

①

[JUNIOR TOPOLOGY SEMINAR — ANDREW GIULIOTTO]
APRIL 9 2008

Biology → huge datasets / multiscale
→ geometric information
→ unknown shape / features

cells 10^{-4}
viruses 10^{-7} m
water mol. 10^{-9} m

Goal: A way to measure topological features
& their relative geometric significance

Bx: Gramicidin A (protein)

Bx: Protein docking (ID features)

Technique: Persistent Homology

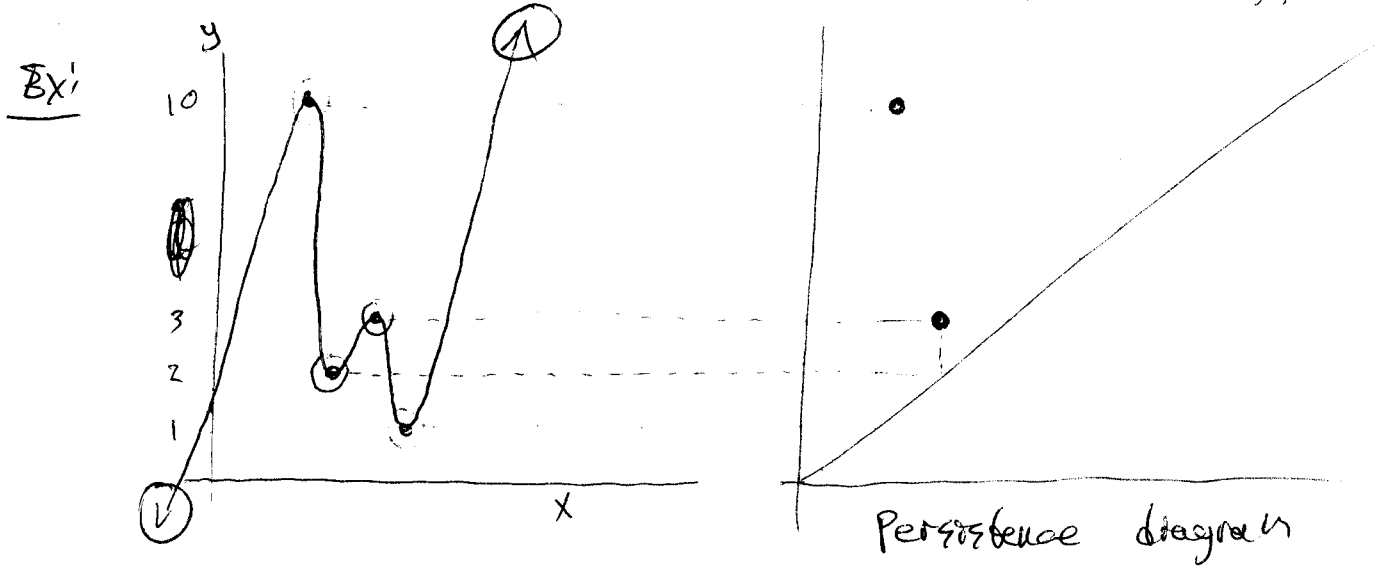
Outline: [I] Basic Idea

[II] The Math

[III] Recent Theoretical Extensions

I Basic Idea

(c.f. $\frac{f_{min}}{(no\ feat)}$ or $\frac{f_{max}}{(2\ feat)}$)



- Let $f: \mathbb{R} \rightarrow \mathbb{R}$ smooth w/ only non-degenerate crit. pts w/ distinct values
- Consider the SUBLEVEL SET $f^{-1}(-\infty, t]$ as t increases
- $\min \Rightarrow$ create component
- $\max \Rightarrow$ merge components; match to higher (younger) of "mergers"
- The PERSISTENCE of a matched pair of critical points (x_1, x_2) is $|f(x_2) - f(x_1)|$
- This = vert. distance of pt to diag in persis. dia
- "Noise" = ~~pts~~ points near diagonal. (c.f. top)

II The Math

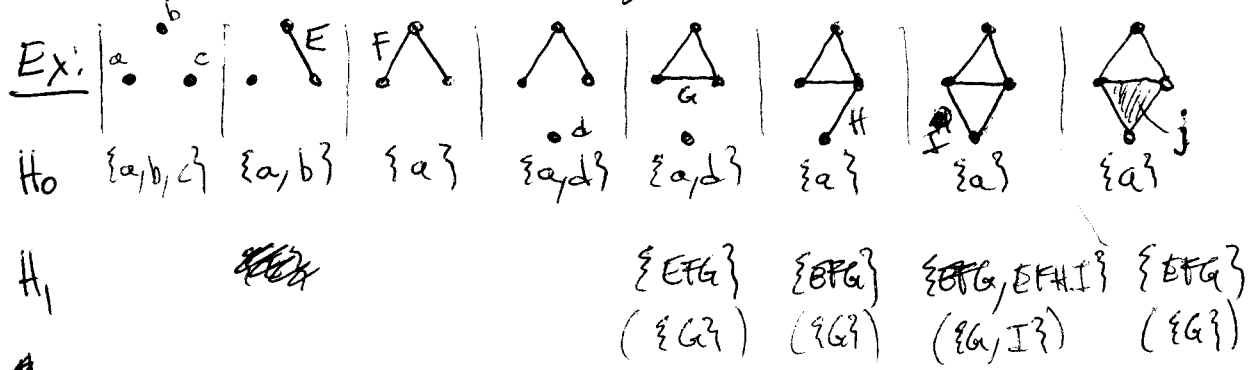
Def: A FILTRATION is a sequence of nested complexes inside a simplicial cplx K :
 $\emptyset = K^0 \subset K^1 \subset \dots \subset K^m = K$

Def: $Z_j^l := j^{\text{th}}$ cycle group in K^l
 $B_j^l := j^{\text{th}}$ boundary group in K^l

$$H_j^{l,p} := \frac{Z_j^l}{(B_j^{l+p} \cap Z_j^l)}$$

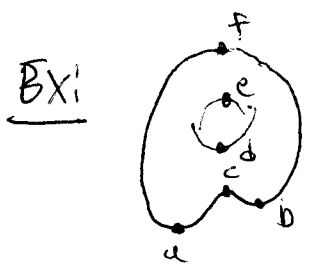
= p-PERSISTENT j^{th} hom. gp. of K^l
 = {cycles in K^l mod ∂ ys in K^{l+p} }

Rmk: IF $H_{j,p}^{l,p} \neq \{0\}$ for large p , \exists "stable" homological j -features.



Def: A POSITIVE simplex creates homology while a NEGATIVE one destroys it, \exists projection between positive simplices & homology bases

III Recent Theoretical Extensions



- a, b - create 0-hom
- c - merge a & b (kills 0-hom)
- d - creates 1-hom
- e - " 1-hom
- f - " 2-hom



Consider Morse function f on a compact surface.

- Problems:
- ① Not all classes are matched
 - ② Highly dependent on "direction" of height fn.

Solution to ①: Extended Persistence (Cohen-Steiner, Edelsbrunner, Harer ≥ 2007)

Let $t_0 < t_1 < \dots < t_n (= \infty)$ be regular values bracketing the critical values of f .

Def: $M_k := f^{-1}(-\infty, t_k]$

$$M_k \xrightarrow{i} M_{k+1} \text{ induces } \begin{cases} i_* : H^r(M_k) \rightarrow H^r(M_{k+1}) \\ i^* : H^r(M_{k+1}) \rightarrow H^r(M_k) \end{cases}$$

(pullback by i)

Thm: POINCARÉ DUALITY: M compact, oriented n -mfd

$$\text{then } H^k(M) \cong (H^{n-k}(M))^* \cong H_{n-k}(M)$$

So we get the sequence

$$H^r(M_0) \xrightarrow{i_*} \dots \rightarrow H^r(M_n) \xrightarrow{\cong \text{ P.D.}} H^{n-r}(M_n) \xrightarrow{i_*} \dots \xrightarrow{i_*} H^{n-r}(M_0)$$

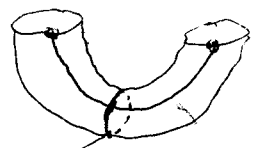
Thm: Lefschetz Duality: \exists non-degenerate pairing

$$\langle \cdot, \cdot \rangle : H_r(M, \partial M) \times H_{n-r}(M) \longrightarrow \mathbb{Z}/2\mathbb{Z}$$

given by counting Pns of cycles in M .

\longrightarrow Poincaré Duality is just Lef. Duality w/ $\partial M = \emptyset$

Bx: M



rep. of $H_1(M)$

rep. of $H_1(M, \partial M)$

any generator of $H_1(M)$ is

any generator of $H_1(M, \partial M)$

exactly once

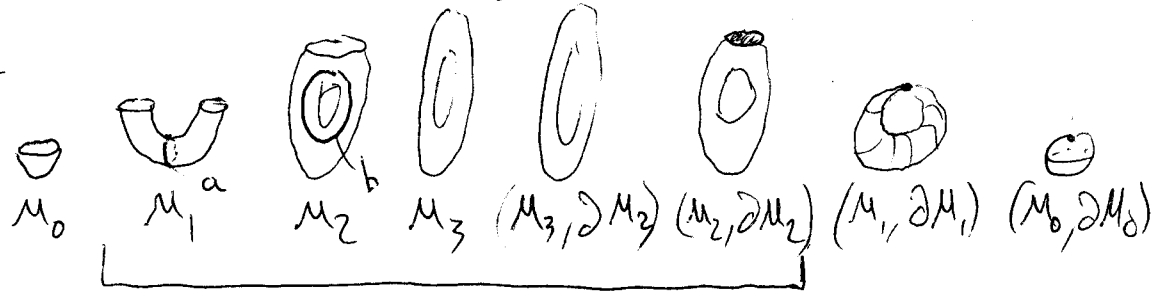
So the sequence becomes

$$H_r(M_0) \longrightarrow \dots \longrightarrow H_r(M_n) \xrightarrow[\cong]{\partial M_n = \emptyset} H_r(M_n, \partial M_n) \longrightarrow \dots \longrightarrow H_r(M_0, \partial M_0)$$

\uparrow \uparrow
 factor thru
 Lefschetz duality

Now all classes get matched!

Bx:



life of a

life of b

⑥

We have the decomposition:

REGULAR (ORDINARY) persistence: classes born & killed by $H_r(M_n)$

EXTENDED persistence: " born before & killed after $H_r(M_n)$

↳ represents essential classes

RELATIVE persistence: " born & killed after $H_r(M_n)$

(Rank: Extended pairs are classes of complementary dimension)

What about choice of direction?

Obs: With extended persistence, all critical points get matched

∴ We gain information on geometrical features from distance between matched pts.

More formally:

Def: The HEIGHT OF $x \in M$ IN DIRECTION $\vec{u} \in S^2$ is

$$h: M \times S^2 \longrightarrow \mathbb{R}$$

where $h(x, \vec{u}) :=$ signed distance from \vec{x} to the plane through the origin w/ normal \vec{u} .

Prmk: h is Morse for a.e. $\vec{u} \in S^2$

Not: Let $\vec{n}_x :=$ normal vector to $T_x M$.

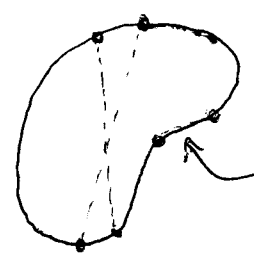
Then x is a crit. point for $h(\cdot, \vec{n}_x)$ & $h(\cdot, -\vec{n}_x)$ & no other $\vec{u} \in S^2$.

$\therefore \exists!$ $y \in M$ s.t. x paired to y by $h(\cdot, \pm \vec{n}_x)$.

Def: The BREVATION AT $x \in M$ where y paired to x .

is $E: M \rightarrow \mathbb{R}_{\geq 0}$ w/ $E(x) = |h(x, \vec{n}_x) - h(y, \vec{n}_x)|$

Ex:



at inflection points $E=0$

Claim: Geometric "features" occur in regions of large E values

Claim: To "dock" two surfaces, features should be aligned.