

Persistent Homology

(Or how I learn this new data analysis methodology in 2020)

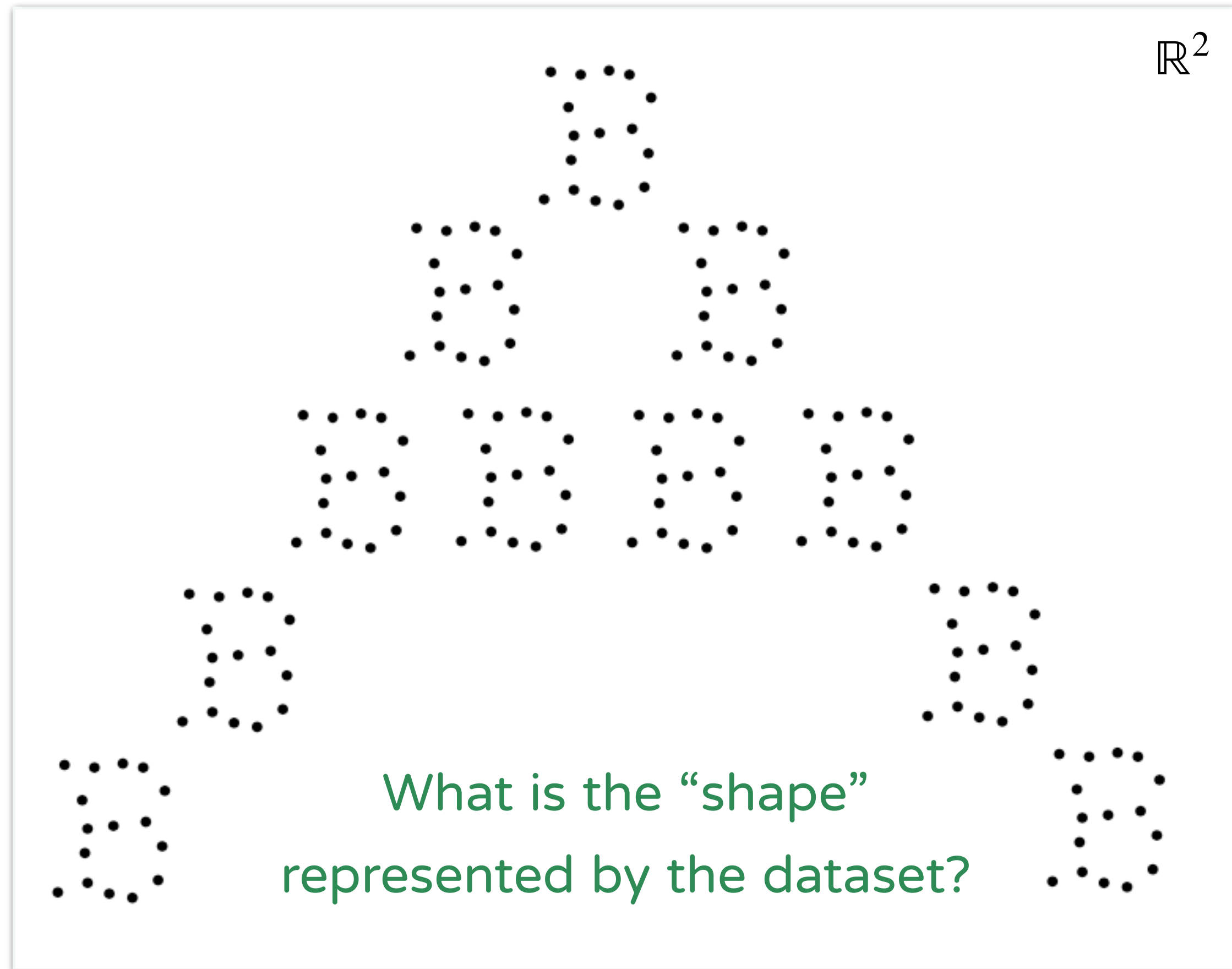
Tzu-Chi Yen

MATH 6220: Introduction to Topology II

Class Presentation

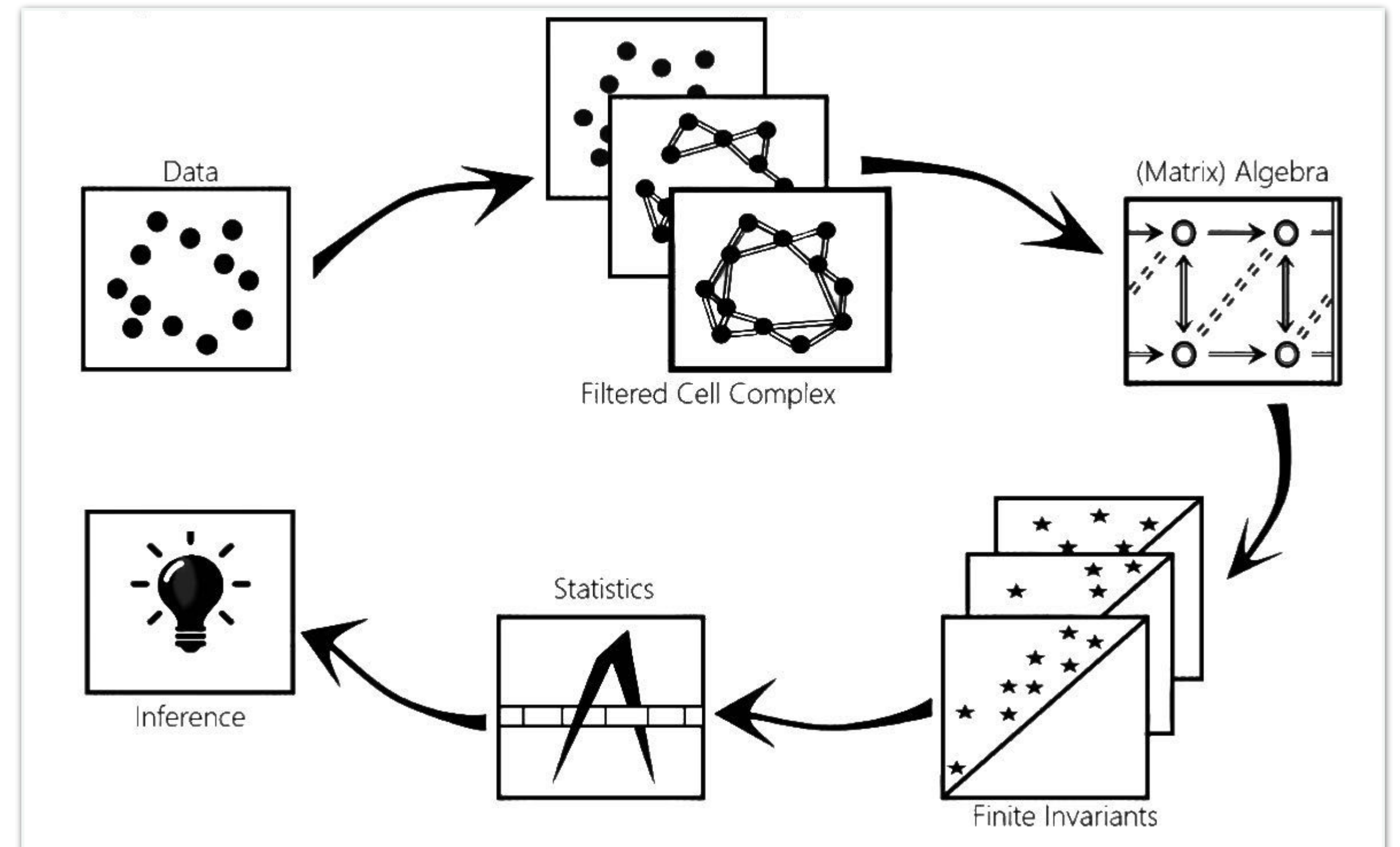
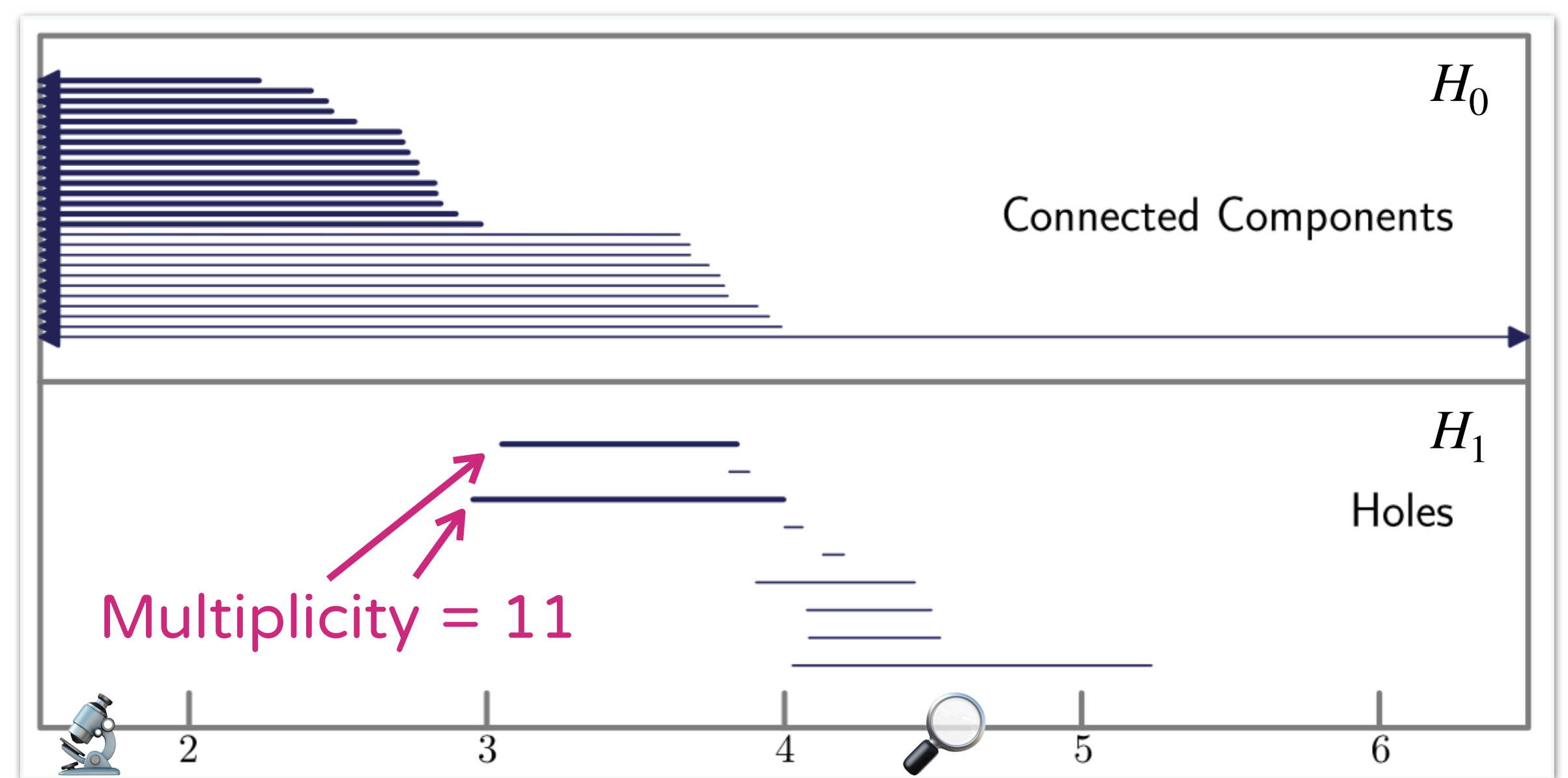
April 17, 2020

A Motivating Example



- Letter A $\times 1$?
- Letter B $\times 11$?
- Points $\times 176$?

Scale matters!



Outline

- ~~A motivating example~~

- Introduction & active research directions

[Gunnar Carlsson “Persistent Homology and Applied Homotopy Theory.” arXiv (2020)]

- Theoretical foundations

Stability theorem

- Topological / algebraic persistence, & stability

Structure theorem

- Computation

[Steve Oudot “Persistence Theory.” AMS monograph (2015)]

[Vidit Nanda’s notes on computational algebraic topology (2020)]

- (Three interesting applications)

[Ann E. Sizemore et al., “TDA for the network neuroscientist.” Network Neuroscience (2019).]

[Tamal K. Dey et al. “An efficient algorithm for 1-dimensional (persistent) path homology.” SoCG (2020).]

[Michelle Feng & Mason A. Porter “Persistent Homology of Geospatial Data: A Case Study with Voting.” SIAM Review (2020).]

- Beyond persistence homology

[Han Riess. “Beyond Persistent Homology: A Mathematical Guide.” Preprint (2019).]

- Conclusion

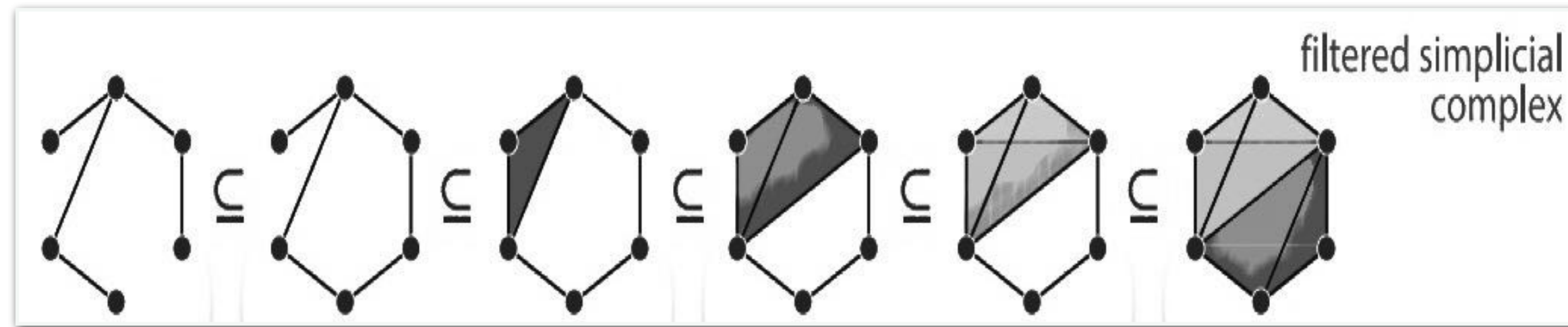
Introduction

- Original motivation: Extend the ideas of algebraic topology from the **category of spaces X** to situations where we only have **a sampling of the space X** .
 - Only 20 years in history!
- Active directions include:
 - Coordinatization of barcodes
 - Stability results
 - Coverage and evasion problems
 - Generalized persistence
 - Probabilistic analysis and inference
 - Symplectic geometry

Topological Persistence

- **Def:** Filtration

A filtration is a sequence of nested topological spaces $X_0 \subseteq X_1 \subseteq \dots \subseteq X_n$.



- **Note:** From topological persistence to algebraic persistence

Applying the “d-dimensional” homology with coefficient in a field \mathbb{F} , i.e., $H_d(\cdot, \mathbb{F})$, to a filtration gives a sequence of vector spaces & linear maps,

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

where f_* is the inclusion simplicial map sending K_* to the next K_{*+1} .

Algebraic Persistence (1 of 2)

- **Def:** Persistence module

A persistence module is a sequence \mathbb{V}_* of vector spaces and linear maps, i.e.,

$$V_0 \xrightarrow{\phi_0} V_1 \xrightarrow{\phi_1} V_2 \xrightarrow{\phi_2} \dots \xrightarrow{\phi_{n-1}} V_n$$

- **Def:** Persistence homology groups

The persistent homology groups of \mathbb{V}_* are $H_i^j(\mathbb{V}_*) = \text{Im} [\psi_{j-1} \circ \dots \circ \psi_{i+1} \circ \psi_i]$, assuming $i \leq j$. For convenience, we can write $\psi_i^j : V_i \rightarrow V_j$. Then, we have the following interpretation:

An element $\alpha \in V_i$ is BORN at i if $\alpha \notin \text{Im } \psi_{i-1}$ and DIES at $j > 1$ if $\psi_i^j(\alpha) = 0$ but $\psi_i^{j-1}(\alpha) \neq 0$.

- **Def:** Interval module

Given $i < j$, the interval module $\mathbb{I}_*^{[i,j)}$ is:

Nicest possible persistence modules

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

Algebraic Persistence (2 of 2)

- Structure theorem

To each persistence module \mathbb{V}_* of vector spaces over \mathbb{F} , one can associate a multi-set of intervals,

$$\text{Bar}(\mathbb{V}_*) = \{[i, j) \mid 0 \leq i < j < \infty\} .$$

such that \mathbb{V}_* is isomorphic to a direct sum of interval modules,

$$\mathbb{V}_* \cong \bigoplus_{[i,j) \in \text{Bar}(V)} \mathbb{I}_*^{[i,j)} .$$

- “proof”

Every persistence module is an “honest module” in the sense of abstract algebra over the polynomial ring $\mathbb{F}[t]$, where t acts on $\alpha \in V_i$ by pushing it to $\psi_i(\alpha) \in V_{i+1}$. These “finitely generated modules” over $\mathbb{F}[t]$ (a principle ideal domain) decompose as follows.

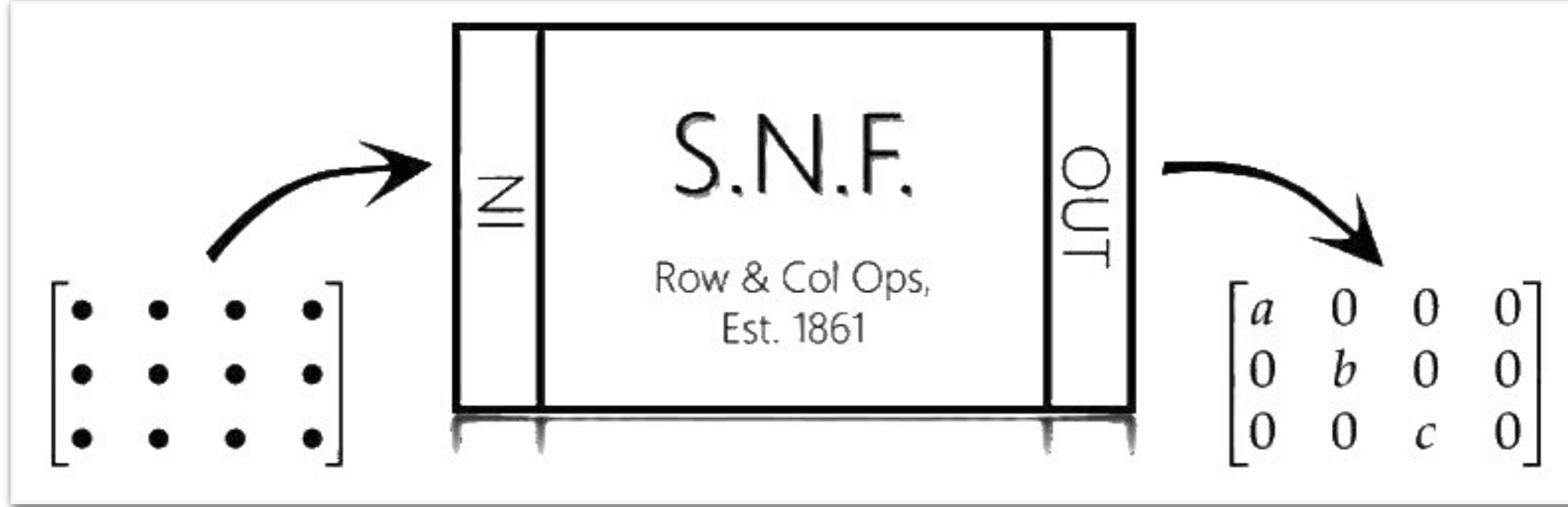
$\exists \{\alpha_i, i \in I\}$ and $\exists \{\beta_j < \gamma_j, j \in J\}$, such that

$$\mathbb{V}_* \cong \underbrace{\bigoplus_{\alpha_i} t^{\alpha_i} \cdot \mathbb{F}[t]}_{\text{“free part”}} \oplus \underbrace{\bigoplus_{\beta_j < \gamma_j} t^{\beta_j} \cdot \mathbb{F}[t]/t^{\gamma_j}}_{\text{“torsion part” (quotient by ideal)}} .$$

And in this case ...

$$\text{Bar}(\mathbb{V}_*) = \coprod_{i,j} \{[\alpha_i, \infty)\} \{[\beta_j, \gamma_j)\} .$$

Computation



Algorithm 1: Matrix reduction

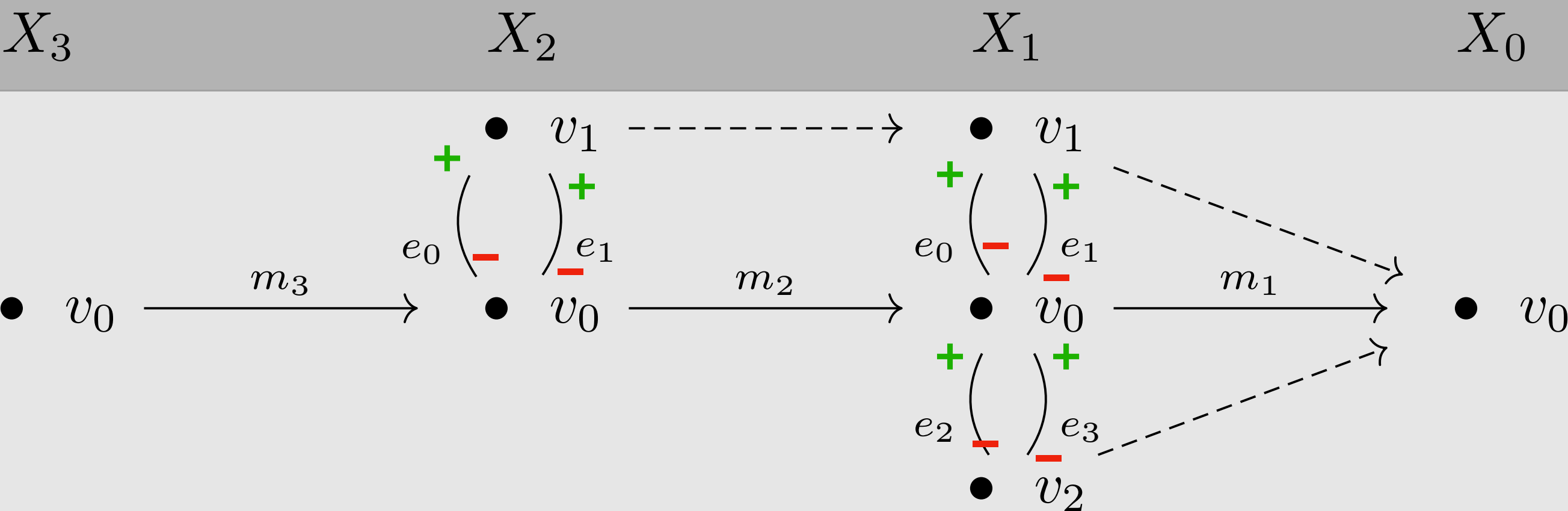
Input: $m \times m$ binary matrix M

```
1 Let  $R = M$ ;  
2 for  $j = 1$  to  $m$  do  
3   while there exists  $k < j$  with  $\text{low}(k, R) = \text{low}(j, R) \neq 0$  do  
4     add (modulo 2) column  $k$  to column  $j$  in  $R$ ;  
5   end  
6 end  
Output:  $R$ 
```

- **Caveat:** The row & col operations are computationally expensive!
The time complexity scales at most cubic in the number m of simplices of K . But m is **combinatorially** large.

Example Persistent Homology Calculation (outcome: barcodes)

Four (small) cellular complexes:

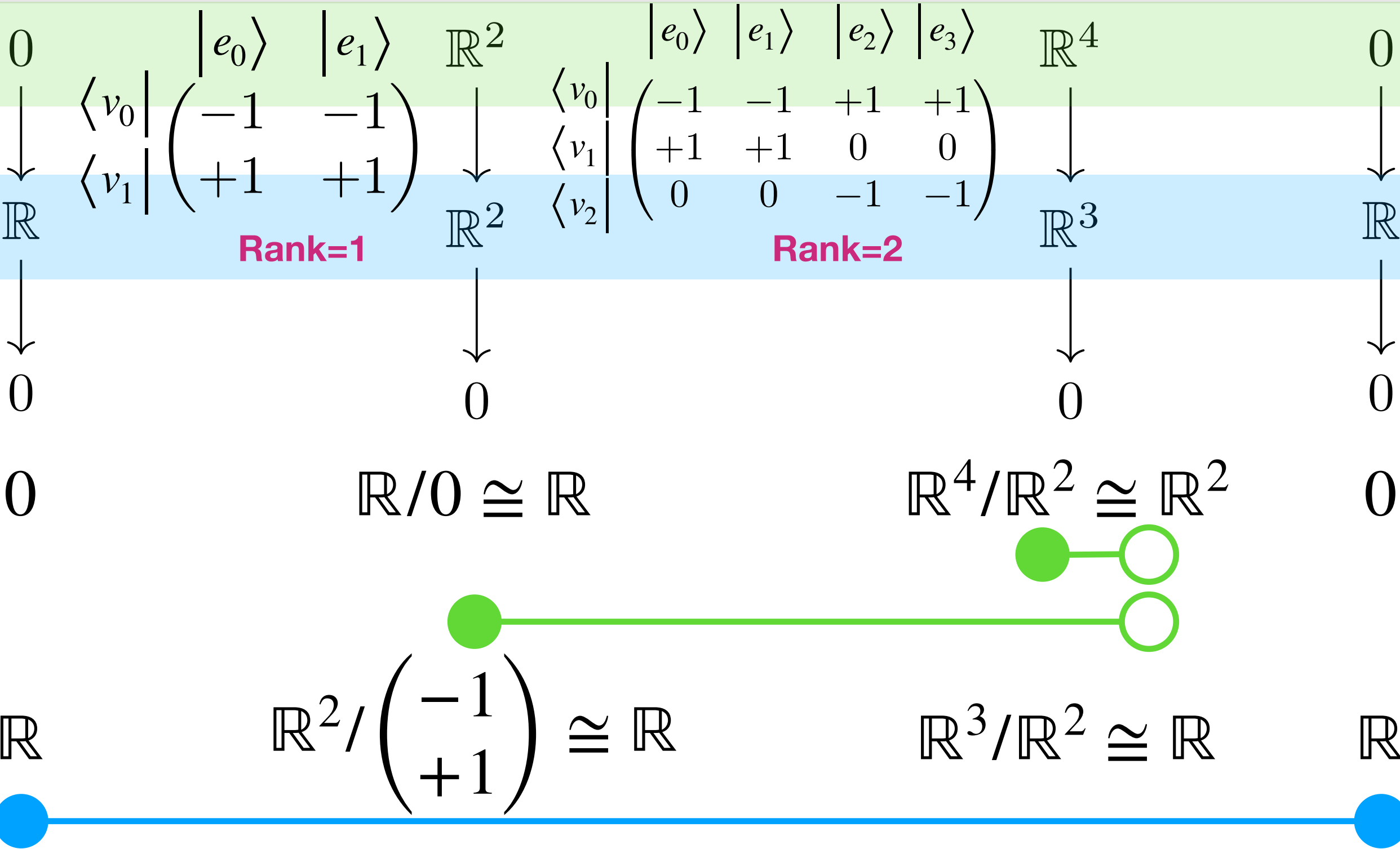


Dimension 1:

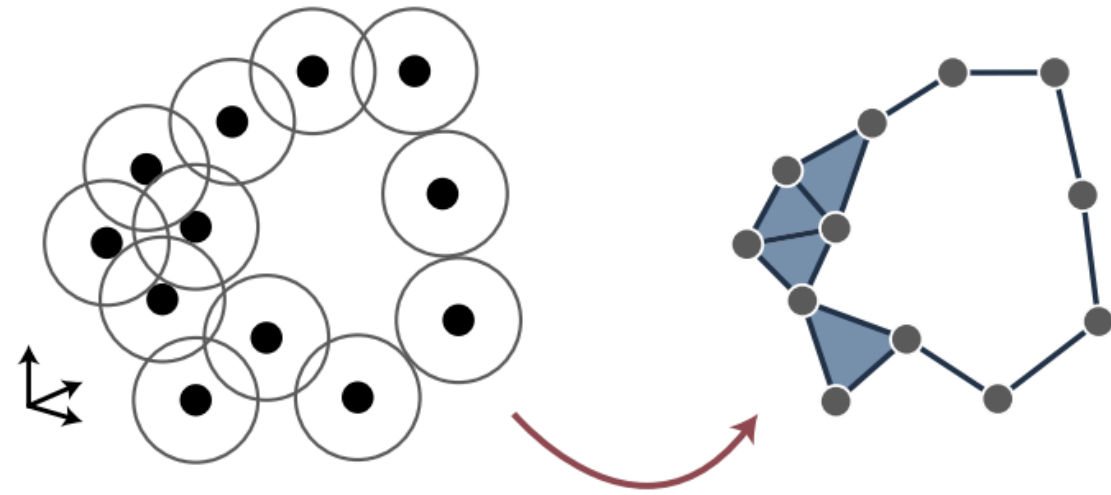
Dimension 0:

$$H_1(X_i; \mathbb{R})$$

$$H_0(X_i; \mathbb{R})$$

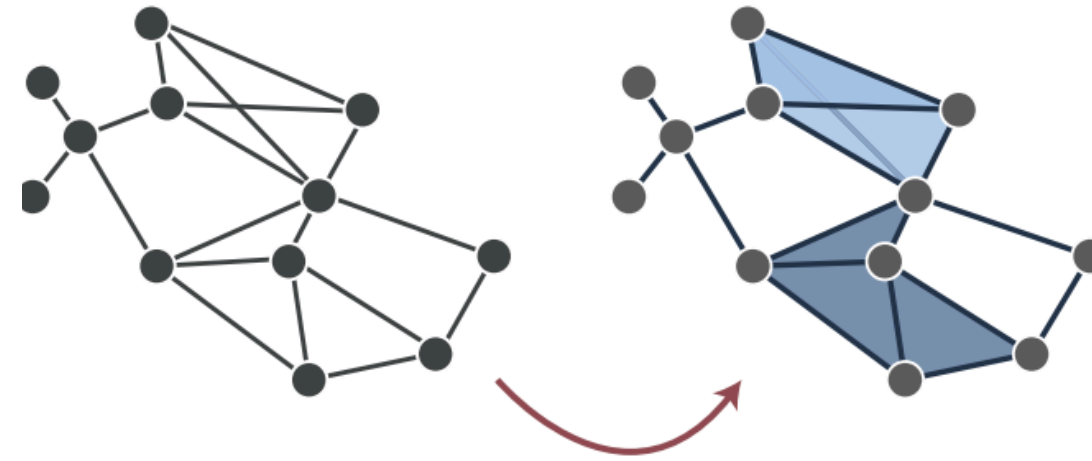


From Data to Simplicial Complex



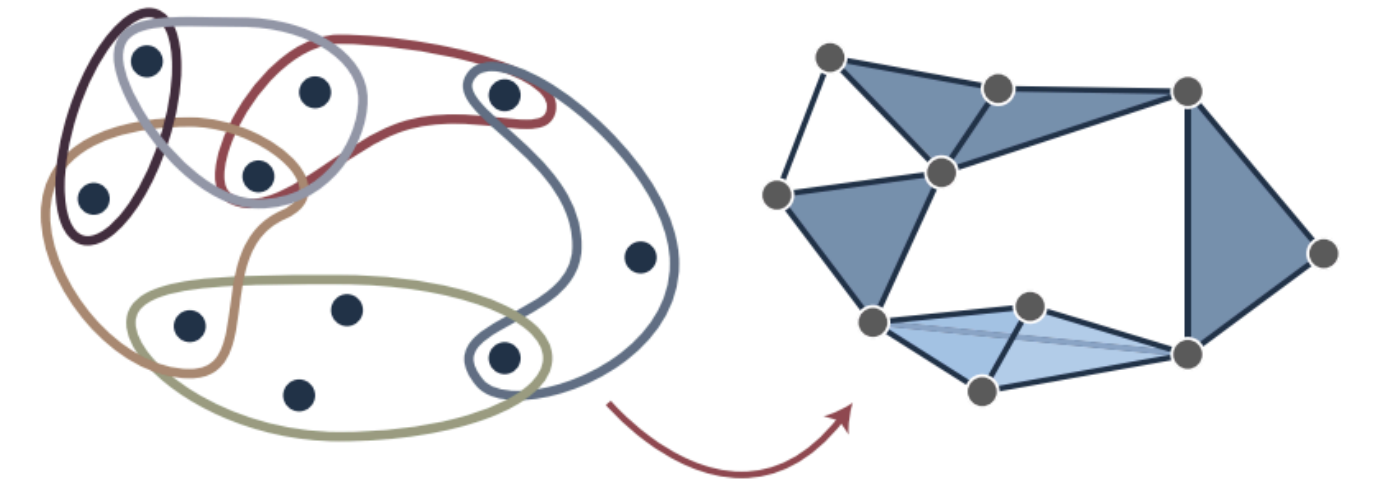
- Vietoris-Rips complex

- Input format: point cloud



- Clique (or flag) complex

- Input format: binary graph



- Nerve complex

- Input format: graph where groups of nodes share a **feature**

- Other flavors include **witness complex**, **Čech complex**, **Alpha complex**, etc. You can even craft your own! For example, **statistically sound filtrations** or **filtrations that better detect the changes** in data.

[Rob Ghrist, "Elementary Applied Topology." (2014)]

- To learn which computational tool to use (e.g., software packages), see Nina Otter et al., "A roadmap for the computation of persistent homology." EPJ Data Science (2017).

Stability (1 of 2; Goal: be able to compare barcodes & persistence modules)

- Def: ϵ -matching

Let B and B' be two barcodes. A ϵ -matching between them is a bijection $\mu : B_0 \xrightarrow{\approx} B'_0$ 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 $|a - a'| < \epsilon$ and $|b - b'| < \epsilon$.

- Def: The Bottleneck distance between barcodes B and B' is

$$d_{\text{Bottle}}(B, B') = \inf\{\epsilon > 0 \mid \exists \epsilon\text{-matching } B \leftrightarrow B'\}.$$

Stability (2 of 2; Goal: be able to compare barcodes & persistence modules)

- **Def: ϵ -interleaving**

Let U_* and V_* be two \mathbb{R}^+ -indexed persistence modules. A ϵ -interleaving between them is a family of maps $\{\phi_t : U_t \rightarrow V_{t+\epsilon} \mid \forall t \in \mathbb{R}^+\}$ and $\{\psi_t : V_t \rightarrow U_{t+\epsilon} \mid \forall t \in \mathbb{R}^+\}$ such that all possible triangles and parallelograms commute, e.g.,

$$\begin{array}{ccc}
 U_s & \xrightarrow{f_{s,s+2\epsilon}} & U_{s+2\epsilon} \\
 \searrow \phi_s & & \nearrow \psi_{s+\epsilon} \\
 & V_{s+\epsilon} &
 \end{array}
 \quad
 \begin{array}{ccc}
 U_s & \xrightarrow{f_{s,t}} & U_t \\
 \searrow \phi_s & & \nearrow \psi_t \\
 & V_{s+\epsilon} & \xrightarrow{g_{s+\epsilon,t+\epsilon}} V_{t+\epsilon}
 \end{array}$$

Note: $f_{s,t} : U_s \rightarrow U_t$ is a linear map for $s \leq t$ such that $f_{s,s} = \text{Id}$ $\forall s$ and $f_{s,u} = f_{t,u} \circ f_{s,t}$ $\forall s \leq t \leq u$. Similarly for $g_{s,t}$ and V_* .

[+ 2 more]

- **Def: The Interleaving distance between U_* and V_* is**

$$d_{\text{Interl}}(U_*, V_*) = \inf\{\epsilon > 0 \mid \exists \epsilon\text{-interleaving } U_* \leftrightarrow V_*\}.$$

- **Stability Theorem**

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

$$d_{\text{Interl}}(U_*, V_*) = d_{\text{Bottle}}(\text{Bar}(U_*), \text{Bar}(V_*)) .$$

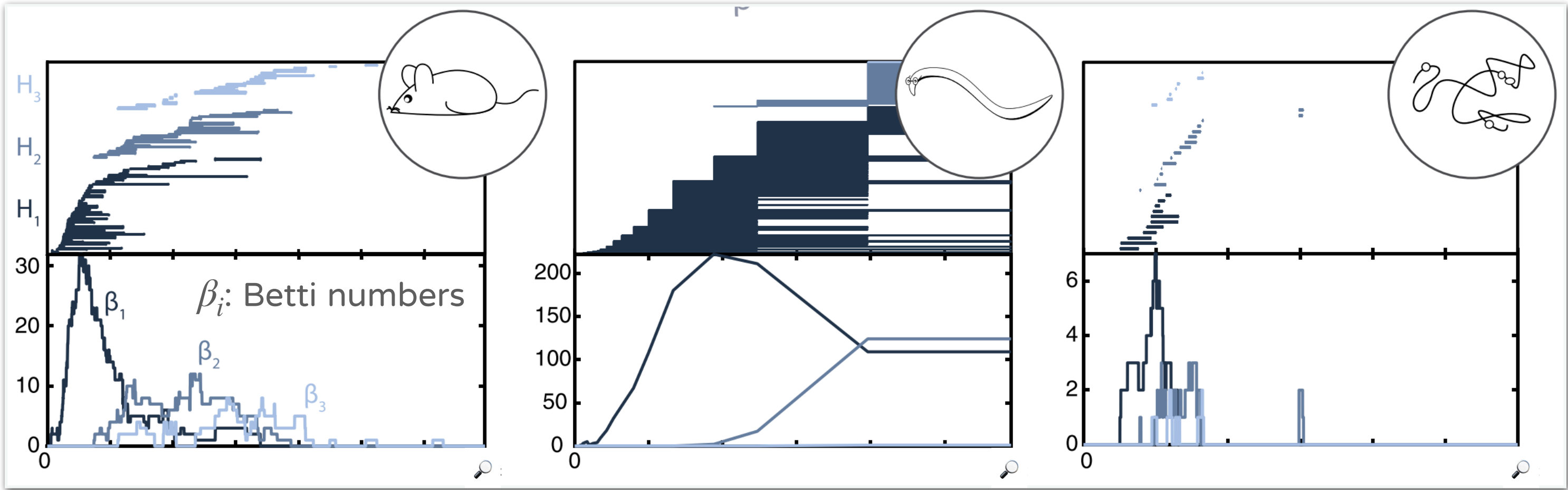
“proof” See Lesnick & Bauer’s “induced matchings” (SOCG’14)

Noise in data is no more than noise in Barcode!

(justifies the use of homology in data analysis)

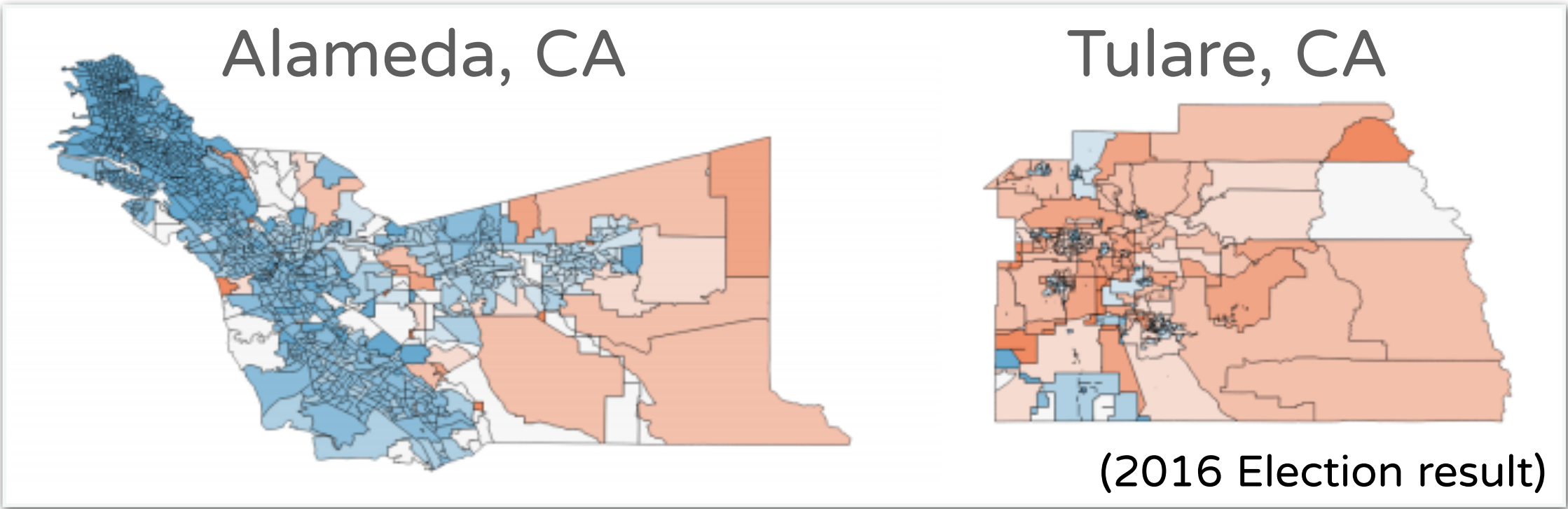
Application 1 of 3: Persistent Homology in Neuroscience

“Find ‘holes’ in the network of interacting brain regions, across organisms”



Application 2 of 3: Persistent Homology of Geospatial Data

“Find a Blue island in the Red sea ...”



Issue	VR	Alpha	Adjacency	Level set
Scaling	✗	✗	✓	✗
Contiguity	✗	✗	✓	✓

“... by constructing better complexes for 2D data”

[Ann E. Sizemore et al., “TDA for the network neuroscientist.” Network Neuroscience (2019).]

[Michelle Feng & Mason A. Porter “Persistent Homology of Geospatial Data: A Case Study with Voting.” SIAM Review (2020).]

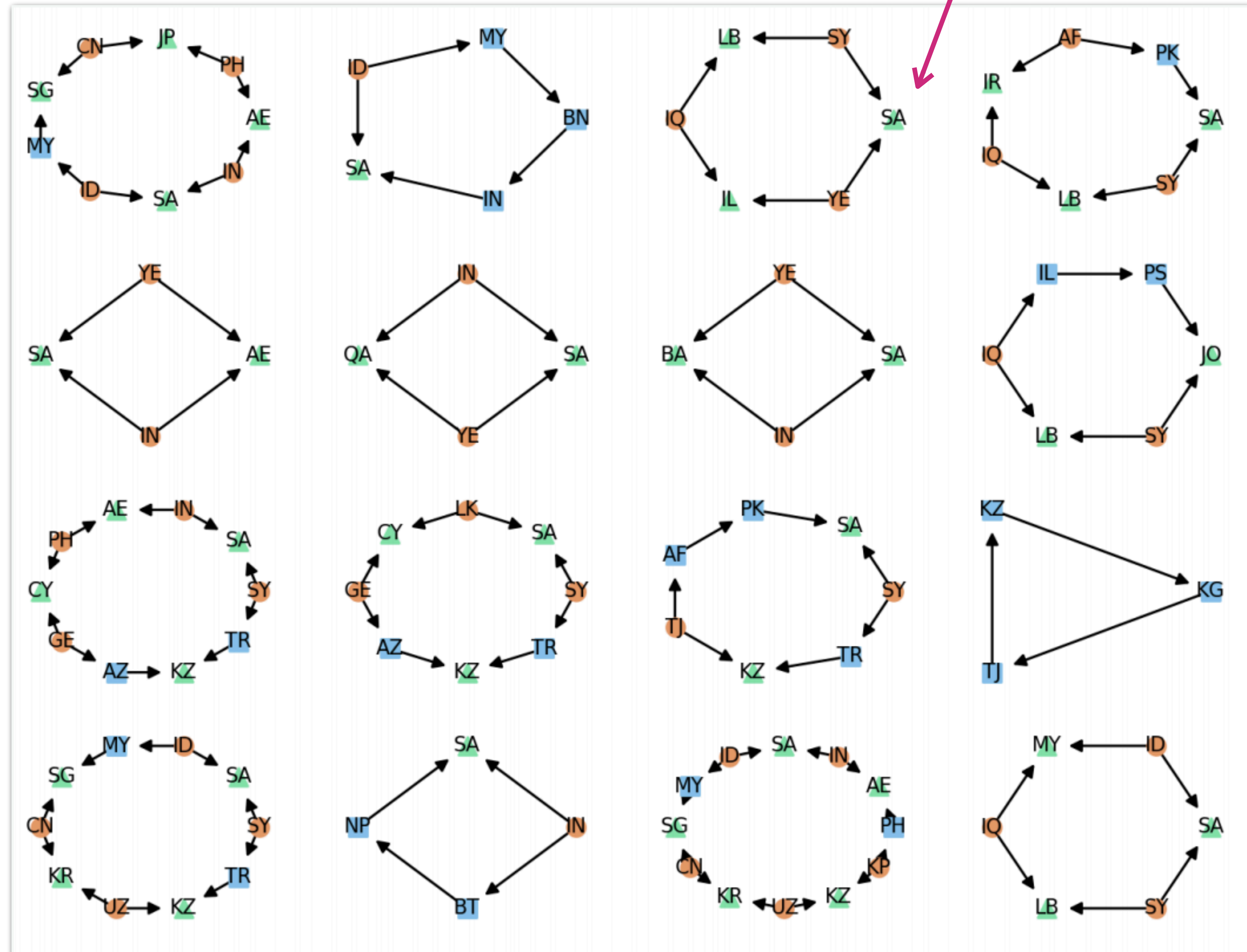
Application 3 of 3: Persistent Path Homology

- On the right 🖱️: Minimal cycles for persistent path homology on migration network
- Dataset 🗄️: UN's net migration network (a weighted directed graph)

Compute “minimal homology basis”

Topological analysis -> Geometric analysis!

2-letter country code



Beyond Persistent Homology

- Computation & math issues (e.g., do we really need all simplices before we can compute homology?)

Han Riess, “Beyond Persistent Homology: A Mathematical Guide.” Preprint (2019).

Justin Curry, Robert Ghrist & Vidi Nanda, “Discrete Morse Theory for Computing Cellular Sheaf Cohomology.” FoCM (2016).

Conclusion

- (see the whole slides)

Thanks!

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