

AMAT 584 Lecture 37 4/27/20

Today: The persistence algorithm, continued

Review: To compute the persistent homology of a filtration  $F$  with largest simplicial complex  $F_{\max}$ :

1) For each  $j \geq 0$ , order simplices of  $F_{\max}$  with respect to their birth time in the filtration.

2) Using these orderings, construct a "boundary matrix"  $D$  containing all the matrices  $[\delta_j]$  as blocks just above the diagonal.

Columns and rows of  $D$  correspond to simplices of  $F_{\max}$ .

3) Use left-to-right column additions to transform  $D$  into a reduced matrix  $R$ .

4) Read each barcode off of  $R$ , using the following formula:

$$\text{Barcode}(H_i(F)) = \{(\text{birth}(\sigma), \text{hirth}(\tau)) \mid \text{pivot of column } \tau \text{ in } R \text{ is } \sigma \text{ and } \dim(\sigma) = i\}$$

$\{[\text{birth}(\sigma), \infty) \mid \text{col } \sigma = 0, \sigma \text{ is not the pivot of any column in } R, \dim(\sigma) = i\}$ .

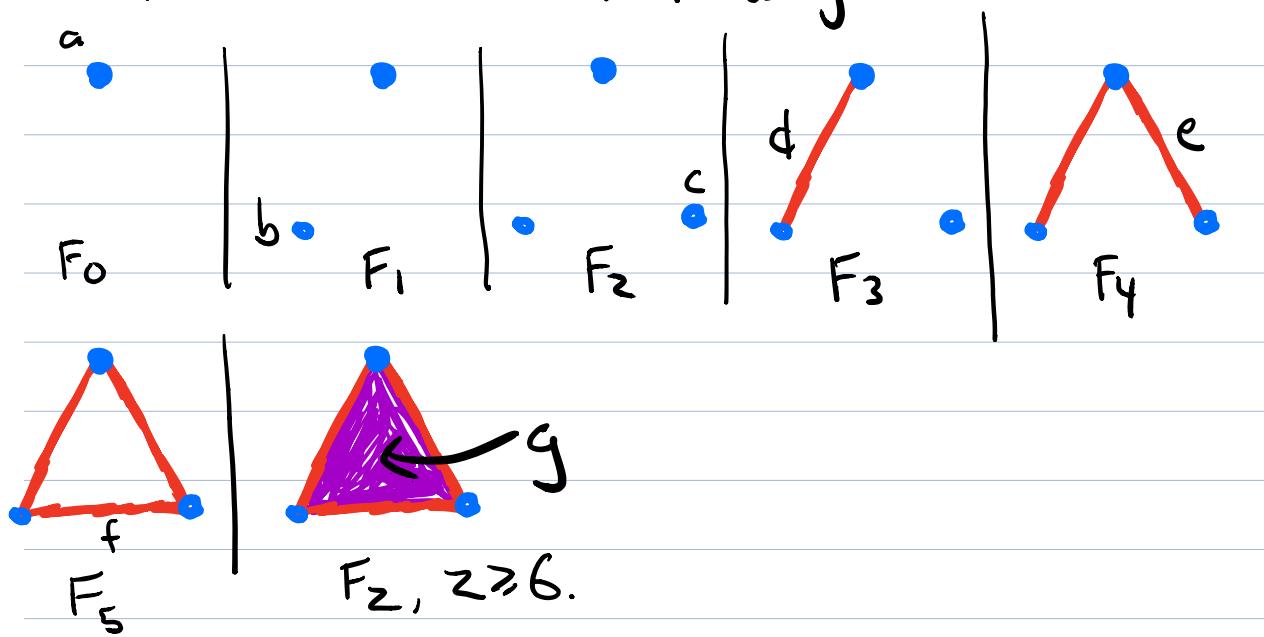
Note: Any interval in the form  $[z, z)$  is ignored.

In words: Every non-zero column in  $R$  gives a finite-length interval in one of the barcodes, by pairing the column with its pivot.

A zero column which doesn't appear as the pivot of any other column gives an infinite interval.

### Example of the last step

Last lecture we considered the following filtration  $F$ :



We saw that for this filtration,

	a	b	c	d	e	f	g
a				1	1	0	
b	0			1	0	1	0
c		0	1		1		
d	0					1	
e	0			0		1	
f					0	1	
g	0			0	0	0	

Applying the standard reduction (Step 3) gives

	a	b	c	d	e	f	g
a				1	1	0	
b	0			1	0	0	0
c		0	1		0	0	
d	0					1	
e	0			0		1	
f					0	1	
g	0			0	0	0	

(The only column of D that was changed was column f).

We get a finite interval in one of the barcodes for each non-zero column:

$$\begin{array}{ccc} F_{\max}^0 & F_{\max}^0 & F_{\max}^1 \\ \text{[birth(b), birth(d)]}, \text{[birth(c), birth(e)]}, \text{[birth(f), birth(g)]} \\ [1, 3) & [2, 4) & [5, 6) \end{array}$$

The zero columns are a, b, c, f. Of these, all but a is a pivot of another column.

$$\text{So the only infinite interval is } \text{[birth(a), } \infty \text{)} \\ [0, \infty)$$

To figure out which interval goes in which barcode, we look at the dimension of the simplex ending the left endpoint.

$$\text{Barcode}(H_0(F)) = \{[1, 3), [2, 4), [0, \infty)\} \\ \text{Barcode}(H_1(F)) = \{[5, 6)\}.$$

Note: If we only want to compute persistent homology up to degree  $k$ , i.e.  $\text{Barcode}(H_i(F))$  for  $i \in \{0, 1, \dots, k\}$ , then we don't need to consider all of  $F$ . It's sufficient to consider the subfiltration consisting of only simplices of dimension  $\leq k+1$ .

This often allows us to keep the size of  $D$  much smaller

An example coming from data

Let  $X = \{(0,0), (2,0), (0,2), (2,2)\} \subset \mathbb{R}^2$ , given the Euclidean metric.

Let  $B_i = \text{Barc}(H_i(\text{Rips}(X)))$

We will compute each  $B_i$ .

Note that  $\text{Rips}(X)$  is a  $[0, \infty)$ -indexed filtration. We will show by example that the persistence algorithm works in essentially the same way for such a filtration, as in the  $\mathbb{N}$ -indexed case.

Let  $F = \text{Rips}(X)$ .  $F_{\max}$  is the 3-simplex with vertex set  $X$ .

Let's give names to all the simplices of  $F_{\max}$ , and record their birth times:

to keep notation simple, we write  $\text{birth}(\sigma)$  as  $\beta(\sigma)$ .

$$a = [a], b = [b], c = [c], d = [d]$$

$$\beta(a) = \beta(b) = \beta(c) = \beta(d) = 0$$

$c = [a, b]$ ,  $f = [b, c]$ ,  $g = [c, d]$ ,  $h = [d, a]$ ,  $i = [a, c]$ ,  $j = [b, d]$

$\beta(e) = \beta(f) = \beta(g) = \beta(h) = 2$ .

$\beta(i) = \beta(j) = 2\sqrt{2}$ .

$k = [a, b, c]$ ,  $l = [a, b, d]$ ,  $m = [a, c, d]$ ,  $n = [b, c, d]$

$\beta(k) = \beta(l) = \beta(m) = \beta(n) = 2\sqrt{2}$

$\sigma = [a, b, c, d]$

$\beta(\sigma) = 2\sqrt{2}$ .

Note: The alphabetical order on each  $X^i$  is in order of increasing birth

to be continued: