

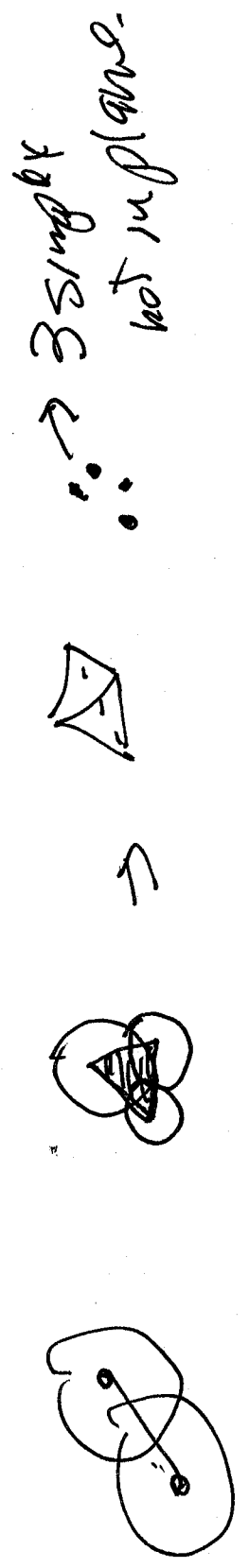
data \xrightarrow{VR} simplicial complex \xrightarrow{Chains} homology

all functional

Recall $X = \sum x_{0,1}, x_{0,2}, \dots, x_{0,n} \subseteq \mathbb{R}^n$
 simplicial complex $VR_X(X)$ via

(1) vertex set is X
 (2) simplex $\{x_{a_1}, \dots, x_{a_k}\} \Leftrightarrow$

$d(\mathbb{R}^n) \subset \mathbb{R}^n$ $\langle x_{a_1}, \dots, x_{a_k} \rangle$
 $\forall i, k$



Look at all scales

NOTE: $\Sigma \hookrightarrow \Sigma'$
 $VR_{\Sigma}(\mathbb{R}) \subseteq VR_{\Sigma'}(\mathbb{R})$

In fact $L_{\Sigma \hookrightarrow \Sigma'}: VR_{\Sigma}(\mathbb{R}) \rightarrow VR_{\Sigma'}(\mathbb{R})$

is a simplicial map.

Fix $\mathbb{R} \xrightarrow{VR} \text{Simp}$ is

a functor $\Sigma \hookrightarrow \Sigma'$ \rightarrow $L_{\Sigma \hookrightarrow \Sigma'}: VR_{\Sigma} \rightarrow VR_{\Sigma'}$
 $\Sigma \rightarrow \Sigma'$
composition works.

So Fix \mathbb{X} , we have a functor.

$$\mathbb{R}^+ \rightarrow \text{Simp} \rightarrow \text{Chains} \rightarrow H_*$$

Keeps track of all scales. For each n

$$\mathbb{Z} \rightarrow H_n(VR_{\mathbb{Z}}(\mathbb{X}))$$

In practice, discretize \mathbb{Z} . For example,

$$\text{Fix } N \quad \mathbb{Z} = \frac{\dim \mathbb{X}}{N} \quad \text{+++++}$$

$$\mathbb{Z} = 1 \cdot \mathbb{Z}_1$$

Functor $\mathbb{N} \rightarrow \text{Ab}$ or vector spaces

~~(Persistence)~~ (Persistent modules)

How do you compute or visualize?

Tool: $i < j \Rightarrow L_{\varepsilon_i, \varepsilon_j} \cdot VR_{\varepsilon_i} \Rightarrow VR_{\varepsilon_j}$

Induces: $(L_{\varepsilon_i, \varepsilon_j})_*$: $H_n(VR_{\varepsilon_i}) \rightarrow H_n(VR_{\varepsilon_j})$

allows us to compare homology of

different scales

Study birth and death of elements
of H_n

3 rows for same ϵ .

DEF

(1) δ is born at index i if δ is not in the image of H_n for some n .

~~$H_n(i, j)$~~

$$H_n(VR_{\epsilon, i}) \rightarrow H_n(VR_{\epsilon, i})$$

$$q \rightarrow \delta \in H_n(VR_{\epsilon, i})$$

and δ is born at i if it becomes

(2) Dies at $j > i$. if it becomes zero in the induced to $H_n(VR_{\epsilon, j})$.

Bar codes keep track of birth and death of homology elements as δ descends

increases

Classification of finitely generated

Persistence modules allow one to compute a coherent basis of ~~coherency~~ that fits together

for all $\epsilon > 0$

This basis is $\{\delta_1, \dots, \delta_k\}$

The barcode of δ_i is

$$\sum_p b(\delta_i), d(\delta_i)$$

birth death.



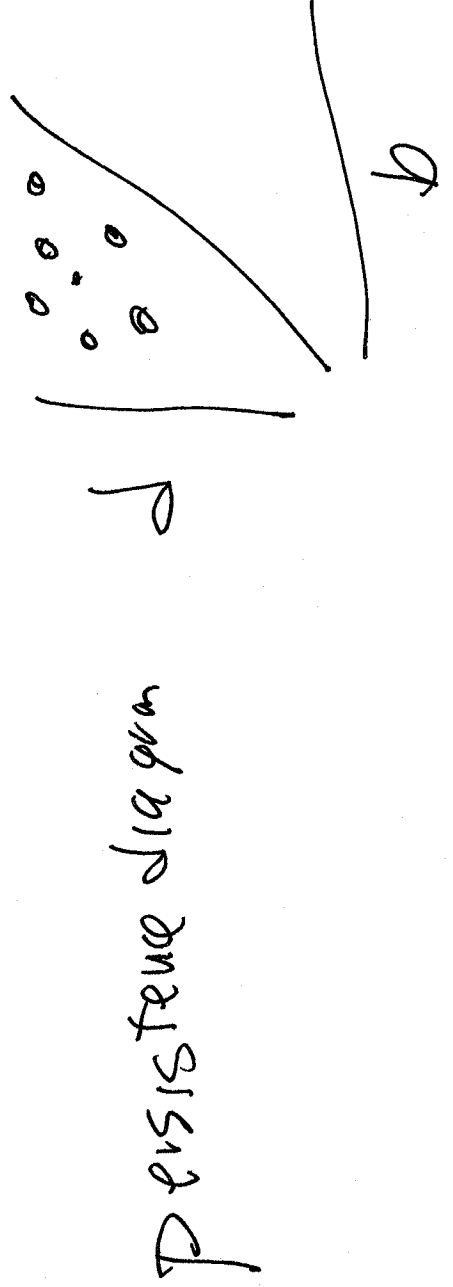
multiset of

The barcode of X is the ~~union~~ of

these barcodes.



$$b(\delta_i), d(\delta_i)$$



Stability: If the barcodes are physically

relevant \Rightarrow small changes in data should
yield small changes in the bar codes.

(or noisy data)

The measure this we need to

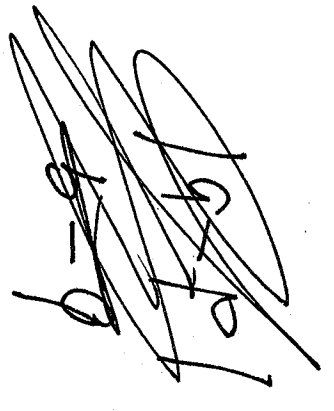
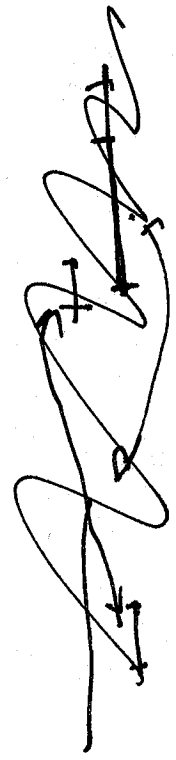
measure the size of changes.

So need a metric on data sets
and one on barcodes.

The metric on data sets is Gromov-Hausdorff distance - which measures the global distance with all matchings



Bottleneck distance on bar codes
compares length over all matches



$$d_{\infty}((b_1, d_1), (b_2, d_2))$$

$$= \max(|b_1 - b_2|, |d_1 - d_2|)$$

For bottle neck each pair

Cohen-Sturtevant - Edelsbrunner + Harer

barcodes of these complex.

Barcode distance ($\overrightarrow{VR}(\mathbb{X}), VR(\mathbb{Y})$)

\leq Gromov Hausdorff (\mathbb{X}, \mathbb{Y})

Stability D_m for persistent homology

Practical Computations (efficient)

and is

require more

work

and exist

a very active area

SEVERAL good codes.