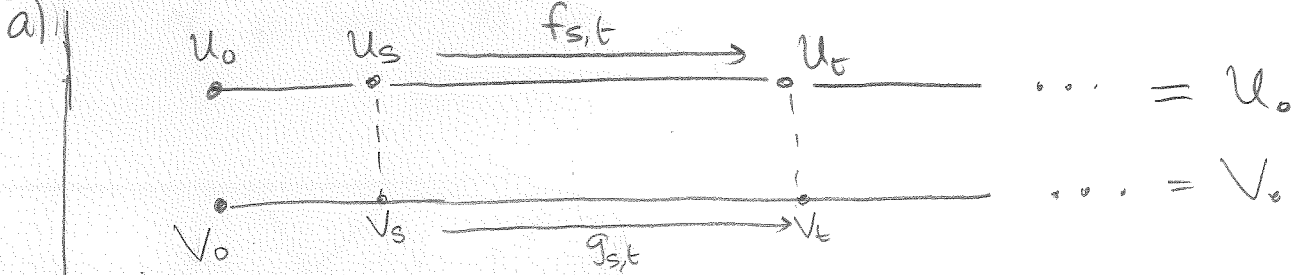
$$d_{\text{Bot}}(B, B') = \inf \{ \epsilon > 0 \mid \exists \epsilon\text{-matching } B \xrightarrow{\mu} B' \}$$

Prop 16  $d_{\text{Bot}}$  is a METRIC on the set of all barcodes with finitely many bars, except for the fact that we allow  $d_{\text{Bot}}(B, B') = \infty$ . [For instance, if the number of infinite-length intervals in  $B$  is different from the number of such intervals in  $B'$ , then there is no possible finite  $\epsilon > 0$  for which there exists an  $\epsilon$ -matching!] ]



Now we can compare barcodes, what about persistence modules?

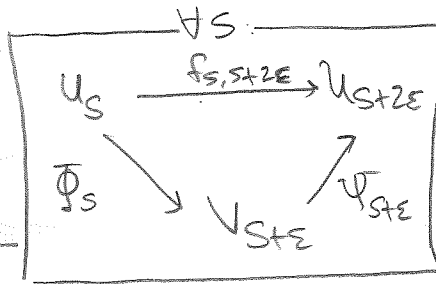
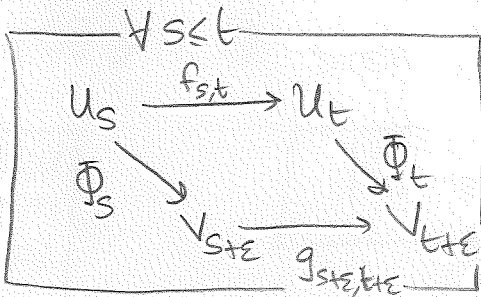
Def 18 Let  $U_\bullet$  and  $V_\bullet$  be two  $\mathbb{R}^+$ -indexed persistence modules.



So: each  $U_t$  is a vector space for  $t \geq 0$ , there is a map  $f_{s,t}: U_s \rightarrow U_t$  for  $s \leq t$  so that  $f_{s,s} = \text{id} \forall s$  and  $f_{s,u} = f_{t,u} \circ f_{s,t} \forall s \leq t \leq u$

An  $\varepsilon$ -INTERLEAVING (for  $\varepsilon > 0$ ) between  $U_\bullet$  and  $V_\bullet$

is a family of maps  $\{\Phi_t: U_t \rightarrow V_{t+\varepsilon} \forall t \in \mathbb{R}^+\}$  and  $\{\Psi_t: V_t \rightarrow U_{t+\varepsilon} \forall t \in \mathbb{R}^+\}$  so that all possible triangles and parallelograms commute, eg.



[+ two more!]

b) The INTERLEAVING DISTANCE between  $U_\bullet$  and  $V_\bullet$  is

$$d_{\text{INT}}(U_\bullet, V_\bullet) = \inf \{ \varepsilon > 0 \mid \exists \varepsilon\text{-interleaving} \dots \}$$

If  $U_\bullet$  and  $V_\bullet$  are tame  $\mathbb{R}^+$ -indexed persistence modules then there is an isometry

$$d_{\text{INT}}(U_\bullet, V_\bullet) = d_{\text{BOT}}(\text{Bar}(U_\bullet), \text{Bar}(V_\bullet))$$

Thm 19 STABILITY THEOREM! (IMPORTANT)

The most elementary proof is Lesnick + Bauer "induced matching"

Prop 20 So what? Well, if point-sets  $P, Q \subseteq \mathbb{R}^n$  have Hausdorff dist  $\varepsilon > 0$ , then  $H_d(\check{C}_\bullet(P))$  and  $H_d(\check{C}_\bullet(Q))$  are  $\varepsilon$ -interleaved [+ same for  $VR_\bullet(P)$  &  $VR_\bullet(Q)$ ] for each dimension  $d \geq 0$ . So,

$$d_{\text{Haus}}(P, Q) \geq d_{\text{INT}}(H_d \check{C}_\bullet(P), H_d \check{C}_\bullet(Q)) = d_{\text{BOT}}(\text{Bar}_d(P), \text{Bar}_d(Q))$$

So, noise in data is no more than noise in Barcode!  
[Here  $\text{Bar}_d(P)$  is shorthand for  $\text{Bar}(H_d \check{C}_\bullet(P))$ , etc]