Persistent Homology: Formalization

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Outline for studying persistent homology

- 1. Intro to persistent homology
 - Build intuitions of persistent homology: what it does, what it produces
- 2. Formalizing persistent homology
 - Introduce its input (filtration) and study an algorithm for computation
- 3. Different ways for building filtrations
 - Vietoris-Rips filtration, sub-levelset filtration
 - Cubical complexes (for images)
- 4. Interpretation and stability of persistence diagram



- Recall the growing space:
 - We have a value α ranging within an interval, say, from 0 to ∞
 - Let each value α corresponds to a topological space so that
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 - We have a value α ranging within an interval, say, from 0 to ∞
 - Let each value α corresponds to a topological space so that
 - The topological space grows as α increases from 0 to ∞
- Suppose I ask you to represent such a growing space in the computer, can you think of any problems?



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 - Each α value may correspond to a possibly different space
 - This means there could be infinitely many spaces that we need to store in the computer, which is impossible



- Solution:
 - While there are infinitely many values for α , our data is still "finite" (e.g., the above point cloud contains finitely many points)



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"The growing space" $\alpha: \xrightarrow[\alpha_1]{\alpha_1} \xrightarrow[\alpha_2]{\alpha_2} \xrightarrow[\alpha_3]{\alpha_3} \xrightarrow[\alpha_4]{\alpha_4}$

- Solution:
 - While there are infinitely many values for α , our data is still "finite" (e.g., the above point cloud contains finitely many points)
 - This means that there are only finitely many values of α where the topological space "essentially changes"
 - So we only need to record finitely many spaces in computer



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 - We will not be very accurate on what the "essential changes" mean here (should be clearer later)

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- Remark
 - We will not be very accurate on what the "essential changes" mean here (should be clearer later)
 - BTW, these values where topological space "essentially changes" are called critical values
 - Critical values are important concepts in "Morse theory", but we will not go very deep on it in this course

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- Problem 2:
 - Even there are finitely many spaces to record, we still need a way to represent each topological space in computer
- Solution:
 - Using simplicial complexes!



• Hence, the "growing space" in computer is represented by a finite sequence of simplicial complexes, called a filtration, which is typically denoted by a calligraphic letter \mathcal{F} ,

 $\mathcal{F}: K_0, K_1, \dots, K_m$



• **Below** is an example of a filtration:



• Another example:



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- How do we account for the fact that the spaces (complexes) grow?
- Answer: We make sure the complexes "grow" by making sure the previous complex is a "subset" (subcomplex) of the next complex.
- **Definition**: A **filtration** is a nested sequence of simplicial complexes

$$\mathcal{F}\colon K_0\subseteq K_1\subseteq\cdots\subseteq K_m$$

such that each K_i is a subcomplex of K_{i+1} .

• Example:



• Another example:



Image source: Patrick Schnider. Introduction to Topological Data Analysis Lecture Notes FS 2023



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- For this, we focus on a single inclusion in a filtration
- Since it's an inclusion, the difference of the two complexes is that K_{i+1} has some additional simplices than K_i
- So we can consider each inclusion $K_i \subseteq K_{i+1}$ in a filtration

$$\mathcal{F}\colon K_0\subseteq K_1\subseteq\cdots\subseteq K_m$$

as an insertion of a bunch of simplices

For the example:



- K_0 to K_1 : insert vertices t and u and edge tu
- K_1 to K_2 : insert edge st
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• More **regulations:** For a filtration

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• **Observation**: (1). Any simplex of K is added exactly once in \mathcal{F}

(2). For any two simplices σ and τ in K such that σ is a face of τ , we have σ cannot be added later than τ .

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cannot be added later than τ .

• (1) is easy to see. To see (2), suppose that σ is added later than τ . Then at a certain time, τ is already added to a complex K_i but σ is not in K_i yet. This contradicts the fact that any face of a simplex in the complex is also in the complex.

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- Filtrations are inputs to the persistent homology pipeline that we want to formalize
- But still we need to formally define a PD on a filtration of simplicial complexes
- Previously, we only saw some examples of PD on a sequence of "growing spaces", which are not exactly a filtration of complexes.
- Moreover, we haven't really formally defined a PD on a growing space other than showing some examples

• Eventually, we will show that, PDs can be formally defined on both a "growing space" (which is continuous) and a "filtration of complexes" (which is discrete).



- Eventually, we will show that, PDs can be formally defined on both a "growing space" (which is continuous) and a "filtration of complexes" (which is discrete).
- We sometimes call the former one a "continuous" filtration and latter a "discrete" filtration (by default, a "filtration" without modifiers is always a discrete one).



- However, formally defining PD on a continuous or a discrete filtration needs a lot of mathematics (a lot of algebra, category theory, or quiver theory), which is beyond the scope of the course.
- So to understand the definition of a PD, we shall see how to compute a PD on a discrete filtration.
- Things can get a bit technical from now on, but I want to stress that this course is trying to focus on applications. So these technical contents are mainly supposed to help build solids skills on applying persistent homology.

- For computing persistence diagram, we focus on a special type of filtration.
- **Definition**: A **simplex-wise filtration** is a filtration such that each consecutive complexes differ by only a single simplex, i.e., in

$$\mathcal{F}\colon \emptyset = K_0 \subseteq K_1 \subseteq \cdots \subseteq K_m = K$$

for each inclusion $K_{i-1} \subseteq K_i$, we have that K_i is derived from K_{i-1} by inserting a single simplex typically denoted σ_i .

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• Because of the constructions, we can also consider a simplex-wise filtration

$$\mathcal{F}: \varnothing = K_0 \stackrel{\sigma_1}{\longrightarrow} K_1 \stackrel{\sigma_2}{\longrightarrow} \cdots \stackrel{\sigma_{m-1}}{\longrightarrow} K_{m-1} \stackrel{\sigma_m}{\longrightarrow} K_m = K$$

as a sequence of simplices $\sigma_0, \sigma_1, \dots, \sigma_{m-1}$ inserted one by one following the order.

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$$\mathcal{F}: \emptyset = K_0 \stackrel{\sigma_1}{\longrightarrow} K_1 \stackrel{\sigma_2}{\longrightarrow} \cdots \stackrel{\sigma_{m-1}}{\longrightarrow} K_{m-1} \stackrel{\sigma_m}{\longleftrightarrow} K_m = K$$

as a sequence of simplices $\sigma_0, \sigma_1, \dots, \sigma_{m-1}$ inserted one by one following the order.

 Fact: Each general filtration (not necessarily simplex-wise) can be made into a simplex-wise one by padding additional complexes (or expanding the inclusions)

- K_0 to K_1 : insert vertices t and u and edge tu
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Image source: Patrick Schnider. Introduction to Topological Data Analysis Lecture Notes FS 2023

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• To convert to simplex-wise, only need to add an empty complex at the beginning and insert two additional complexes between K_0 to K_1 .



Algorithm

• Notice that the input filtration \mathcal{F} must be simplex-wise

nput: a filtration \mathcal{F} as a sequence of simplices $\sigma_1, \sigma_2, \ldots, \sigma_m$ Dutput: <i>p</i> -th PD of \mathcal{F} , PD _{<i>p</i>} (\mathcal{F}), for each dimension <i>p</i>		
1:	set each σ_i in \mathcal{F} as "unpaired"	
2:	ζ = a table mapping each σ_i to a cycle $\zeta(\sigma_i)$ initially undefined	
3:	for $\sigma_i = \sigma_1, \sigma_2, \ldots, \sigma_m$ do	
4:	$z = \partial(\sigma_i)$	
5:	while $z \neq 0$ do	
6:	let σ_j be the simplex with maximum index in z	
7:	if σ_i is unpaired then break	
8:	$z = z + \zeta(\sigma_j)$	
9:	if $z \neq 0$ then	
0:	pair σ_j with σ_i and set σ_j, σ_i as "paired"	
11:	$\zeta(\sigma_j)=z$	
2:	$p = $ dimension of σ_j	
3:	add (j,i) to $PD_p(\mathcal{F})$	
4:	for each each unpaired σ_i do	
5:	$p = \operatorname{dimension} \operatorname{of} \sigma_i$	
6:	add (i,∞) to $PD_p(\mathcal{F})$	



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- Black: *PD*₀
- Red: *PD*₁
- Blue: *PD*₂



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- Notice: instead of drawing each pair of birth / death as a point on 2D plane, we just let each pair of birth and death form an interval, indicating the "time" in which a certain homology hole persists (will see examples later)
- The above is also called the **persistence barcode**
- So persistence barcodes and persistence diagrams are just the same things displayed in different ways (we sometimes also use the two terms interchangeably)



- 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
- Notice: instead of drawing each pair of birth / death as a point on 2D plane, we just let each pair of birth and death form an interval, indicating the "time" in which a certain homology hole persists (will see examples later)
- The above is also called the **persistence barcode**
- So persistence barcodes and persistence diagrams are just the same things displayed in different ways (we sometimes also use the two terms interchangeably)
- Also notice: In persistence barcode, we always draw each interval as left-closed, right open (there is a technical reason for this but explaining this a little beyond scope)



• We also notice that the cycle recorded in the " ζ table" indeed captures the homology hole born and died with a birth-death interval in the barcode (point in the PD)



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- i.e., for an interval [b, d), $\zeta[\sigma_b]$ represents the homology feature born at the index b and dying at index d.



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- i.e., for an interval [b, d), $\zeta[\sigma_b]$ represents the homology feature born at the index b and dying at index d.
- This $\zeta[\sigma_b]$ is also called the **representative** for the interval [b, d).



1d hole captured by interval $[12,15) \in PD_1$



1d hole captured by interval $[8,16) \in PD_1$



- Od hole captured by interval $[3,10) \in PD_0$, which is the gap between s and u.
- The gap disappears when the two points become connected

More interpretations of the algorithm:

• When processing each σ_i , if the while loop ends with z = 0, then the simplex σ_i is called **positive** Input: a filtration \mathcal{F} as a sequence of simplices $\sigma_1, \sigma_2, \ldots, \sigma_m$ Output: p-th PD of \mathcal{F} , PD_p(\mathcal{F}), for each dimension p 1: set each σ_i in \mathcal{F} as "unpaired" 2: $\zeta = a$ table mapping each σ_i to a cycle $\zeta(\sigma_i)$ initially undefined 3: for $\sigma_i = \sigma_1, \sigma_2, \ldots, \sigma_m$ do 4: $z = \partial(\sigma_i)$ while $z \neq 0$ do 5: let σ_i be the simplex with maximum index in z 6: 7: if σ_i is unpaired then break $z = z + \zeta(\sigma_i)$ 8: if $z \neq 0$ then 9: pair σ_i with σ_i and set σ_i, σ_i as "paired" 10: $\zeta(\sigma_i) = z$ 11: 12: $p = \text{dimension of } \sigma_i$ add (j, i) to $\mathsf{PD}_p(\mathcal{F})$ 13: 14: for each each unpaired σ_i do p =dimension of σ_i 15: add (i,∞) to $\mathsf{PD}_p(\mathcal{F})$ 16:

More interpretations of the algorithm:

- When processing each σ_i , if the while loop ends with z = 0, then the simplex σ_i is called **positive**
- It means that inserting σ_i creates a new homology hole

Input: a filtration \mathcal{F} as a sequence of simplices $\sigma_1, \sigma_2, \ldots, \sigma_m$ Output: *p*-th PD of \mathcal{F} , PD_{*p*}(\mathcal{F}), for each dimension *p* 1: set each σ_i in \mathcal{F} as "unpaired" 2: $\zeta = a$ table mapping each σ_i to a cycle $\zeta(\sigma_i)$ initially undefined 3: for $\sigma_i = \sigma_1, \sigma_2, \ldots, \sigma_m$ do 4: $z = \partial(\sigma_i)$ while $z \neq 0$ do 5: let σ_i be the simplex with maximum index in z 6: if σ_i is unpaired then break 7: $z = z + \zeta(\sigma_i)$ 8: if $z \neq 0$ then 9: pair σ_i with σ_i and set σ_i, σ_i as "paired" 10: $\zeta(\sigma_i) = z$ 11: p =dimension of σ_i 12: add (j, i) to $\mathsf{PD}_p(\mathcal{F})$ 13: 14: for each each unpaired σ_i do p =dimension of σ_i 15: add (i,∞) to $\mathsf{PD}_p(\mathcal{F})$ 16:

• E.g., inserting $\sigma_8 = tw$ creates the blue 1d hole



• If the while loop ends with $z \neq 0$, then the simplex σ_i is called **negative** Input: a filtration \mathcal{F} as a sequence of simplices $\sigma_1, \sigma_2, \ldots, \sigma_m$ Output: p-th PD of \mathcal{F} , PD_p(\mathcal{F}), for each dimension p 1: set each σ_i in \mathcal{F} as "unpaired" 2: $\zeta = a$ table mapping each σ_i to a cycle $\zeta(\sigma_i)$ initially undefined 3: for $\sigma_i = \sigma_1, \sigma_2, \ldots, \sigma_m$ do 4: $z = \partial(\sigma_i)$ while $z \neq 0$ do 5: let σ_i be the simplex with maximum index in z 6: 7: if σ_i is unpaired then break $z = z + \zeta(\sigma_i)$ 8: if $z \neq 0$ then 9: pair σ_i with σ_i and set σ_i, σ_i as "paired" 10: 11: $\zeta(\sigma_i) = z$ 12: $p = \text{dimension of } \sigma_i$ add (j, i) to $\mathsf{PD}_p(\mathcal{F})$ 13: 14: for each each unpaired σ_i do p =dimension of σ_i 15: add (i, ∞) to $\mathsf{PD}_p(\mathcal{F})$ 16:

- If the while loop ends with $z \neq 0$, then the simplex σ_i is called **negative**
- It means that inserting σ_i creates a homology hole die (becomes trivial)

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• E.g., inserting $\sigma_{16} = stu \text{ kills the}$ blue 1d hole



We have that line 10 in the algorithm is always pairing

• a positive simplex σ_i

with

• a negative simplex σ_i

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4: $z = O(\sigma_i)$ 5: while $z \neq 0$ do
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First of all, summing two cycles in line 8 takes O(m) time

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• You could either represent a cycle z (a set of simplices) as a 0-1 list where the i-th item is 1 iff σ_i is in z Input: a filtration \mathcal{F} as a sequence of simplices $\sigma_1, \sigma_2, \ldots, \sigma_m$ Output: *p*-th PD of \mathcal{F} , PD_{*p*}(\mathcal{F}), for each dimension *p*

- 1: set each σ_i in \mathcal{F} as "unpaired"
- 2: $\zeta = a$ table mapping each σ_i to a cycle $\zeta(\sigma_i)$ initially undefined
- 3: for $\sigma_i = \sigma_1, \sigma_2, \ldots, \sigma_m$ do
- 4: $z = \partial(\sigma_i)$

6:

7:

8:

- 5: while $z \neq 0$ do
 - let σ_j be the simplex with maximum index in z
 - if σ_j is unpaired then break
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- 10: pair σ_j with σ_i and set σ_j, σ_i as "paired"
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- 12: $p = \text{dimension of } \sigma_j$
- 13: add (j,i) to $\mathsf{PD}_p(\mathcal{F})$

14: for each each unpaired σ_i do 15: $p = \text{dimension of } \sigma_i$

16: add (i,∞) to $\mathsf{PD}_p(\mathcal{F})$

First of all, summing two cycles in line 8 takes O(m) time

- You could either represent a cycle z (a set of simplices) as a 0-1 list where the i-th item is 1 iff σ_i is in z
- Or represent z as a sorted list of integers such that i is in the list iff σ_i is in z

Input: a filtration \mathcal{F} as a sequence of simplices $\sigma_1, \sigma_2, \ldots, \sigma_m$ Output: *p*-th PD of \mathcal{F} , PD_{*p*}(\mathcal{F}), for each dimension *p* 1: set each σ_i in \mathcal{F} as "unpaired" 2: $\zeta = a$ table mapping each σ_i to a cycle $\zeta(\sigma_i)$ initially undefined 3: for $\sigma_i = \sigma_1, \sigma_2, \ldots, \sigma_m$ do $z = \partial(\sigma_i)$ 4: while $z \neq 0$ do 5: let σ_i be the simplex with maximum index in z 6: if σ_i is unpaired then break 7: $z = z + \zeta(\sigma_i)$ 8: if $z \neq 0$ then 9: pair σ_i with σ_i and set σ_i, σ_i as "paired" 10: $\zeta(\sigma_i) = z$ 11: $p = \text{dimension of } \sigma_i$ 12: add (j, i) to $\mathsf{PD}_p(\mathcal{F})$ 13: 14: for each each unpaired σ_i do $p = \text{dimension of } \sigma_i$ 15: add (i,∞) to $\mathsf{PD}_p(\mathcal{F})$ 16:

First of all, summing two cycles in line 8 takes O(m) time

- You could either represent a cycle z (a set of simplices) as a 0-1 list where the *i*-th item is 1 iff σ_i is in z
- Or represent z as a sorted list of integers such that *i* is in the list iff σ_i is in z

In the worst case, both inner and outer loop iterates O(m) time, and hence $O(m^3)$ oveall

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PD for General Filtration

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 - 4. During the contraction, some intervals in $PD(\mathcal{F}')$ may disappear (birth and death coincide)



Image source: Patrick Schnider. Introduction to Topological Data Analysis Lecture Notes FS 2023



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• Another interactive example for correspondence between a general filtration and its simplex-wise version: <u>https://iuricichf.github.io/ICT/algorithm.html</u>

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"Contracting" $[4,10) \in PD(\mathcal{F}')$ into one for $PD(\mathcal{F})$:

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- So the birth of the corresponding interval in $PD(\mathcal{F})$ is 2



"Contracting" $[4,10) \in PD(\mathcal{F}')$ into one for $PD(\mathcal{F})$:

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- $[4,10) \in PD(\mathcal{F}')$ dies in K'_{10} , which specifically is when go from K'_9 to K'_{10}
- In \mathcal{F} , the homology feature dies when we go from K_3 to K_4 , aka in K_4
- So the corresponding interval in $PD(\mathcal{F})$ is [2,4)

$$\mathcal{F}: K_{0} \hookrightarrow K_{1} \hookrightarrow K_{2} \hookrightarrow K_{1} \hookrightarrow K_{2} \hookrightarrow K_{3} \hookrightarrow K_{4} \hookrightarrow K_{5} \hookrightarrow K_{6} \hookrightarrow K_{7} \hookrightarrow K_{8} \hookrightarrow K_{9} \hookrightarrow K_{10} \hookrightarrow K_{11} \hookrightarrow K_{12} \hookrightarrow K_{13} \hookrightarrow K_{13} \hookrightarrow K_{10} \hookrightarrow K_{10} \hookrightarrow K_{11} \hookrightarrow K_{12} \hookrightarrow K_{13} \to K_{13}$$

 $[5,8) \in PD(\mathcal{F}')$ does not correspond to any interval in $PD(\mathcal{F})$:

• In \mathcal{F} , the homology feature is born in K_3 and dies also K_3 (so it's ephemeral)

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Image source: Edelsbrunner, Letscher, and Zomorodian. Topological persistence and simplification.

- For the previous simplex-wise filtration, we can skip some complexes and renumber them
- Then [8,16) in the simplex-wise filtration becomes [5,10) in the non-simplex-wise
- But they are essential "same" interval (representatives are the same)



Image source: Edelsbrunner, Letscher, and Zomorodian. Topological persistence and simplification.