USING TOPOLOGY TO MEASURE DYNAMICS OF BIOLOGICAL AGGREGATIONS

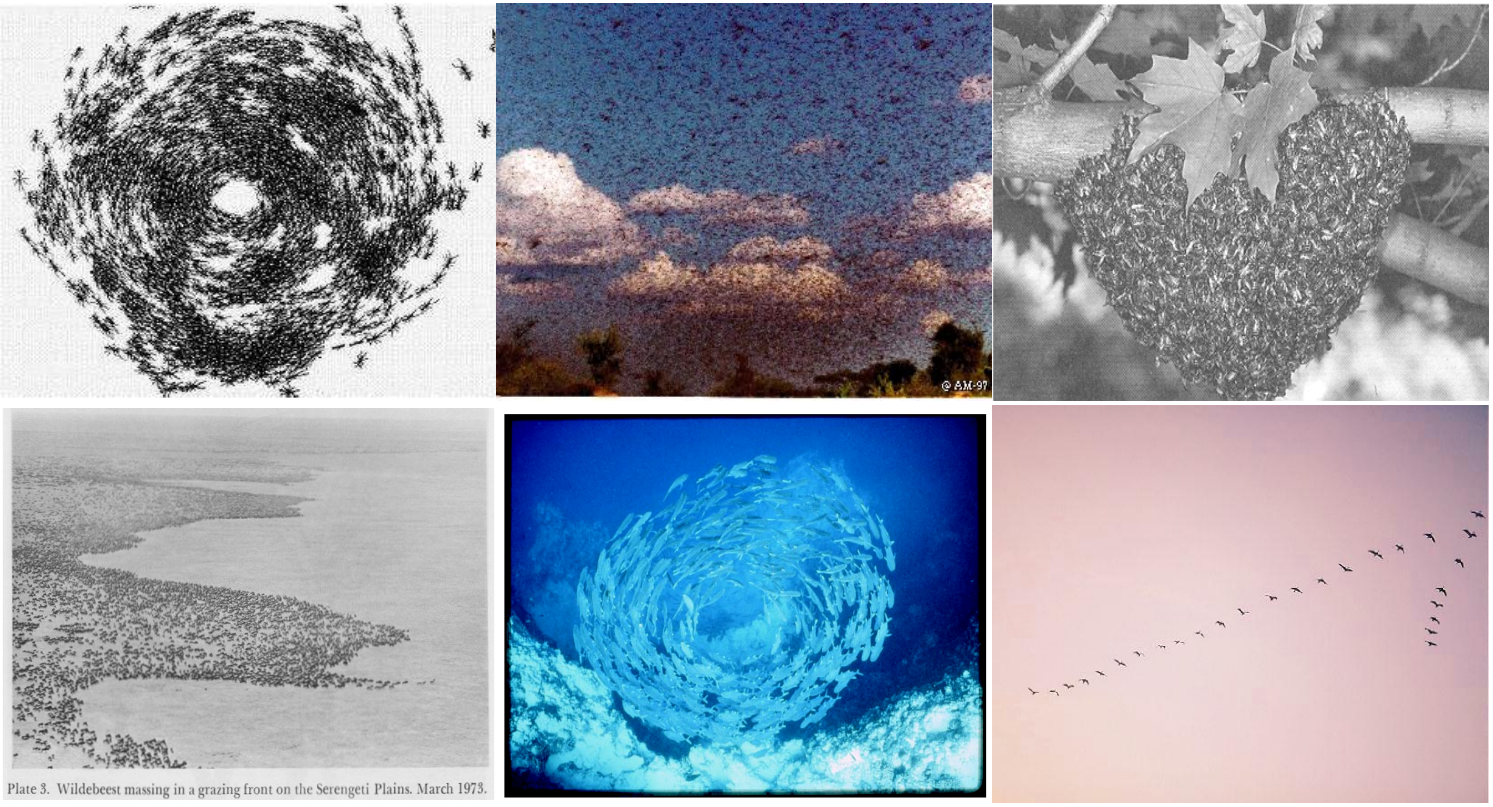
August 7, 2019

Lori Ziegelmeier, Macalester College

ICERM Workshop: Applied Mathematical Modeling with Topological Techniques

INTRODUCTION

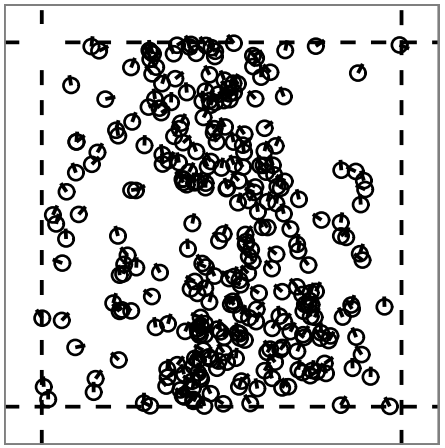
BIOLOGICAL AGGREGATIONS



In many natural systems, particles, organisms, or agents interact locally according to rules that produce aggregate behavior.

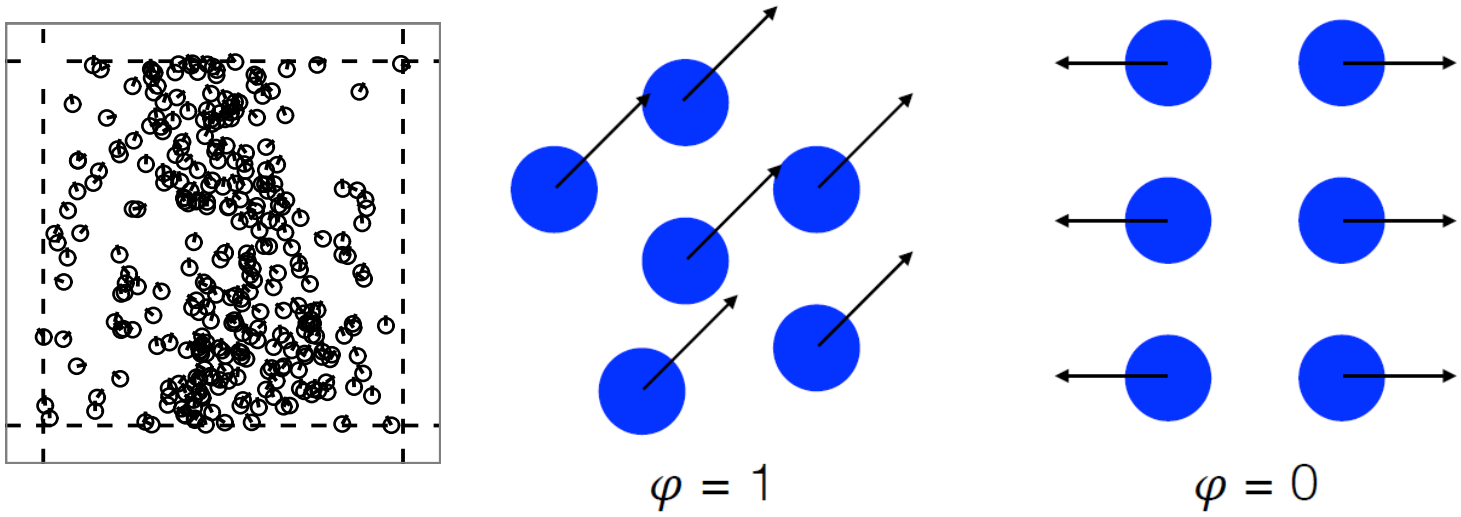
CLASSIC WAY TO ANALYZE BIOLOGICAL AGGREGATIONS

Alignment Order Parameter: $\varphi(t) = \frac{1}{Nv_0}\left|\sum_{i=1}^{N} \vec{v}_i(t)\right|$



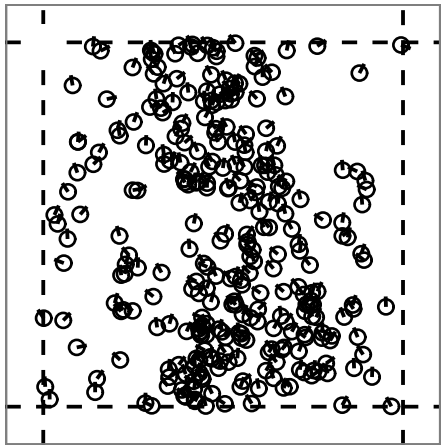
CLASSIC WAY TO ANALYZE BIOLOGICAL AGGREGATIONS

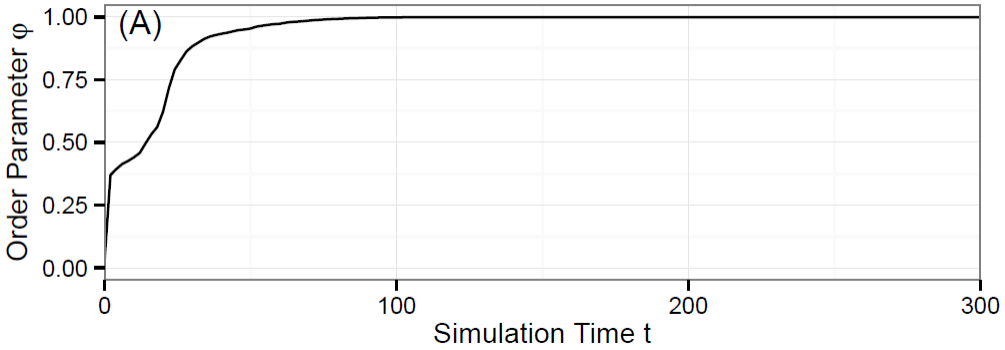
Alignment Order Parameter: $\varphi(t) = \frac{1}{Nv_0}\left|\sum_{i=1}^{N} \vec{v}_i(t)\right|$



CLASSIC WAY TO ANALYZE BIOLOGICAL AGGREGATIONS

Alignment Order Parameter: $\varphi(t) = \frac{1}{Nv_0}\left|\sum_{i=1}^{N} \vec{v}_i(t)\right|$

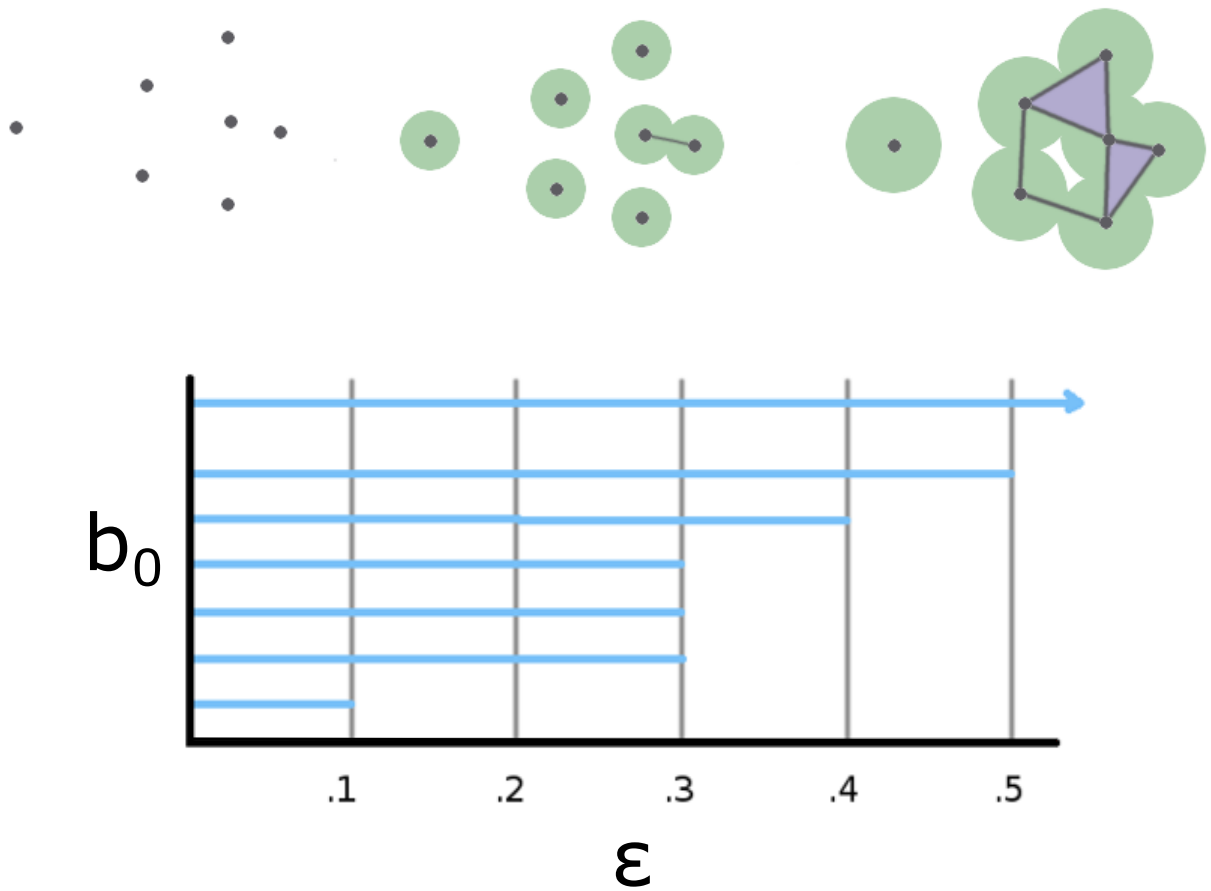




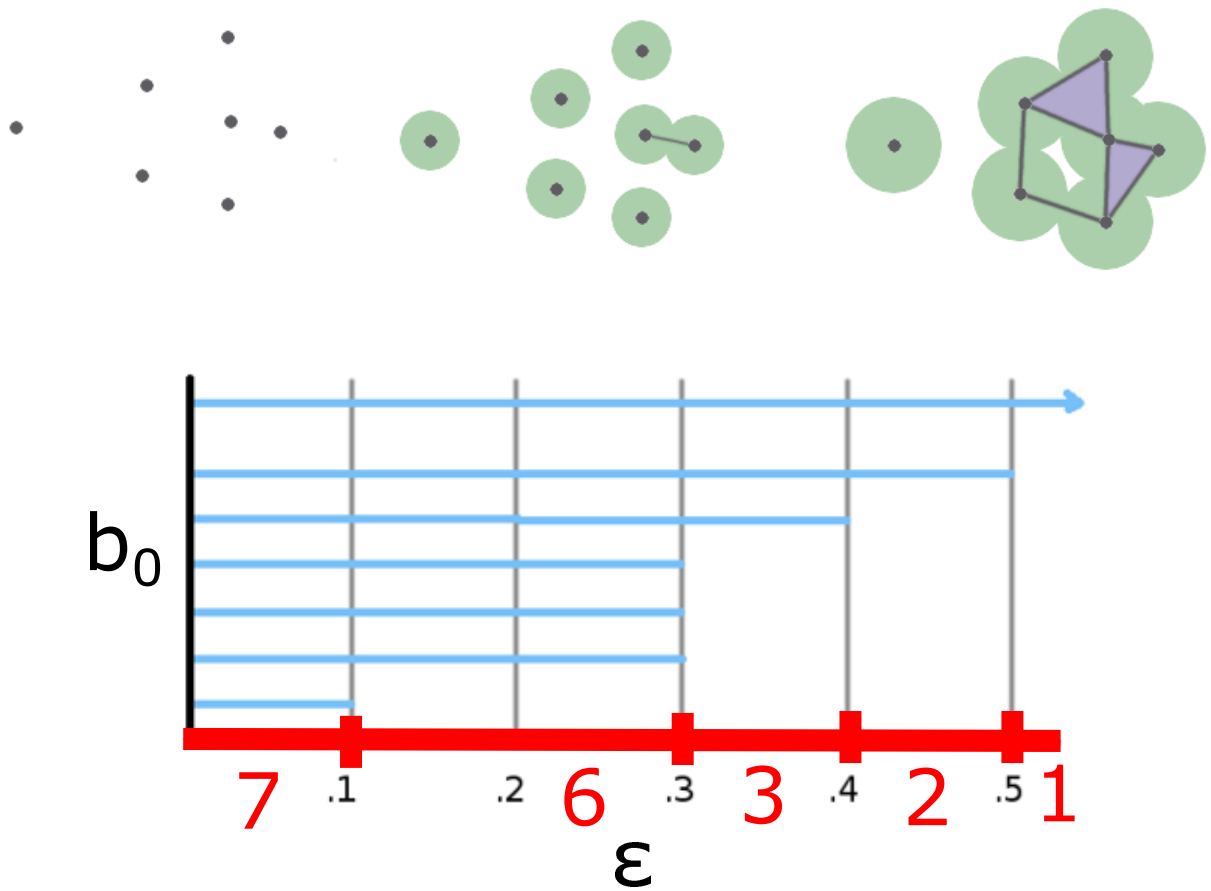
TOPOLOGICAL DATA ANALYSIS

1. Envision data as a point cloud
   - *e.g.* position-velocity for one snapshot in time
2. Create connections between proximate points
   - build simplicial complex
3. Determine topological structure of complex
   - compute homology (measure # holes)
4. Vary proximity parameter to assess different scales
   - calculate persistent homology

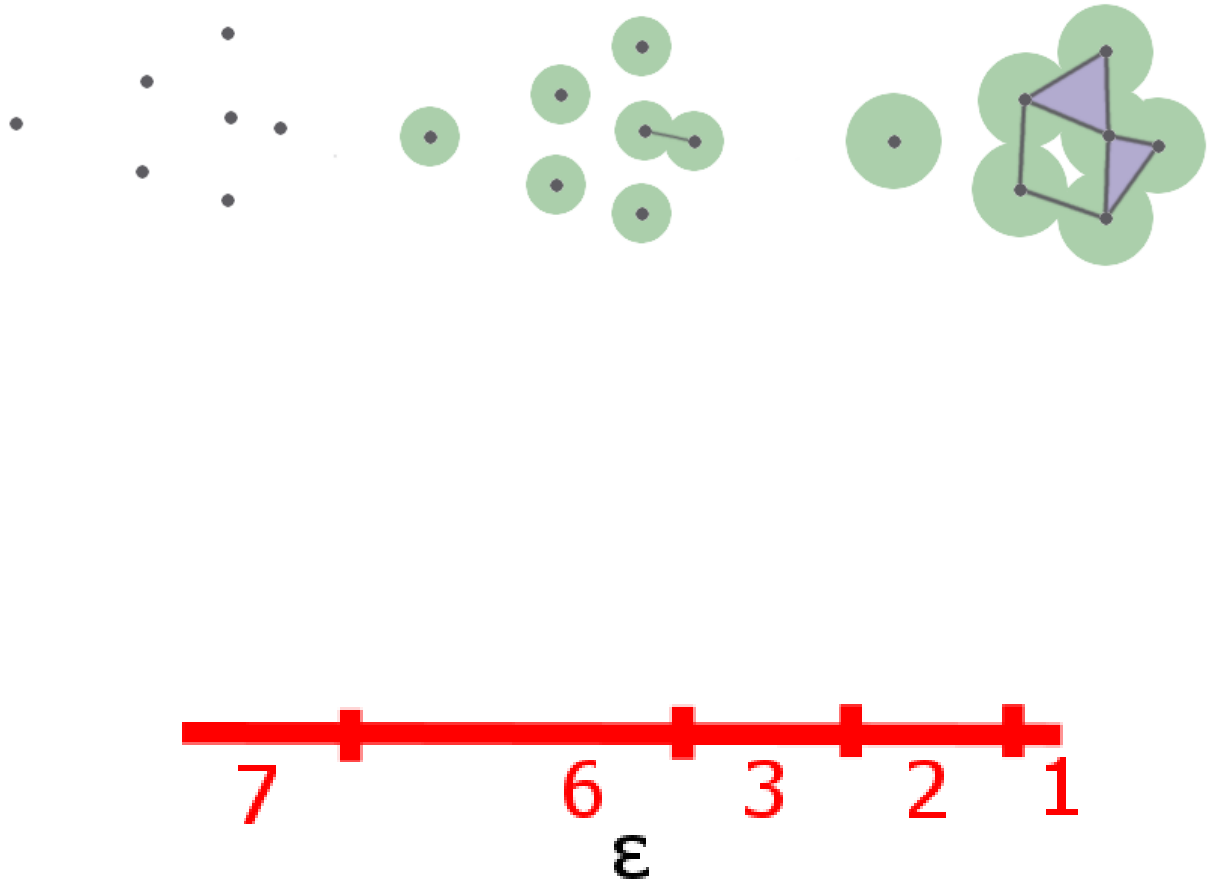
COMPUTE PERSISTENT HOMOLOGY



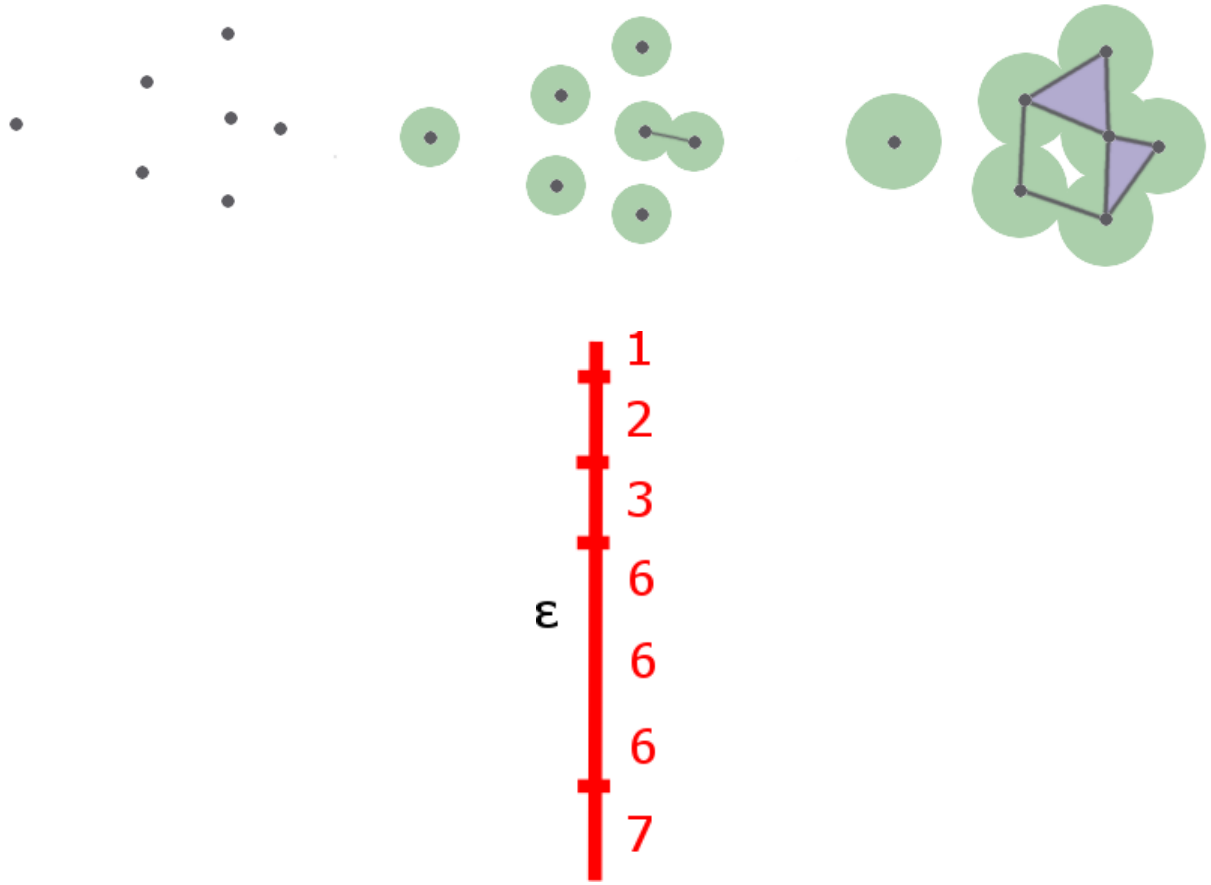
COMPUTE PERSISTENT HOMOLOGY



COMPUTE PERSISTENT HOMOLOGY



COMPUTE PERSISTENT HOMOLOGY



TOPOLOGICAL DATA ANALYSIS

1. Envision data as a point cloud
   - *e.g.* position-velocity for one snapshot in time

2. Create connections between proximate points
   - build simplicial complex

3. Determine topological structure of complex
   - compute homology (measure # holes)

4. Vary proximity parameter to assess different scales
   - calculate persistent homology

TOPOLOGICAL DATA ANALYSIS

1. Envision data as a point cloud
   - *e.g.* position-velocity for one snapshot in time

2. Create connections between proximate points
   - build simplicial complex

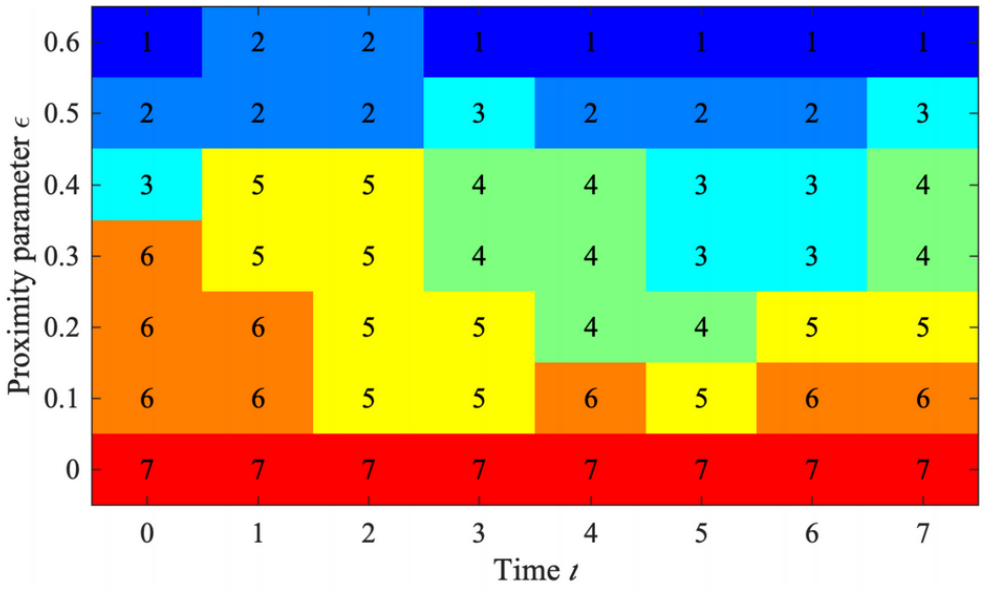
3. Determine topological structure of complex
   - compute homology (measure # holes)

4. Vary proximity parameter to assess different scales
   - calculate persistent homology

5. **Measure topology as time evolves.**
   - **Crocker plots**

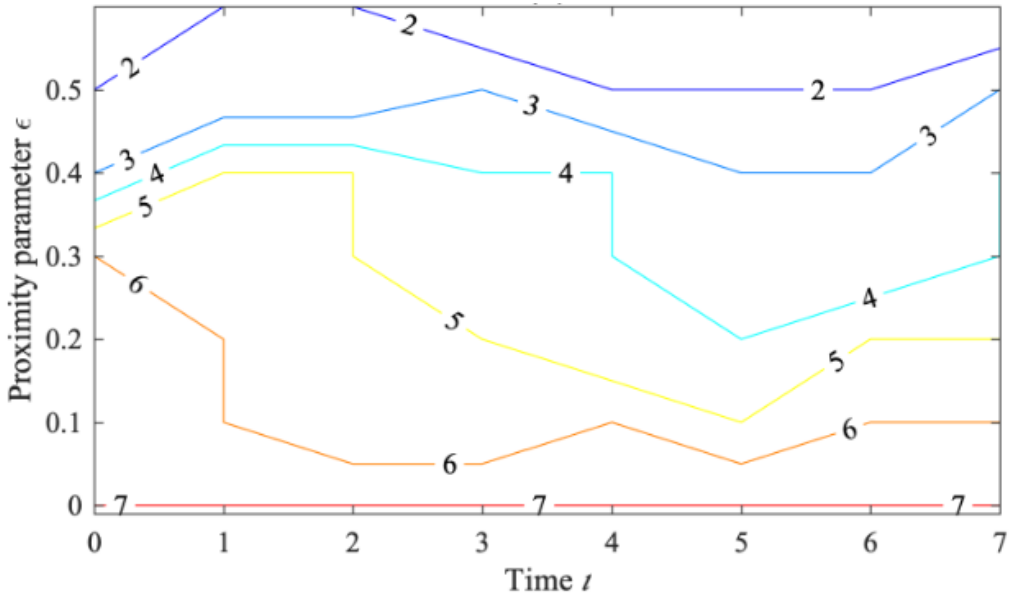
EVOLVE IN TIME

Compute the kth Betti number $b_k(\varepsilon, t)$,



EVOLVE IN TIME

Compute the kth Betti number $b_k(\varepsilon, t)$,



CROCKER plot

Contour Realization Of Computed K-dimensional hole Evolution in the Rips complex (CROCKER)

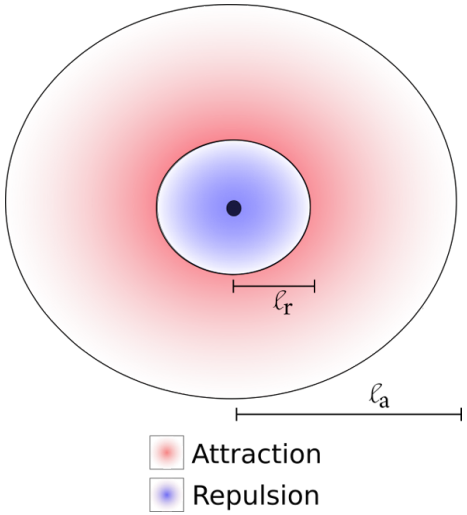
(Topaz, Z., Halverson 2015) Topological Data Analysis of Biological Aggregation Models

CROCKER AS EXPLORATORY TOOL

D'ORSOGNA MODEL

- Dynamical system describing motion of interacting point particles in an unbounded plane in continuous time.
- Model written as:

$$
\begin{aligned}
\dot{\vec{x}}_i &= \vec{v}_i \qquad\qquad i = 1, \ldots, N \\
m\dot{\vec{v}}_i &= \left(\alpha - \beta|\vec{v}_i|^2\right)\vec{v}_i - \nabla_i U_i \\
U_i &= \sum_{j \neq i} C_r \mathrm{e}^{-|\vec{x}_i - \vec{x}_j|/\ell_r} - C_a \mathrm{e}^{-|\vec{x}_i - \vec{x}_j|/\ell_a}
\end{aligned}
$$

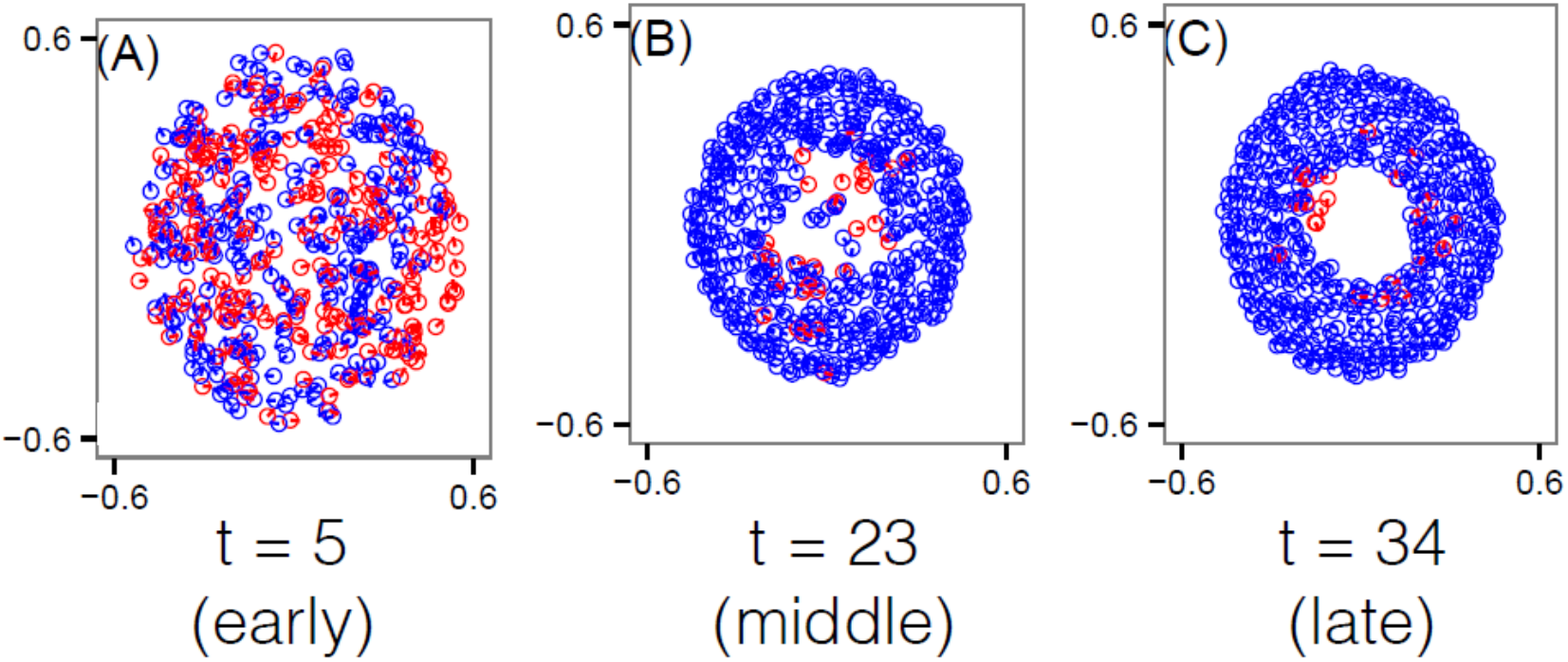


- After nondimensionalization, we have 4 parameters:

$$\alpha, \beta, C = \frac{C_r}{C_a}, \ell = \frac{\ell_r}{\ell_a}$$

(D'Orsogna, et al 2006) Self-Propelled Particles with Soft-Core Interactions: Patterns, Stability, and Collapse

SNAPSHOTS IN TIME



$\alpha = 1.5, \beta = 0.5, C = 2, \ell = 0.25$ with $N = 500$ particles

Clockwise motion

Counter Clockwise motion

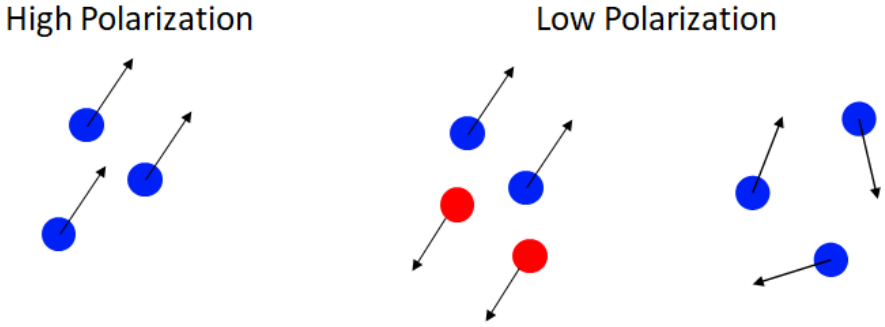
ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

Are the particles moving in the same direction?



ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

Angular Momentum:

$M_{ang}(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{r}_i(t) \times \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$

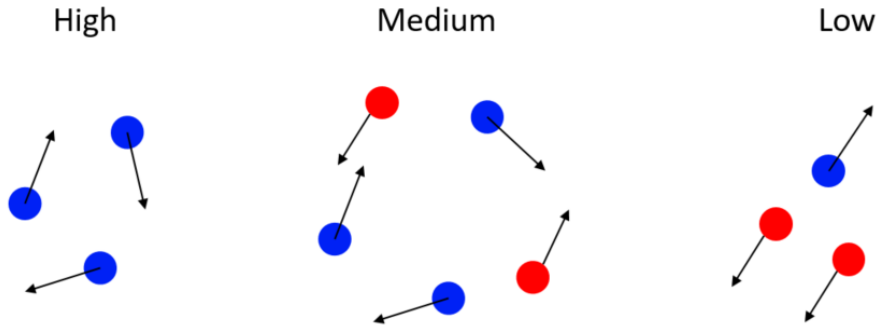
ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

Angular Momentum:

$M_{ang}(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{r}_i(t) \times \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$

Are the particles rotating (in the same direction)?



ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

Angular Momentum:

$M_{ang}(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{r}_i(t) \times \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$

Absolute Angular Momentum:

$M_{abs}(t) = \left| \frac{\sum_{i=1}^{N} |\mathbf{r}_i(t) \times \mathbf{v}_i(t)|}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$

ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

Angular Momentum:

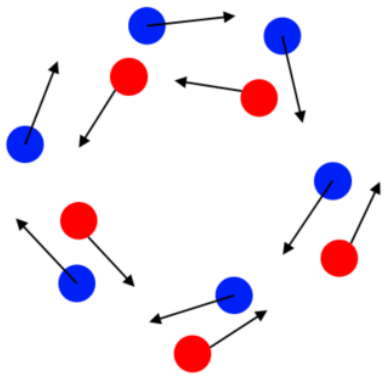
$$M_{ang}(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{r}_i(t) \times \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$$

Absolute Angular Momentum:

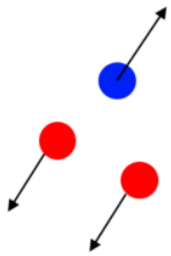
$$M_{abs}(t) = \left| \frac{\sum_{i=1}^{N} |\mathbf{r}_i(t) \times \mathbf{v}_i(t)|}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$$

Are the particles rotating?

High absolute angular momentum



Low absolute angular momentum



ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

Angular Momentum:
$M_{ang}(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{r}_i(t) \times \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$

Absolute Angular Momentum:
$M_{abs}(t) = \left| \frac{\sum_{i=1}^{N} |\mathbf{r}_i(t) \times \mathbf{v}_i(t)|}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$

Average Nearest Neighbor Distance:

$$D_{nn}(t) = \frac{1}{N} \sum_{i=1}^{N} \min_{1 \le j \le N} |\mathbf{x}_i(t) - \mathbf{x}_j(t)|$$

ORDER PARAMETERS TO SUMMARIZE COLLECTIVE BEHAVIOR

Polarization: $P(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{v}_i(t)|} \right|$

Angular Momentum:

$$M_{ang}(t) = \left| \frac{\sum_{i=1}^{N} \mathbf{r}_i(t) \times \mathbf{v}_i(t)}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$$

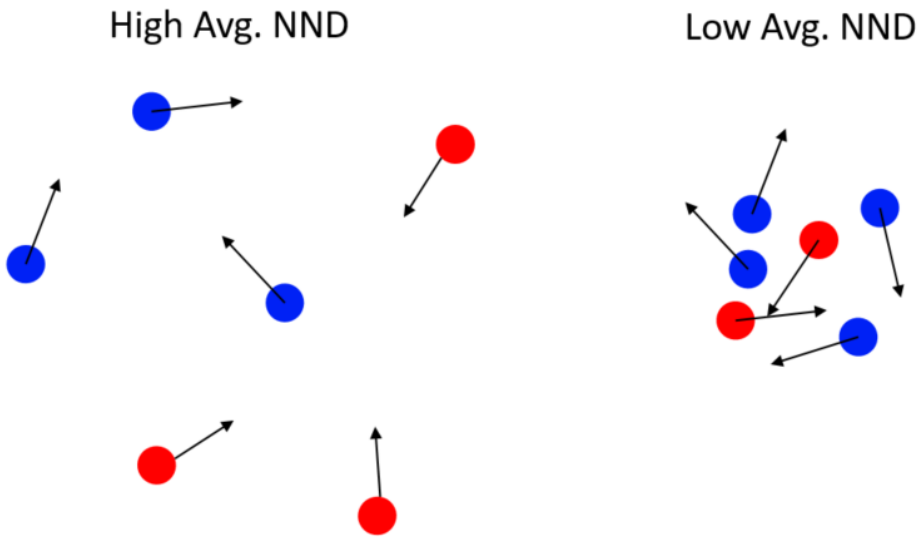
Absolute Angular Momentum:

$$M_{abs}(t) = \left| \frac{\sum_{i=1}^{N} |\mathbf{r}_i(t) \times \mathbf{v}_i(t)|}{\sum_{i=1}^{N} |\mathbf{r}_i(t)||\mathbf{v}_i(t)|} \right|$$

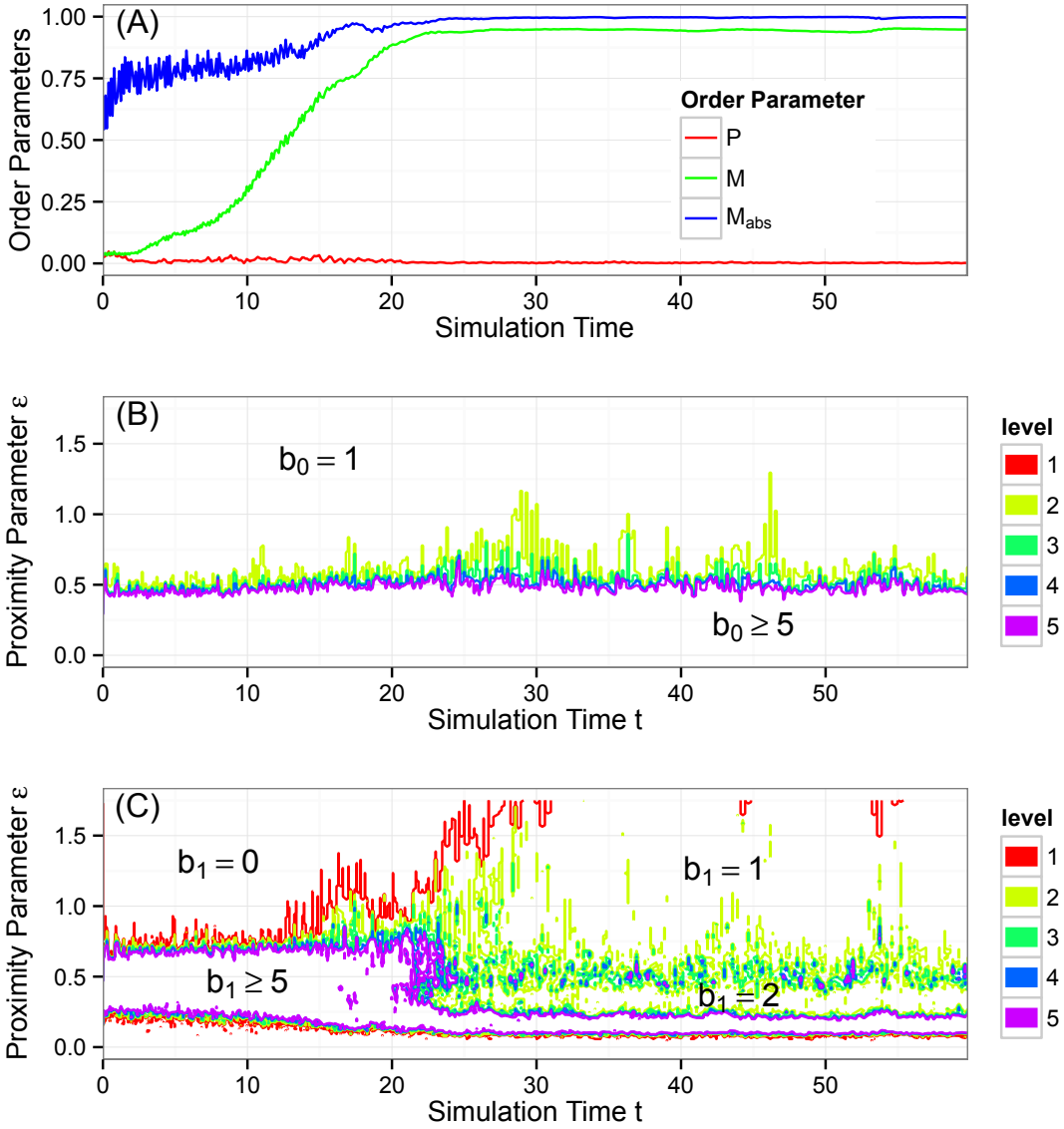
Average Nearest Neighbor Distance:

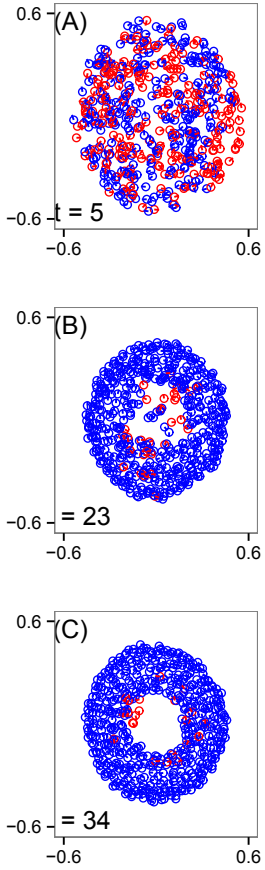
$$D_{nn}(t) = \frac{1}{N} \sum_{i=1}^{N} \min_{1 \le j \le N} |\mathbf{x}_i(t) - \mathbf{x}_j(t)|$$

How close are the particles?

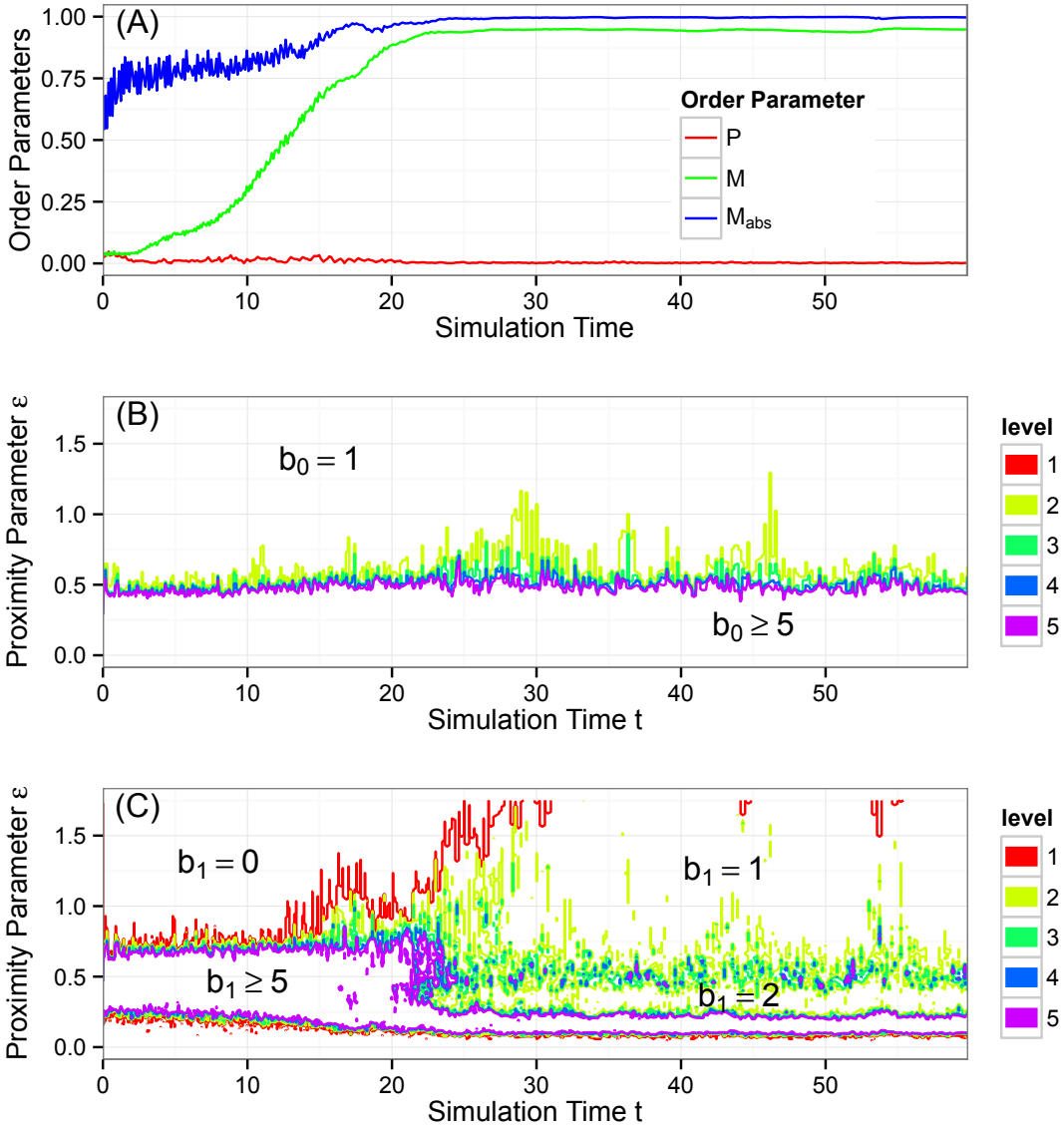


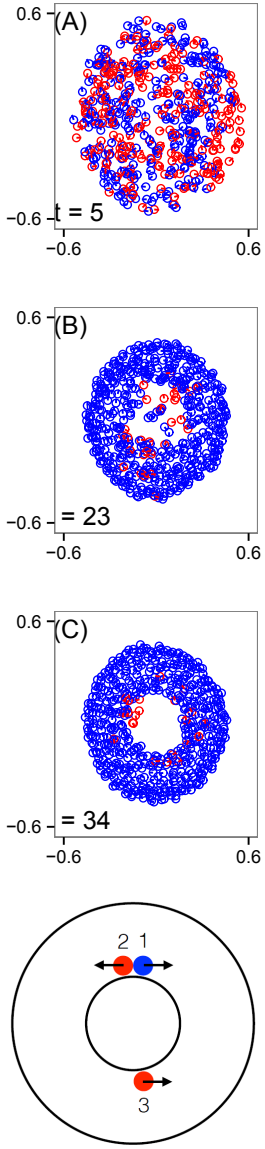
D'ORSOGNA SIMULATION ANALYSIS





D'ORSOGNA SIMULATION ANALYSIS





PARAMETER IDENTIFICATION

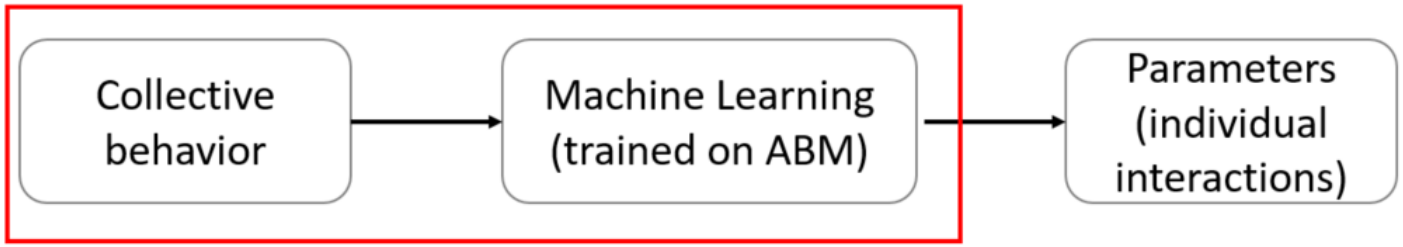
QUESTION OF INTEREST

Forward Problem:

QUESTION OF INTEREST

Forward Problem:

Inverse Problem:



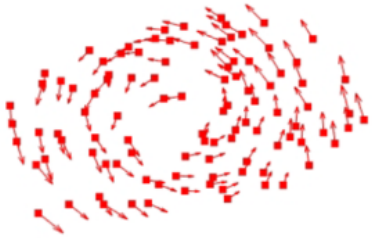
Research Question

What is an informative way to summarize collective behavior for machine learning techniques?

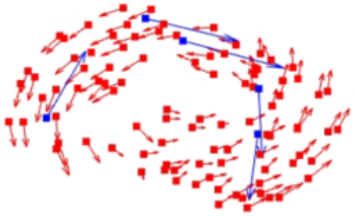
PHENOTYPES IN THE D'ORSOGNA MODEL

Different patterns emerge by altering parameters C and ℓ

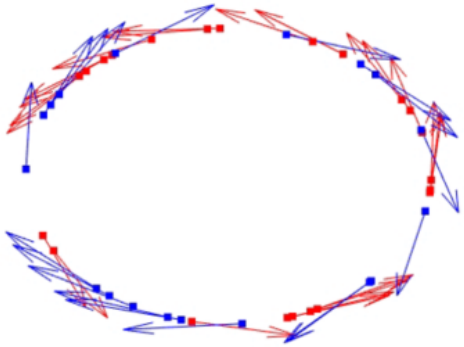
Single Mill



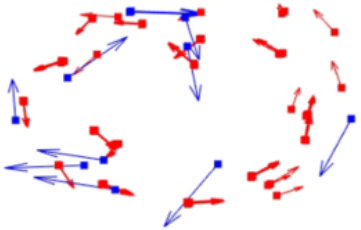
Double Mill



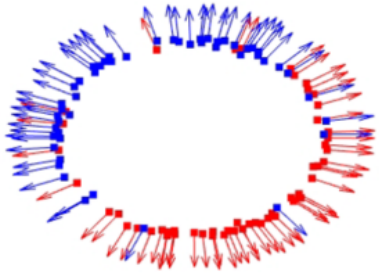
Double Ring



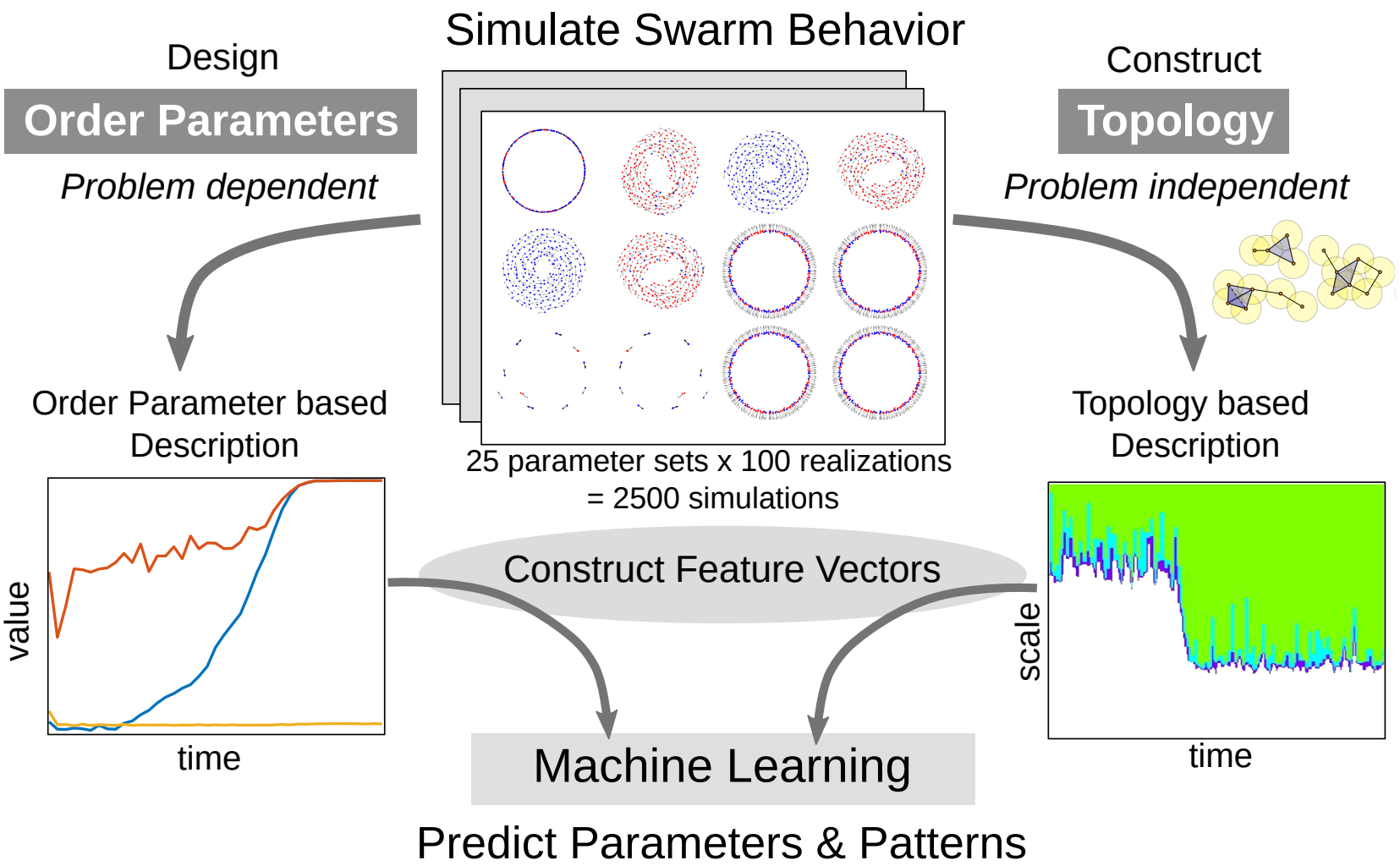
Collective Swarm



Escape

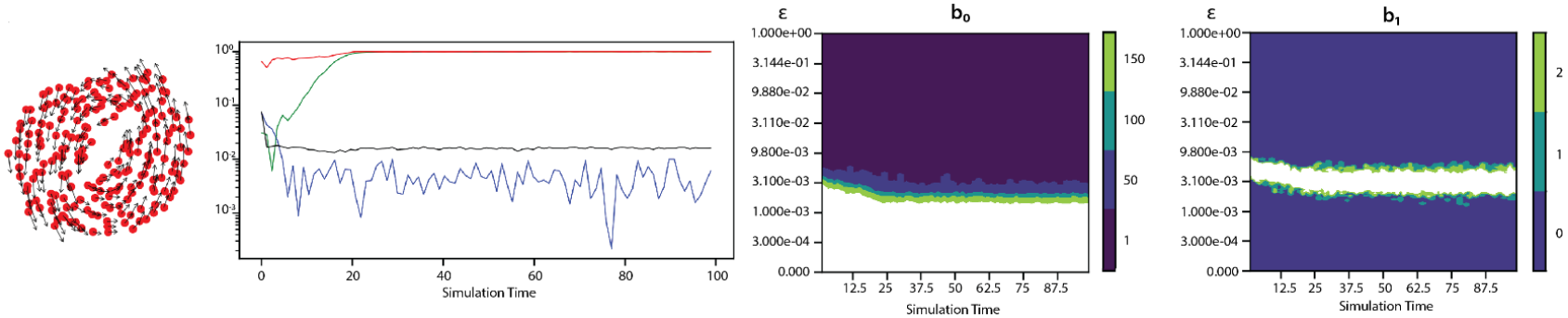


PIPELINE

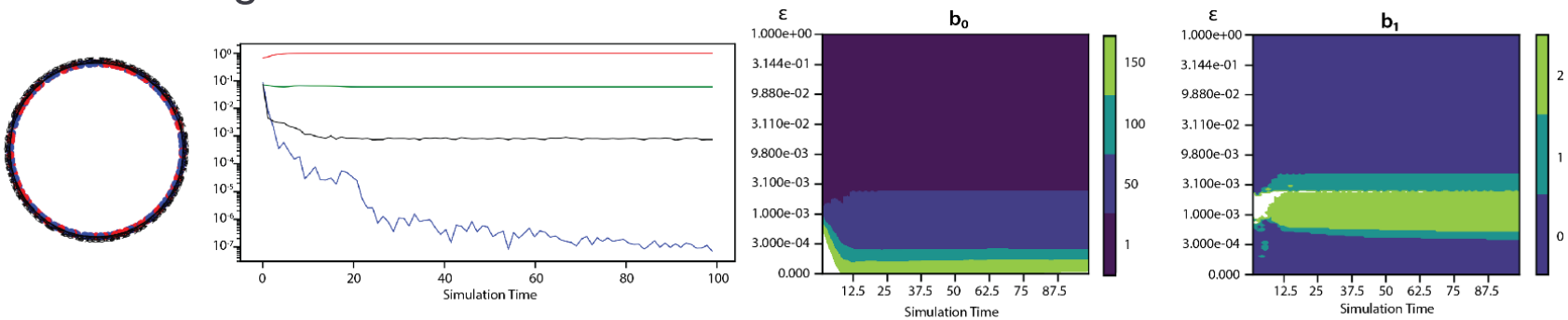

Simulate Swarm Behavior
Design
Order Parameters
Problem dependent
Construct
Topology
Problem independent
Order Parameter based Description
25 parameter sets x 100 realizations
= 2500 simulations
Topology based Description
value
time
Construct Feature Vectors
scale
time
Machine Learning
Predict Parameters & Patterns

PHENOTYPES AND FEATURE VECTORS

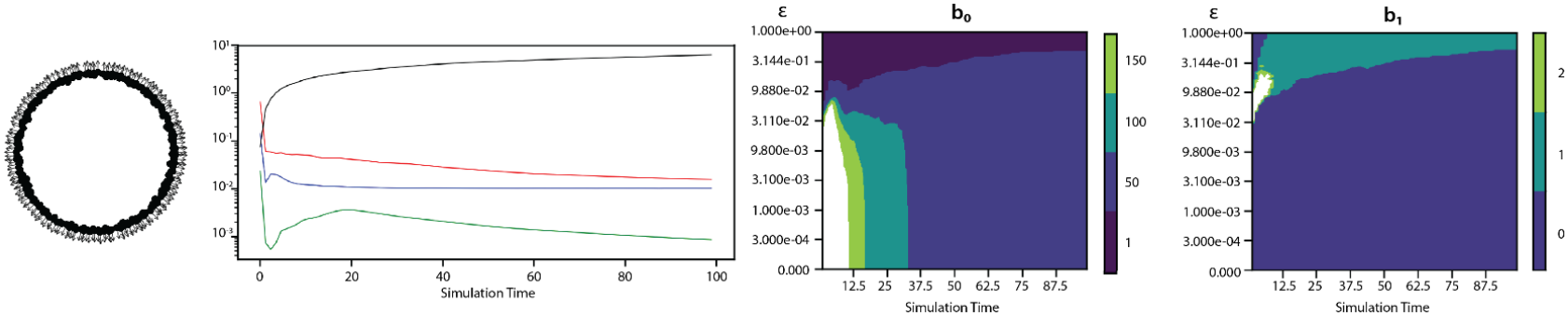
Single Mill:



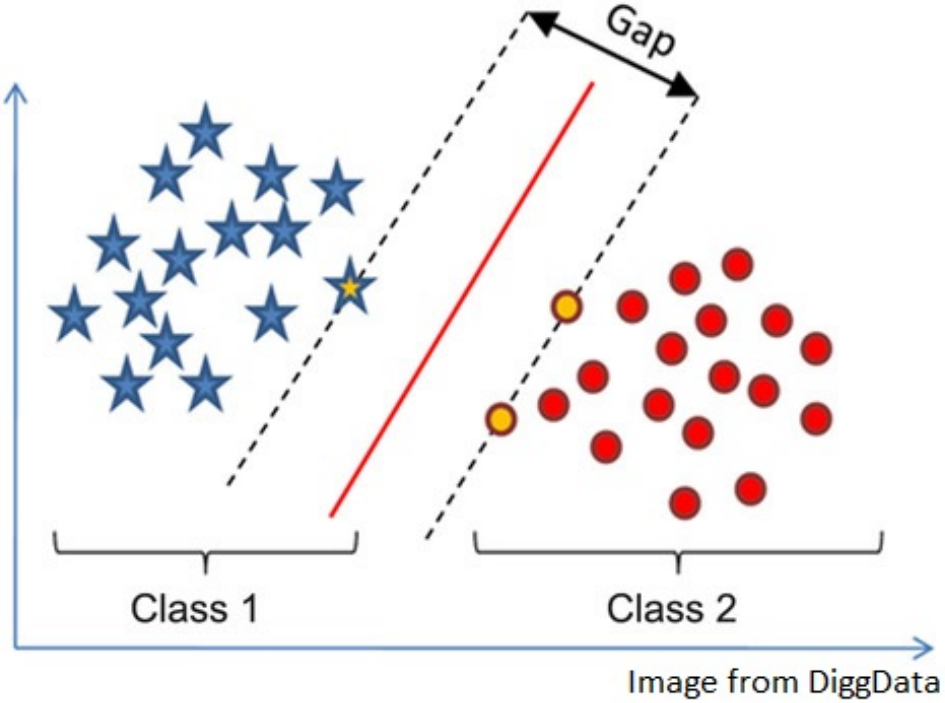
Double Ring:



Escape:



SUPPORT VECTOR MACHINE



- Supervised machine learning algorithm
- 5-fold cross validation, with each training simulation labeled with (C, ℓ), 20% of data used for each test
- Accuracy $= \dfrac{\text{out-of-sample simulations with } (C,\ell) \text{ correct}}{\text{out-of-sample simulations}}$

CLASSIFICATION RESULTS

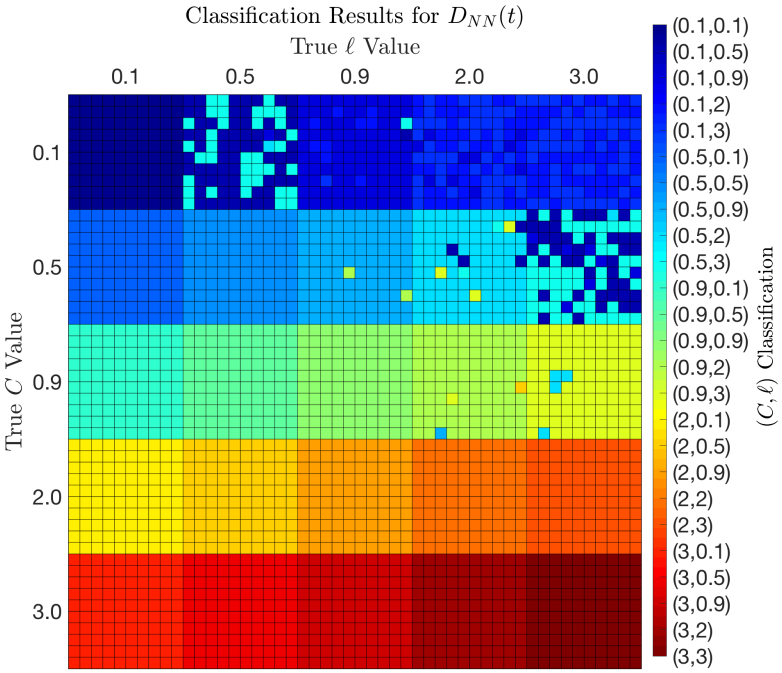
Summary	Feature	Dimension	Accuracy
Order Parameters	$P(t)$	87	57.7%
	$M_{ang}(t)$	87	34.4%
	$M_{abs}(t)$	87	68.0%
	$D_{NN}(t)$	87	91.1%
	All	4*87	89.2%
TDA (time-delayed position)	b_0	200*86	99.6%
	b_1	200*86	99.3%
	b_0 & b_1	2*200*86	99.1%

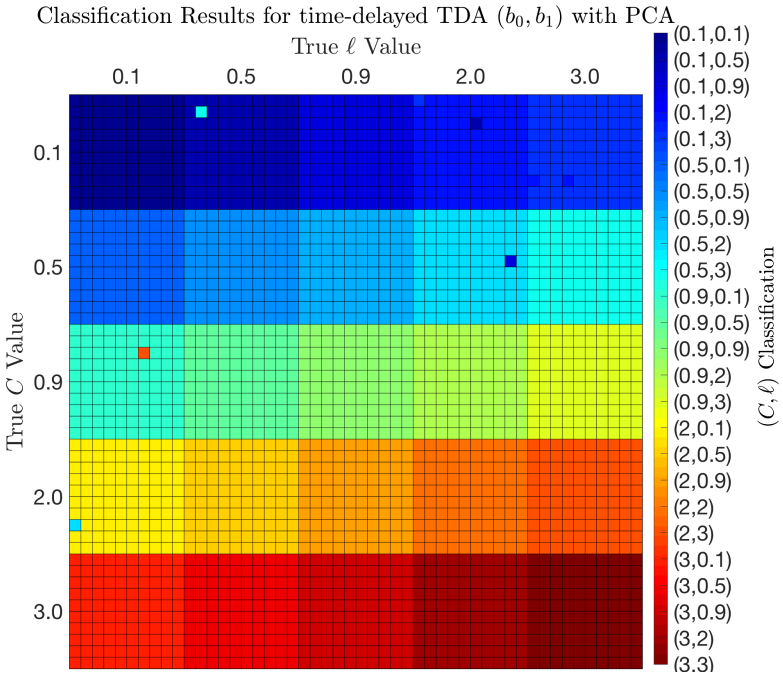
CLASSIFICATION RESULTS

Summary	Feature	Dimension	Accuracy
Order Parameters	$P(t)$	87	57.7%
	$M_{ang}(t)$	87	34.4%
	$M_{abs}(t)$	87	68.0%
	$D_{NN}(t)$	87	91.1%
	All	4*87	89.2%
TDA (time-delayed position)	b_0	200*86	99.6%
	b_1	200*86	99.3%
	b_0 & b_1	2*200*86	99.1%

Summary	Feature	Dimension	Accuracy
Order Parameters	$P(t)$ (PCA)	3	46.7%
	$M_{ang}(t)$ (PCA)	3	30.0%
	$M_{abs}(t)$ (PCA)	3	58.8%
	$D_{NN}(t)$ (PCA)	3	81.5%
	All (PCA)	3	68.6%
TDA (time-delayed position)	b_0 (PCA)	87	99.7%
	b_1 (PCA)	87	99.9%
	b_0 & b_1 (PCA)	87	99.7%
	b_0 (PCA)	3	89.7%
	b_1 (PCA)	3	82.8%
	b_0 & b_1 (PCA)	3	89.6%

CLASSIFICATION RESULTS





(Bhaskar, Manhart, Milzman, Nardini, Storey, Topaz, Z. forthcoming) Analyzing Collective Motion with Machine Learning and Topology

ASSESSING MODEL VALIDITY

MOVEMENT OF PEA APHIDS

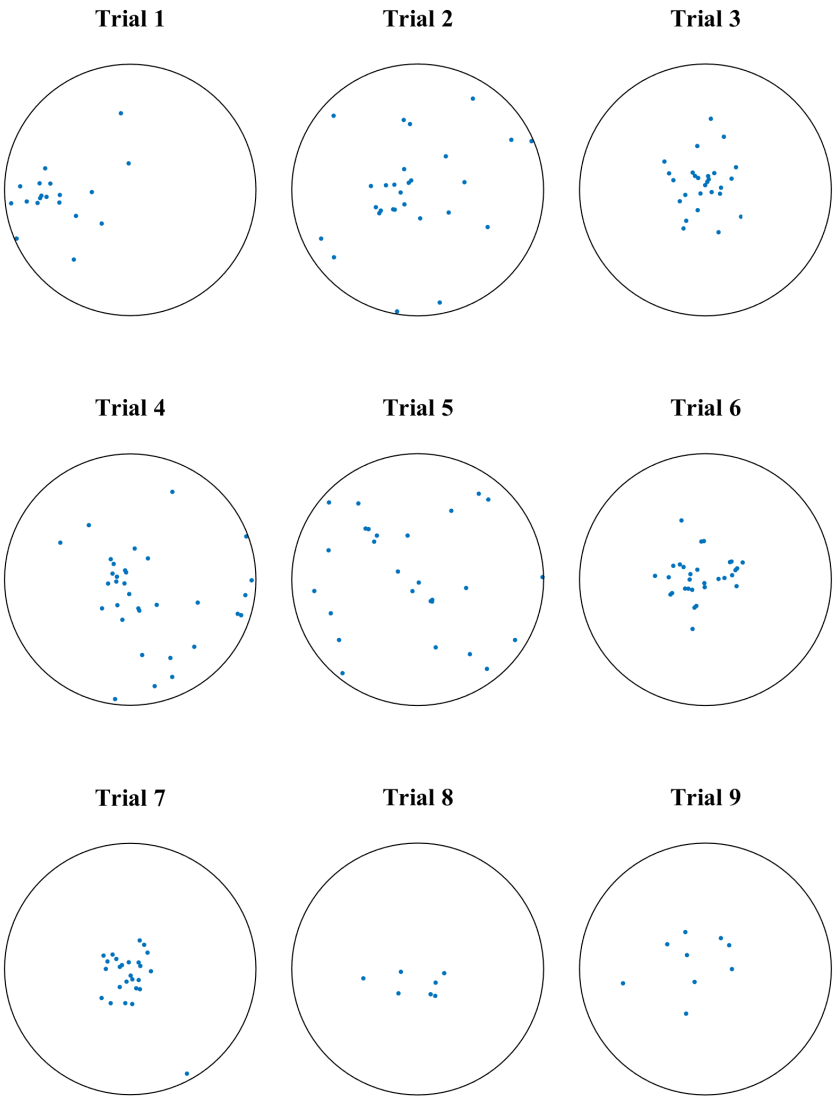
OPEN ACCESS Freely available online

PLOS | ONE

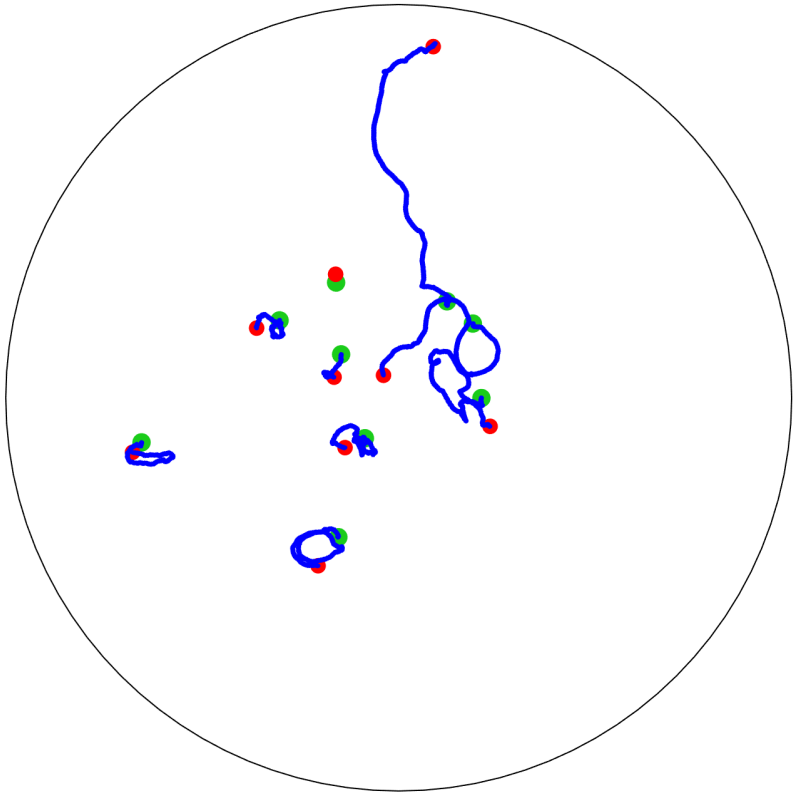
Social Aggregation in Pea Aphids: Experiment and Random Walk Modeling

Christa Nilsen[1], John Paige[1], Olivia Warner[1], Benjamin Mayhew[1], Ryan Sutley[1], Matthew Lam[2], Andrew J. Bernoff[2], Chad M. Topaz[1]*

MOVEMENT OF PEA APHIDS

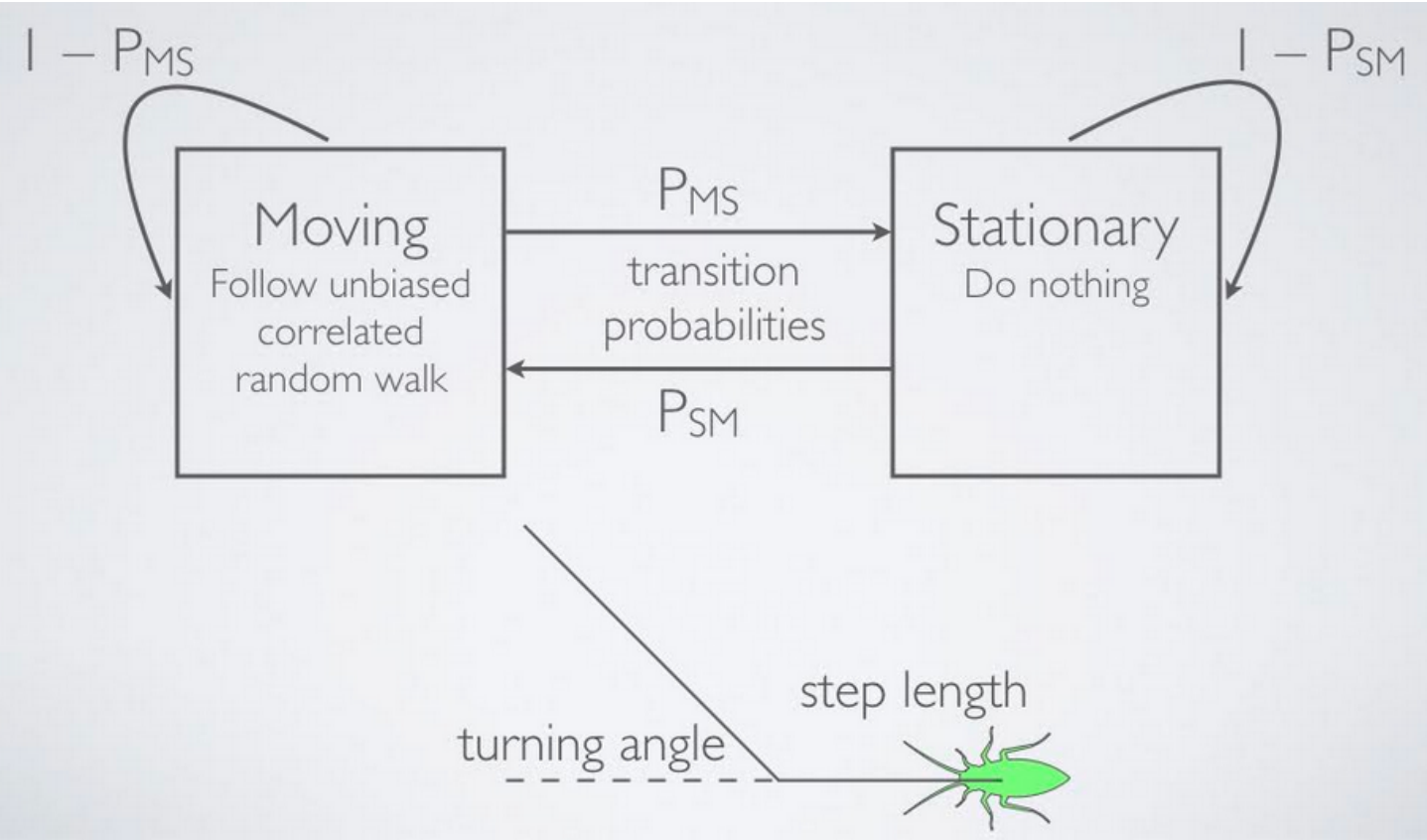


MOVEMENT OF PEA APHIDS



PEA APHID MODELS

- Classifies each aphid according to two motion states, moving or stationary.
- Transitions between these states are probabilistic, depending on distance *d* to each aphid's nearest neighbor.



PEA APHID MODELS

- Classifies each aphid according to two motion states, moving or stationary.
- Transitions between these states are probabilistic, depending on distance d to each aphid's nearest neighbor.
- Model written as:
  - Probability of transition state

$$P_{MS}(d) = P_{MS}^{\infty} + \left(P_{MS}^{0} - P_{MS}^{\infty}\right) \mathrm{e}^{-d/d_{MS}}$$

$$P_{SM}(d) = P_{SM}^{0} \mathrm{e}^{-d/d_{SM}} + P_{SM}^{\infty} \frac{d}{d + \Delta_{SM}}$$

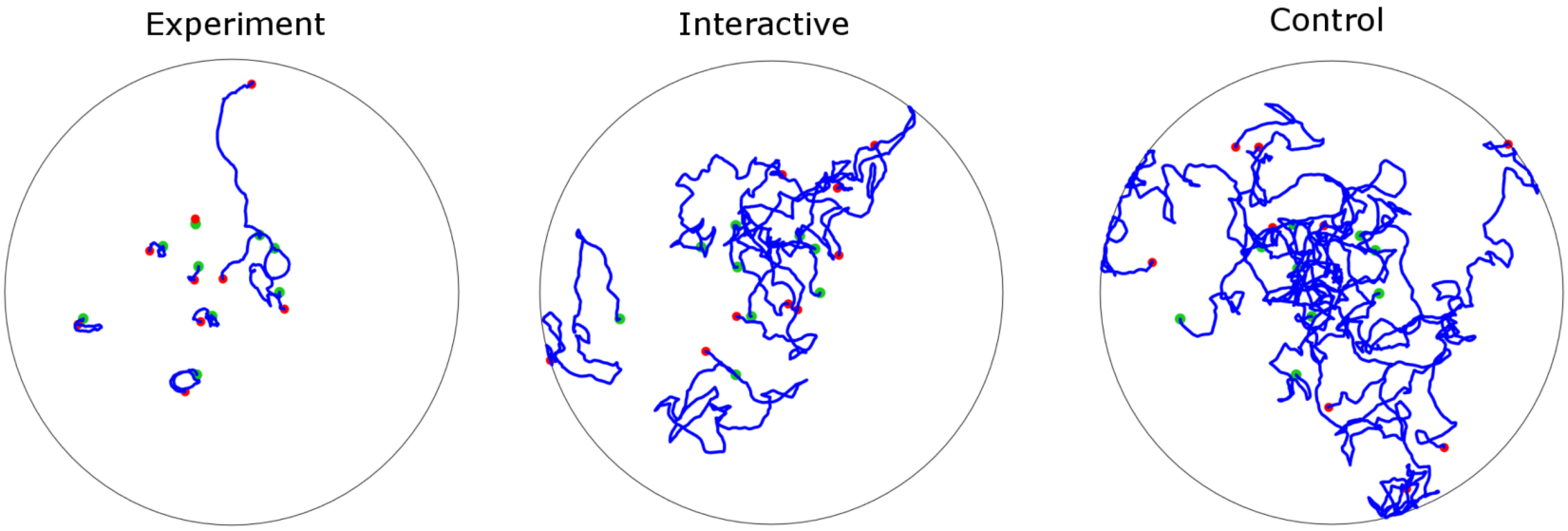
  - Step length ℓ

$$\ell(d) = \ell^{\infty} + \left(\ell^{0} - \ell^{\infty}\right) \mathrm{e}^{-d/d_{\ell}}$$

  - Turning angle θ drawn from a wrapped Cauchy distribution centered at zero, with parameter $\rho(d)$ controlling the spread of the distribution.

PEA APHID MODELS

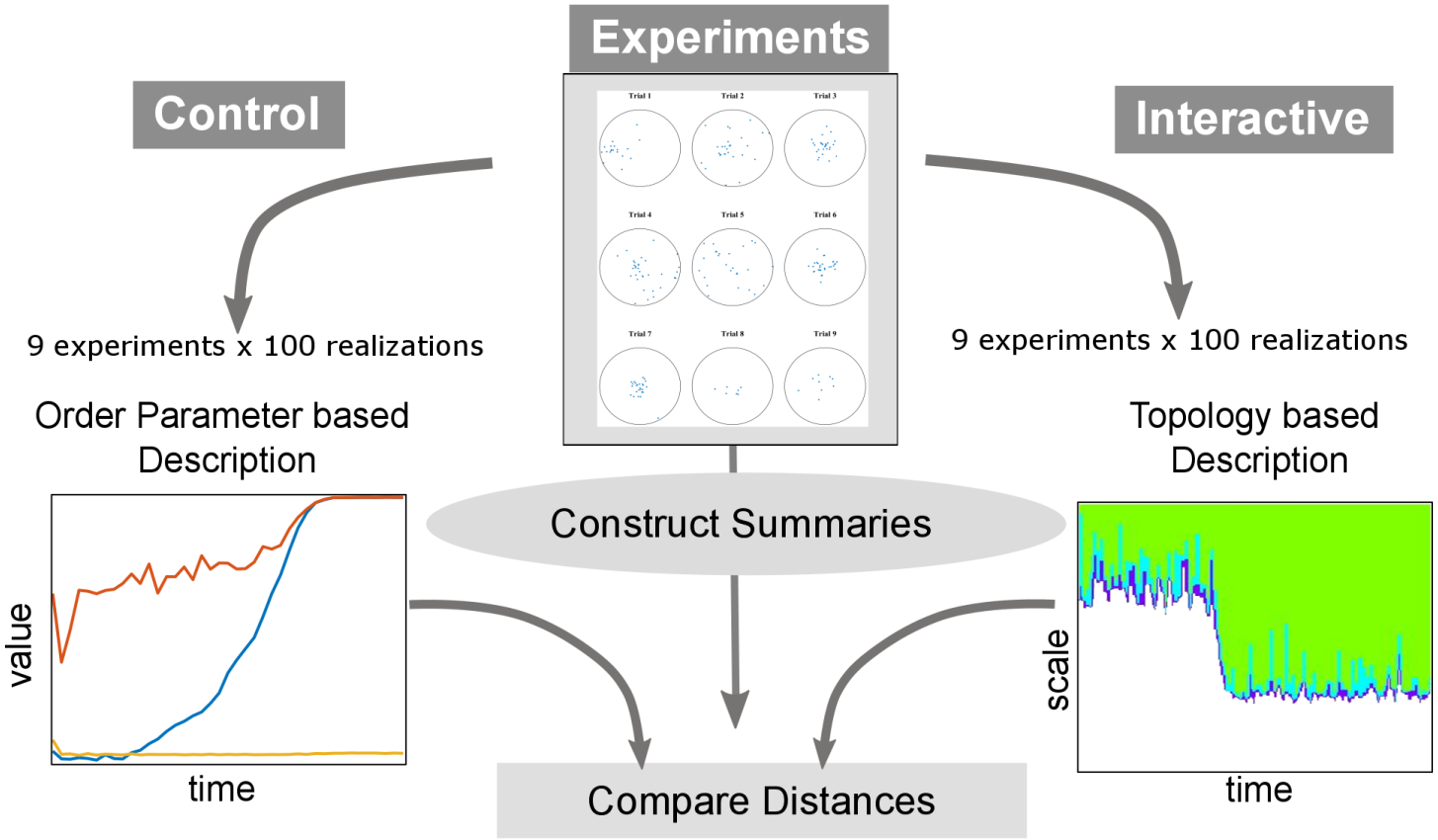
- Classifies each aphid according to two motion states, moving or stationary.
- Transitions between these states are probabilistic, depending on distance d to each aphid's nearest neighbor.
- Two models: Interactive and Noninteractive (Control)



ASSESSING MODEL VALIDITY

Goal:

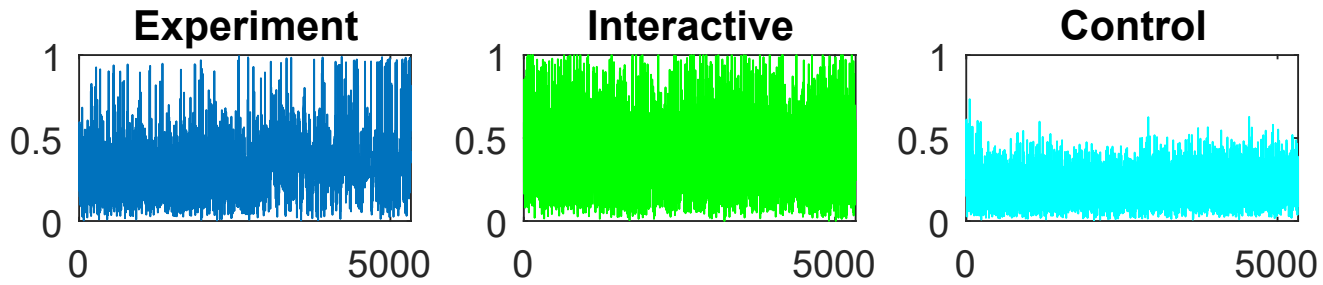
Use order parameters and crocker plots to compare each of the interactive and control models to experimental data



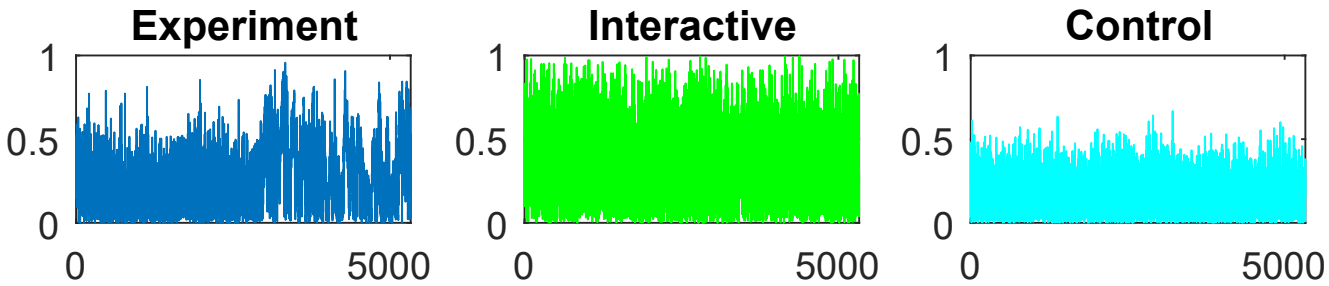
Two Sample t-Test to Assess Model Validity

ORDER PARAMETERS OF EXPERIMENT AND SIMULATIONS

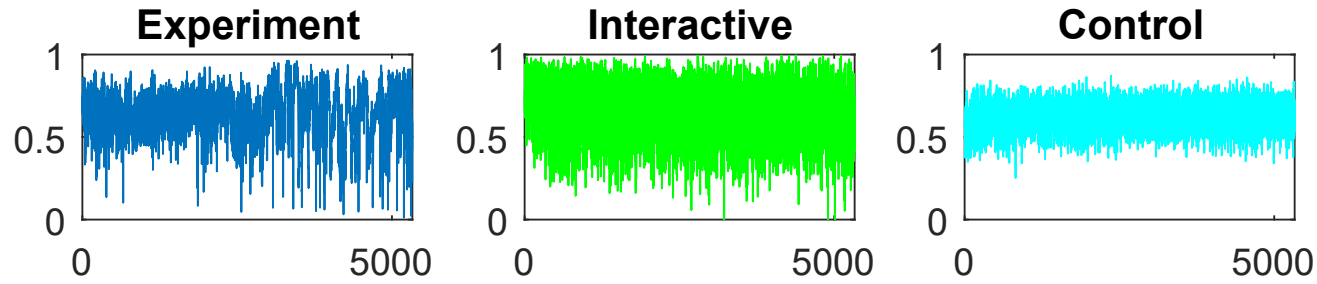
Polarization



Angular Momentum

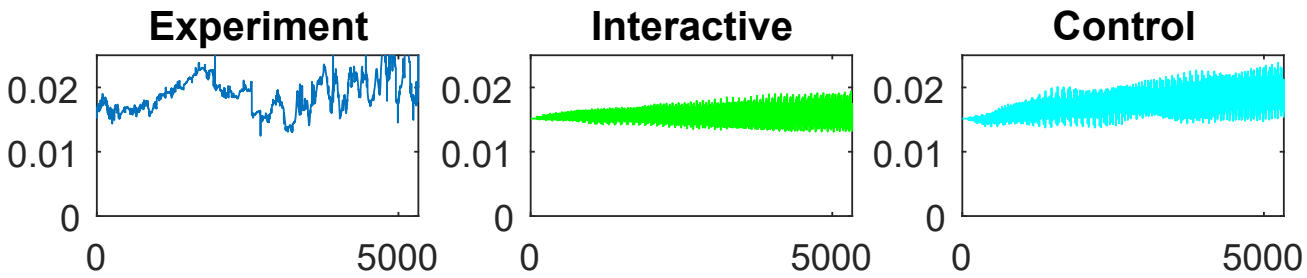


Absolute Angular Momentum

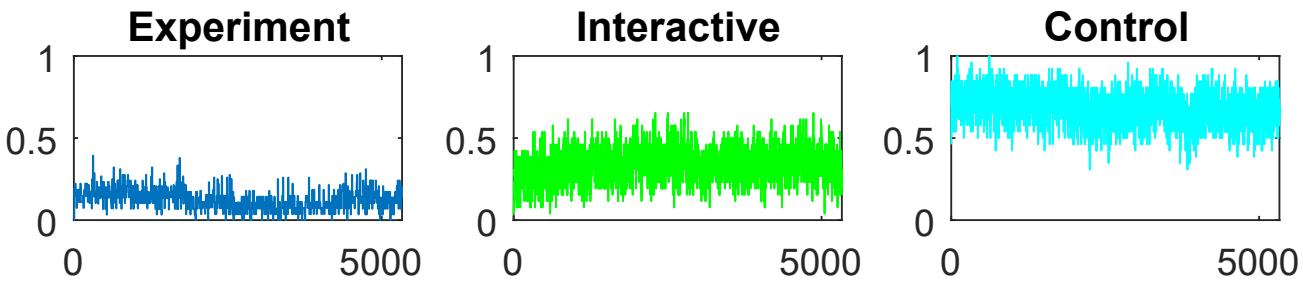


ORDER PARAMETERS OF EXPERIMENT AND SIMULATIONS

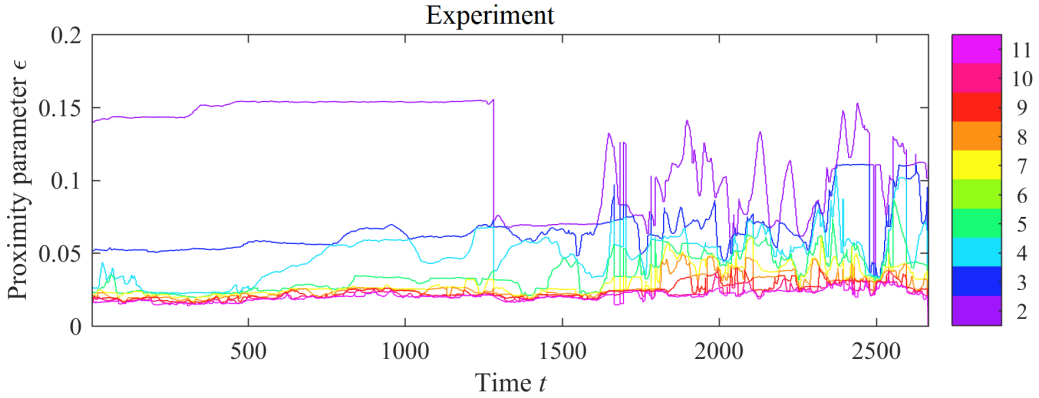
Average Nearest Neighbor Distance

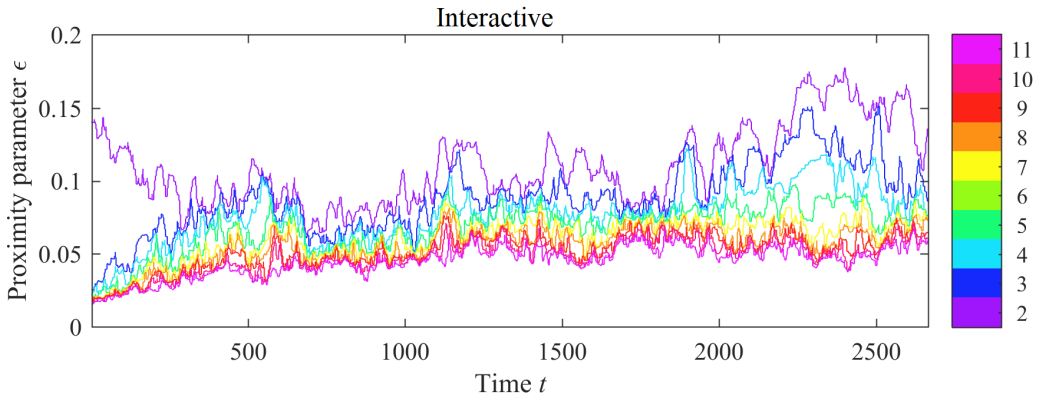


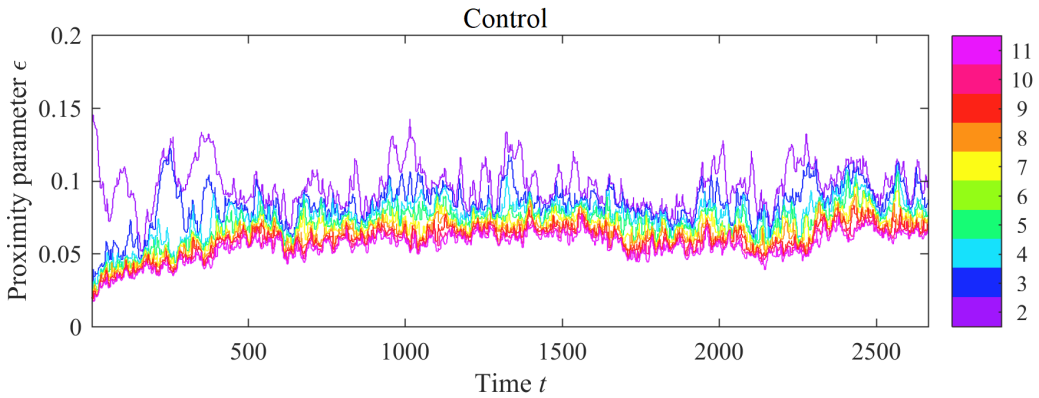
Percent of Aphids Moving



$B_{0(POS)}$ CROCKER PLOTS OF EXPERIMENT AND SIMULATIONS

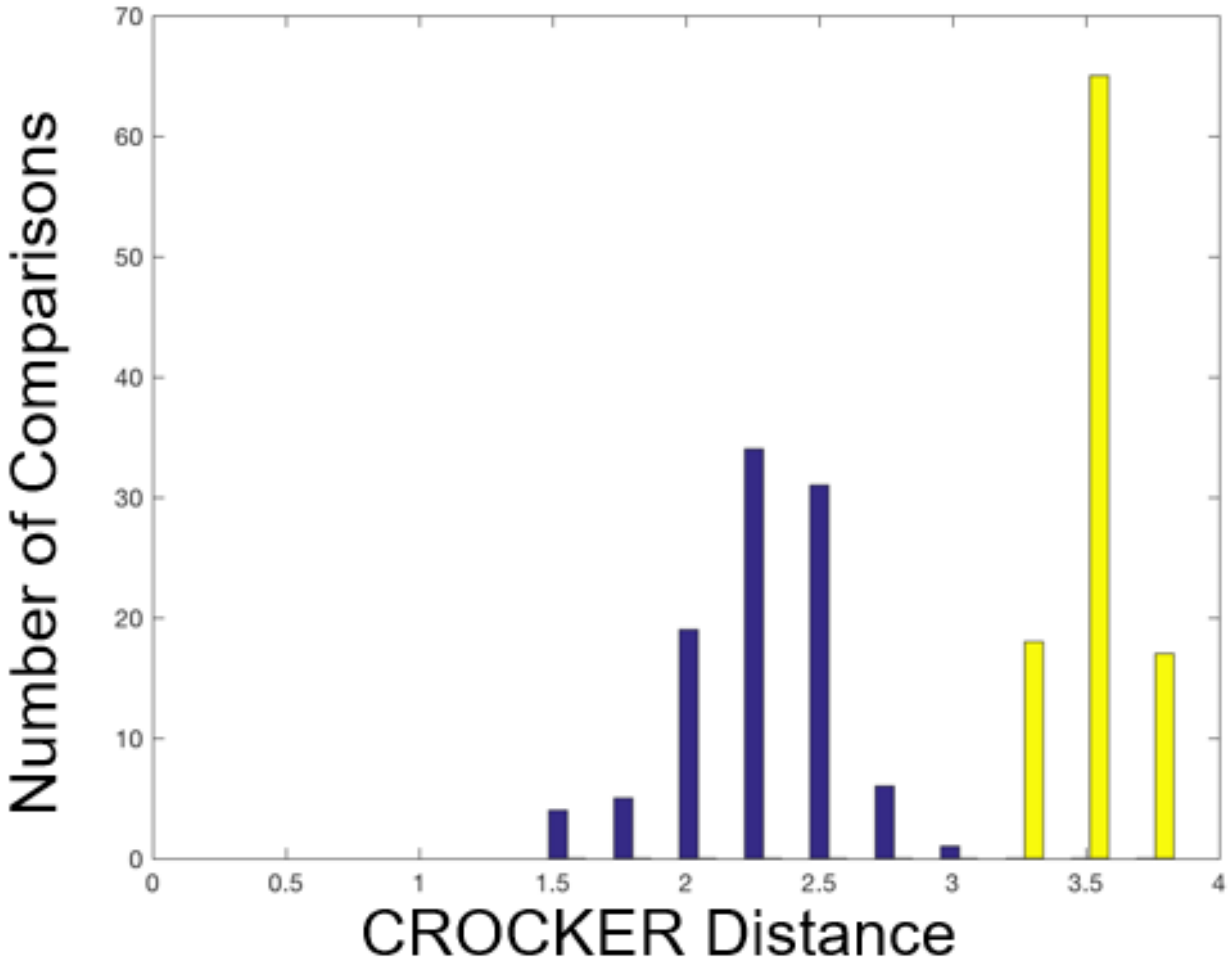






EXPERIMENT VS MODEL COMPARISON

Histogram of crocker difference between control/experiment and interactive/experiment



SUMMARY OF STATISTICAL TESTS COMPARING MODELS

Summaries of statistical tests comparing models of aphid motion using order parameters.

	P		M_{ang}		M_{abs}	
Exp	D	$R_{95\%}$	D	$R_{95\%}$	D	$R_{95\%}$
1	0.17	0.13	1.50	0.16	-2.00	0.15
2	-0.25	0.10	-0.97	0.11	-1.66	0.09
3	1.09	0.10	0.40	0.11	-1.71	0.10
4	1.70	0.08	-0.78	0.09	-1.24	0.07
5	-2.22	0.09	-0.63	0.09	-1.10	0.07
6	1.04	0.09	-0.49	0.10	-1.68	0.09
7	-0.97	0.11	-1.28	0.13	-1.99	0.11
8	-3.30	0.25	-2.11	0.22	-2.87	0.26
9	-4.69	0.25	-3.14	0.22	-2.81	0.20

SUMMARY OF STATISTICAL TESTS COMPARING MODELS

Summaries of statistical tests comparing models of aphid motion using order parameters.

	P		M_{ang}		M_{abs}		d_a		$Mov_{\%}$	
Exp	D	$R_{95\%}$	D	$R_{95\%}$	D	$R_{95\%}$	D	$R_{95\%}$	D	$R_{95\%}$
1	0.17	0.13	1.50	0.16	-2.00	0.15	0.26	0.05	20.2	0.40
2	-0.25	0.10	-0.97	0.11	-1.66	0.09	0.25	0.02	0.78	0.24
3	1.09	0.10	0.40	0.11	-1.71	0.10	0.54	0.04	25.1	0.26
4	1.70	0.08	-0.78	0.09	-1.24	0.07	0.16	0.02	1.68	0.21
5	-2.22	0.09	-0.63	0.09	-1.10	0.07	0.31	0.03	7.68	0.24
6	1.04	0.09	-0.49	0.10	-1.68	0.09	0.53	0.04	24.0	0.26
7	-0.97	0.11	-1.28	0.13	-1.99	0.11	0.57	0.04	23.9	0.29
8	-3.30	0.25	-2.11	0.22	-2.87	0.26	0.57	0.25	13.2	0.63
9	-4.69	0.25	-3.14	0.22	-2.81	0.20	0.48	0.15	11.7	0.34

SUMMARY OF STATISTICAL TESTS COMPARING MODELS

Summaries of statistical tests comparing models of aphid motion using order parameters.

	P		M_{ang}		M_{abs}		d_a		$Mov_{\%}$	
Exp	D	$R_{95\%}$	D	$R_{95\%}$	D	$R_{95\%}$	D	$R_{95\%}$	D	$R_{95\%}$
1	0.17	0.13	1.50	0.16	-2.00	0.15	0.26	0.05	20.2	0.40
2	-0.25	0.10	-0.97	0.11	-1.66	0.09	0.25	0.02	0.78	0.24
3	1.09	0.10	0.40	0.11	-1.71	0.10	0.54	0.04	25.1	0.26
4	1.70	0.08	-0.78	0.09	-1.24	0.07	0.16	0.02	1.68	0.21
5	-2.22	0.09	-0.63	0.09	-1.10	0.07	0.31	0.03	7.68	0.24
6	1.04	0.09	-0.49	0.10	-1.68	0.09	0.53	0.04	24.0	0.26
7	-0.97	0.11	-1.28	0.13	-1.99	0.11	0.57	0.04	23.9	0.29
8	-3.30	0.25	-2.11	0.22	-2.87	0.26	0.57	0.25	13.2	0.63
9	-4.69	0.25	-3.14	0.22	-2.81	0.20	0.48	0.15	11.7	0.34

Summaries of statistical tests comparing models of aphid motion using topology.

	$\mathsf{b}_{0(pos)}$		$\mathsf{b}_{1(pos)}$		$\mathsf{b}_{0(posvel)}$		$\mathsf{b}_{1(posvel)}$	
Exp	D^*	$R^*_{95\%}$	D^*	$R^*_{95\%}$	D^*	$R^*_{95\%}$	D^*	$R^*_{95\%}$
1	1147	38.73	135.1	5.149	831.9	42.81	124.2	5.640
2	1703	23.98	297.0	6.500	858.9	16.88	261.1	7.258
3	1893	37.36	290.4	6.836	1347	35.60	271.3	7.218
4	1825	18.36	359.0	5.741	552.3	19.04	332.5	6.301
5	1370	15.81	249.2	6.039	270.8	15.25	225.1	6.401
6	2086	40.53	322.9	7.061	1484	37.35	307.7	7.116
7	1747	34.32	264.8	6.235	1289	33.69	247.5	6.69
8	298.5	20.81	10.28	1.920	147.9	19.81	3.573	1.641
9	467.5	19.66	22.34	2.148	245.3	21.10	10.93	2.067

(Ulmer, Z., Topaz 2018) Assessing Biological Models Using Topological Data Analysis

PERSISTENT CROCKER PLOTS

BENEFITS AND DRAWBACKS OF CROCKERS

Benefits:

- Can be used to summarize time-varying metric spaces
- Displays topological information at all times simultaneously
- Can be vectorized and applied to statistical and machine learning tasks

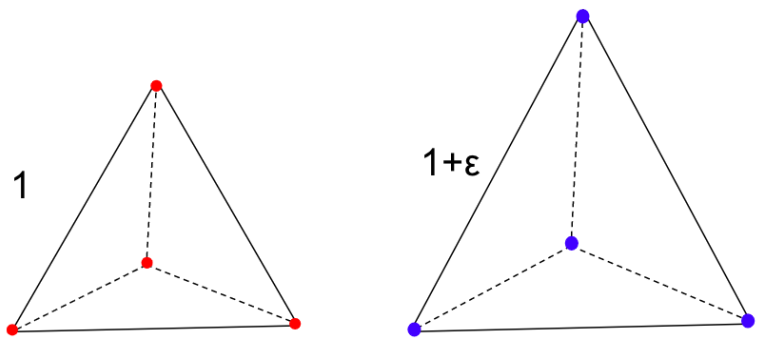
BENEFITS AND DRAWBACKS OF CROCKERS

Benefits:

- Can be used to summarize time-varying metric spaces
- Displays topological information at all times simultaneously
- Can be vectorized and applied to statistical and machine learning tasks

Drawbacks:

- Crockers are not stable. Perturbing the dynamic metric space only slightly could produce changes of unbounded size.



STABILITY OF PERSISTENCE DIAGRAMS

Stability

Ideal if tools for data analysis are stable with respect to small perturbations of the inputs.

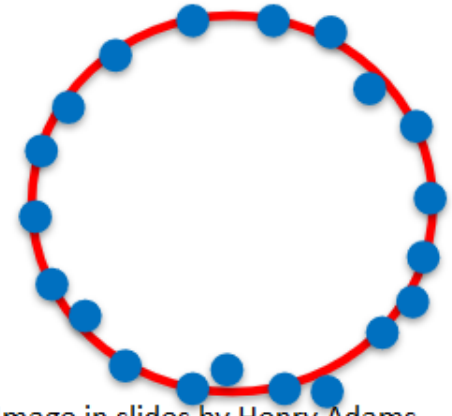


Image in slides by Henry Adams

STABILITY OF PERSISTENCE DIAGRAMS

Stability

Ideal if tools for data analysis are stable with respect to small perturbations of the inputs.

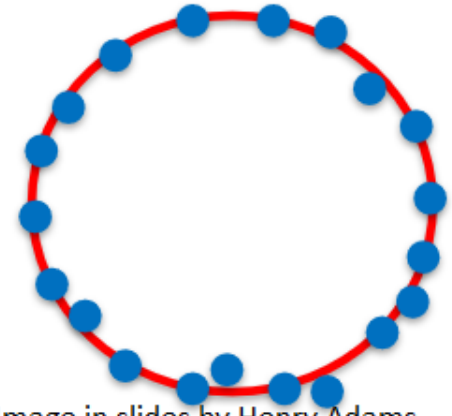
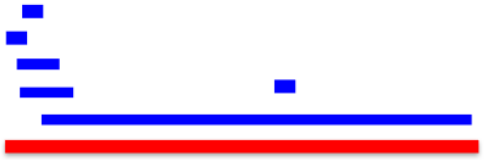
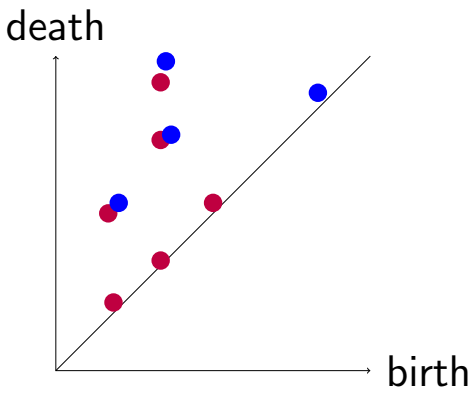


Image in slides by Henry Adams



DISTANCE BETWEEN PERSISTENCE DIAGRAMS



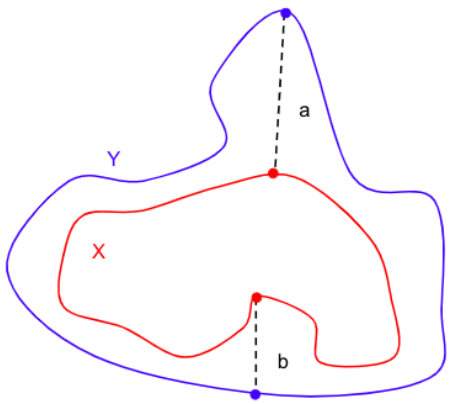
Definition

The *bottleneck distance* between two PDs B and B' is given by

$$d_\infty(B, B') = \inf_{\gamma : B \to B'} \sup_{u \in B} ||u - \gamma(u)||_\infty,$$

ranging over all bijections between B and B'.

DISTANCE BETWEEN METRIC SPACES



Definition

If X and Y are two subsets of a metric space Z, then the *Hausdorff distance* between X and Y is

$$d_H^Z(X,Y) = \max\{\sup_{x\in X}\inf_{y\in Y} d(x,y), \sup_{y\in Y}\inf_{x\in X} d(x,y)\}.$$

The *Gromov–Hausdorff* distance between metric spaces X and Y is

$$d_{\mathrm{GH}}(X,Y) = \inf_{Z,f,g} d_H^Z(f(X),g(Y)),$$

where the infimum is taken over all metric spaces Z and isometric embeddings $f\colon X \to Z$ and $g\colon Y \to Z$.

PERSISTENCE DIAGRAMS ARE STABLE

Stability of PDs

(Chazal, de Silva, Oudot 2013) PDs are stable (Lipschitz) with respect to the bottleneck metric

$$d_\infty(PD(VR(X)), PD(VR(Y))) \leq 2d_{GH}(X, Y)$$

for metric spaces X and Y.

RANK INVARIANT

Definition

For a persistence module V and $\varepsilon < \varepsilon'$, the *rank* of the map $V(\varepsilon) \to V(\varepsilon')$, is the number of intervals in the persistence barcode that contain the interval $[\varepsilon, \varepsilon']$.

The collection of all natural numbers $\mathrm{rank}(V(\varepsilon) \to V(\varepsilon'))$ for all $\varepsilon < \varepsilon'$ is called the *rank invariant*.

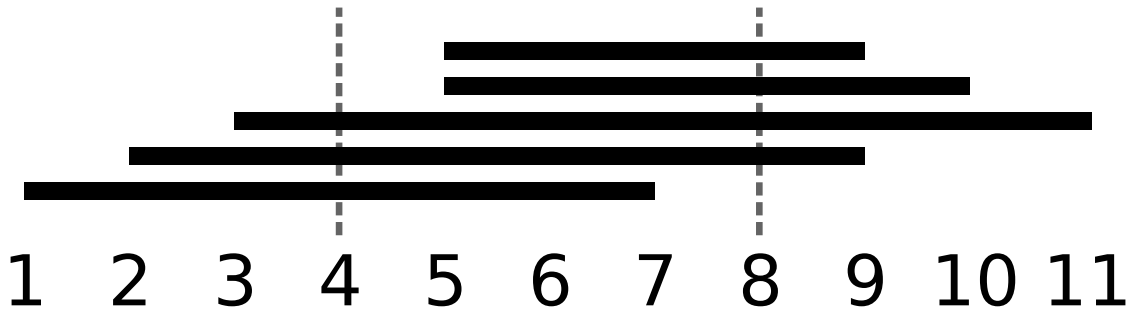


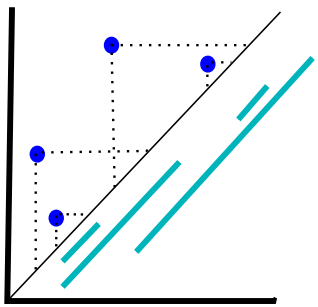
Figure: $\mathrm{rank}(V(4) \to V(8)) = 2$

- The rank invariant is equivalent to a persistence barcode i.e. can obtain one from the other (Carlsson and Zomorodian, 2009).

α-SMOOTHED CROCKER PLOT

- Let **X** be a time-varying metric space, with X_t the space at time t.
- An *α-smoothed crocker plot,* for $\alpha \geq 0$, at time t and scale ε is equal to $\mathrm{rank}(H_k(\mathrm{VR}(X_t; \varepsilon - \alpha)) \to H_k(\mathrm{VR}(X_t; \varepsilon + \alpha)))$.
- A standard crocker plot is a 0-smoothed crocker plot.

Persistence Diagram

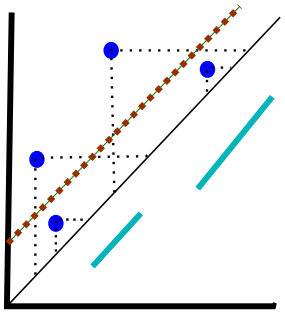


Persistence Intervals

Vertical Slice of Crocker

0
1
2
2
1
2
2
2
1
0

Persistence Diagram



Persistence Intervals

Vertical Slice of
α- persistence Crocker

0
0
1
1
1
1
0
1
1
0

CROCKER VIDEO

Definition (Crocker Video)

A *crocker video* is a sequence of α-smoothed crocker plots as α increases continuously from 0. It is an integer-valued function

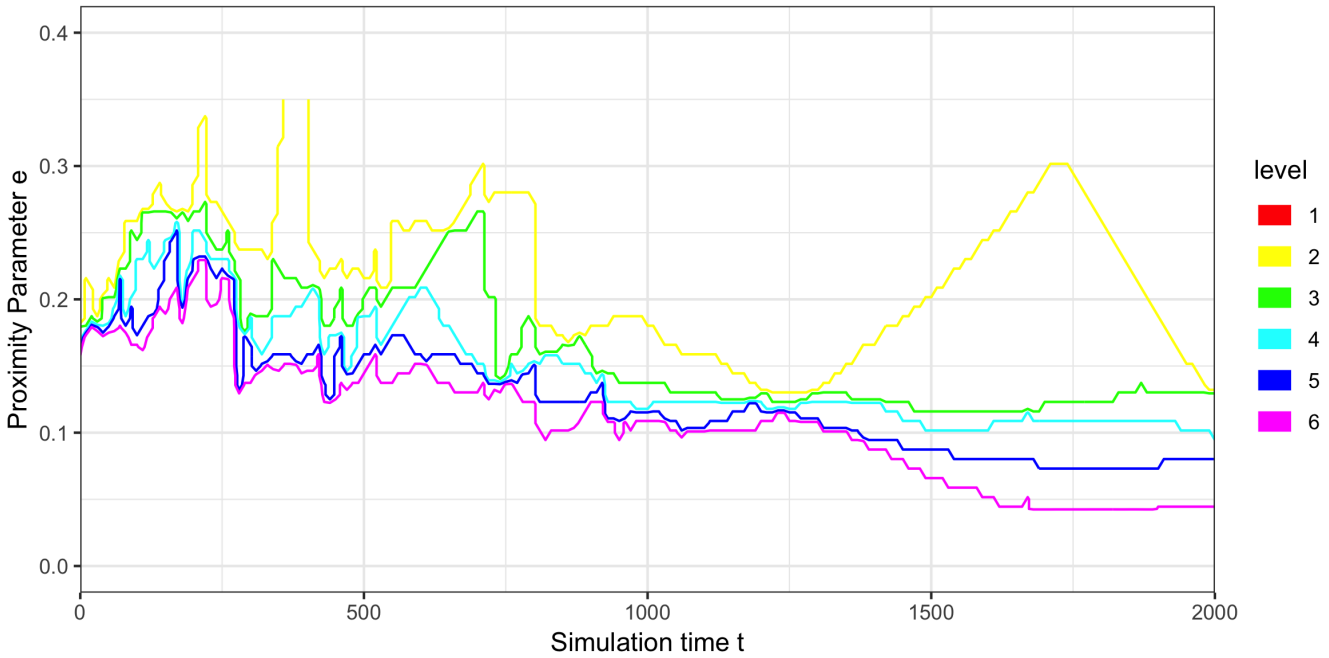
$$f : \mathbb{R}^3 \to \mathbb{N}$$

$$f(t, \varepsilon, \alpha) = \mathrm{rank}(H_k(\mathrm{VR}(X_t; \varepsilon - \alpha)) \to H_k(\mathrm{VR}(X_t; \varepsilon + \alpha))).$$

CROCKER VIDEOS

A crocker video is a non-increasing function,

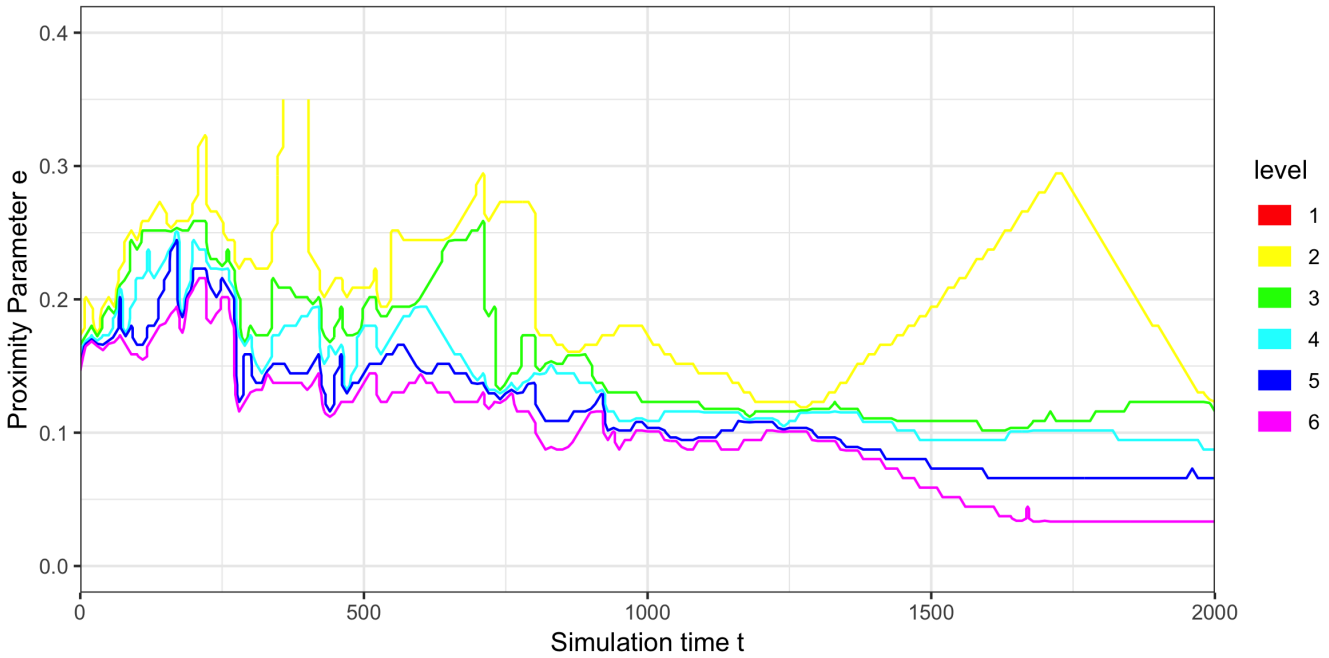
$$f(t, \varepsilon, \alpha) \leq f(t, \varepsilon, \alpha') \text{ for } \alpha \geq \alpha'.$$



CROCKER VIDEOS

A crocker video is a non-increasing function,

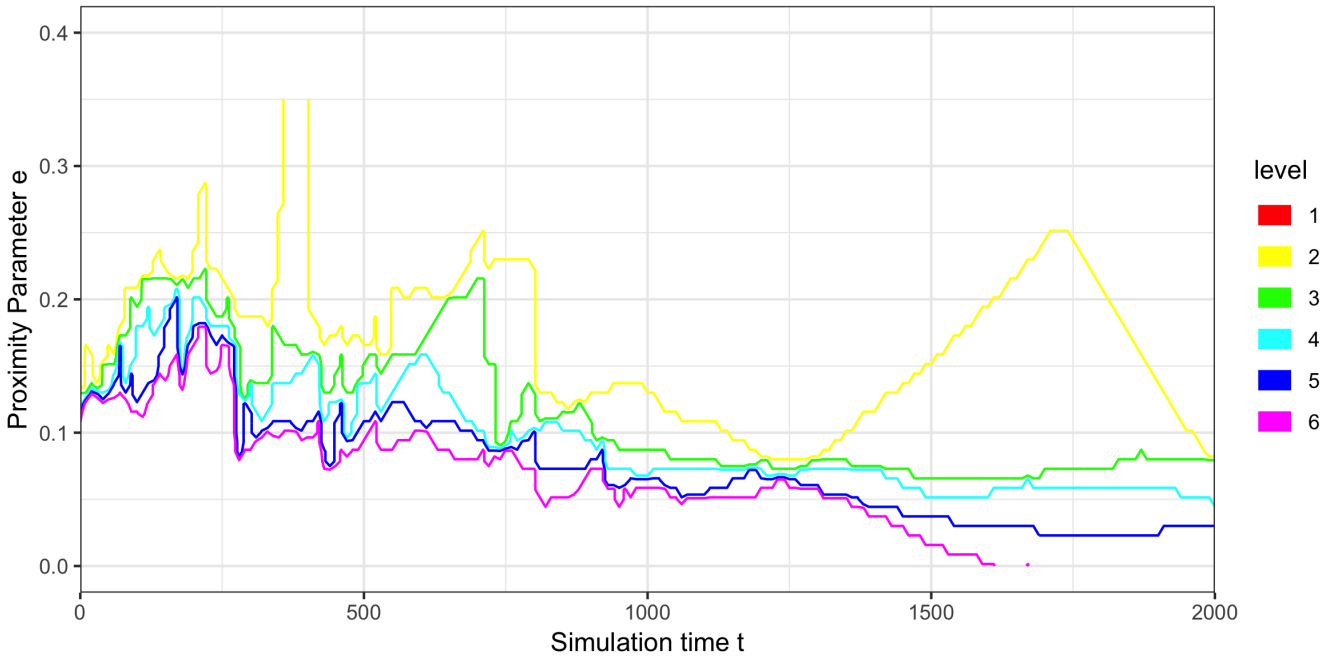
$$f(t, \varepsilon, \alpha) \leq f(t, \varepsilon, \alpha') \text{ for } \alpha \geq \alpha'.$$



CROCKER VIDEOS

A crocker video is a non-increasing function,

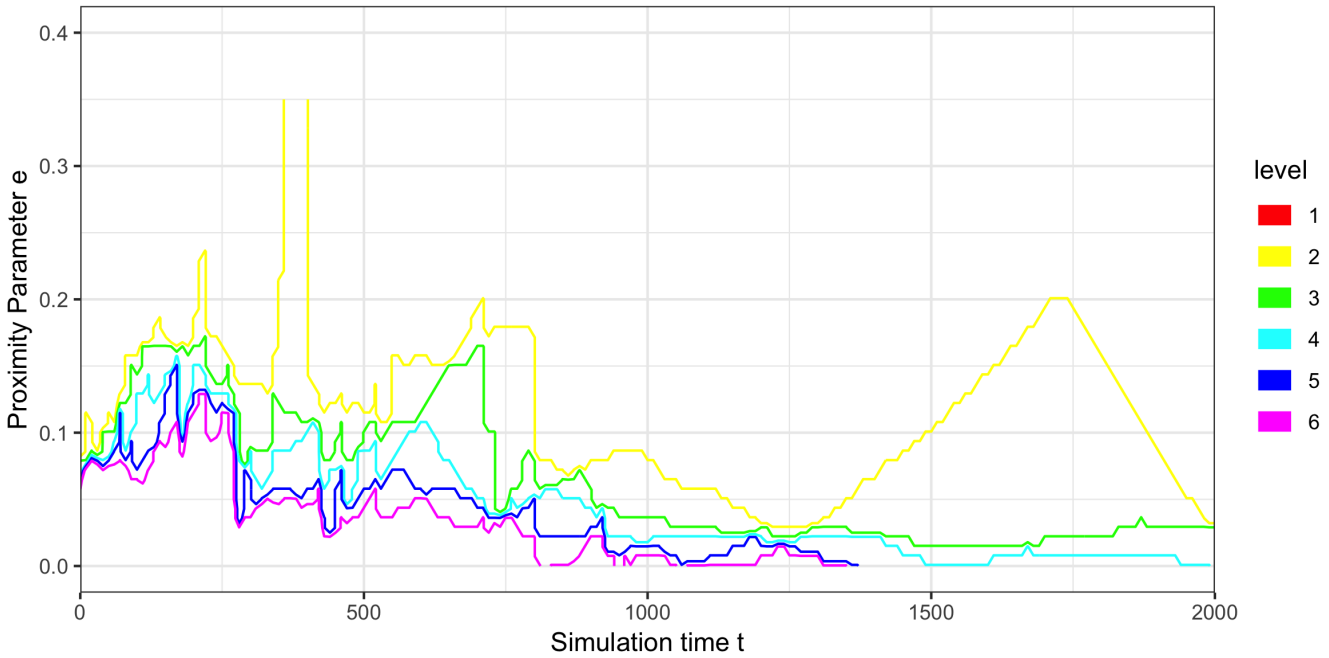
$$f(t, \varepsilon, \alpha) \leq f(t, \varepsilon, \alpha') \text{ for } \alpha \geq \alpha'.$$



CROCKER VIDEOS

A crocker video is a non-increasing function,

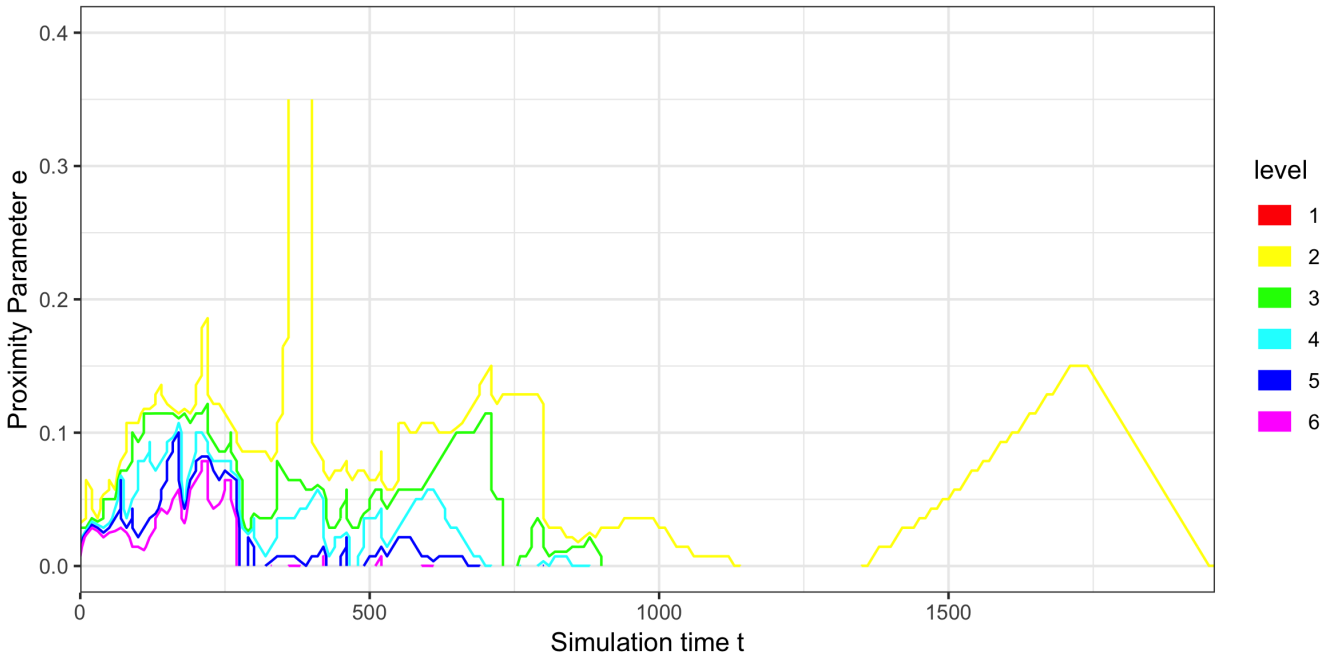
$$f(t, \varepsilon, \alpha) \leq f(t, \varepsilon, \alpha') \text{ for } \alpha \geq \alpha'.$$



CROCKER VIDEOS

A crocker video is a non-increasing function,

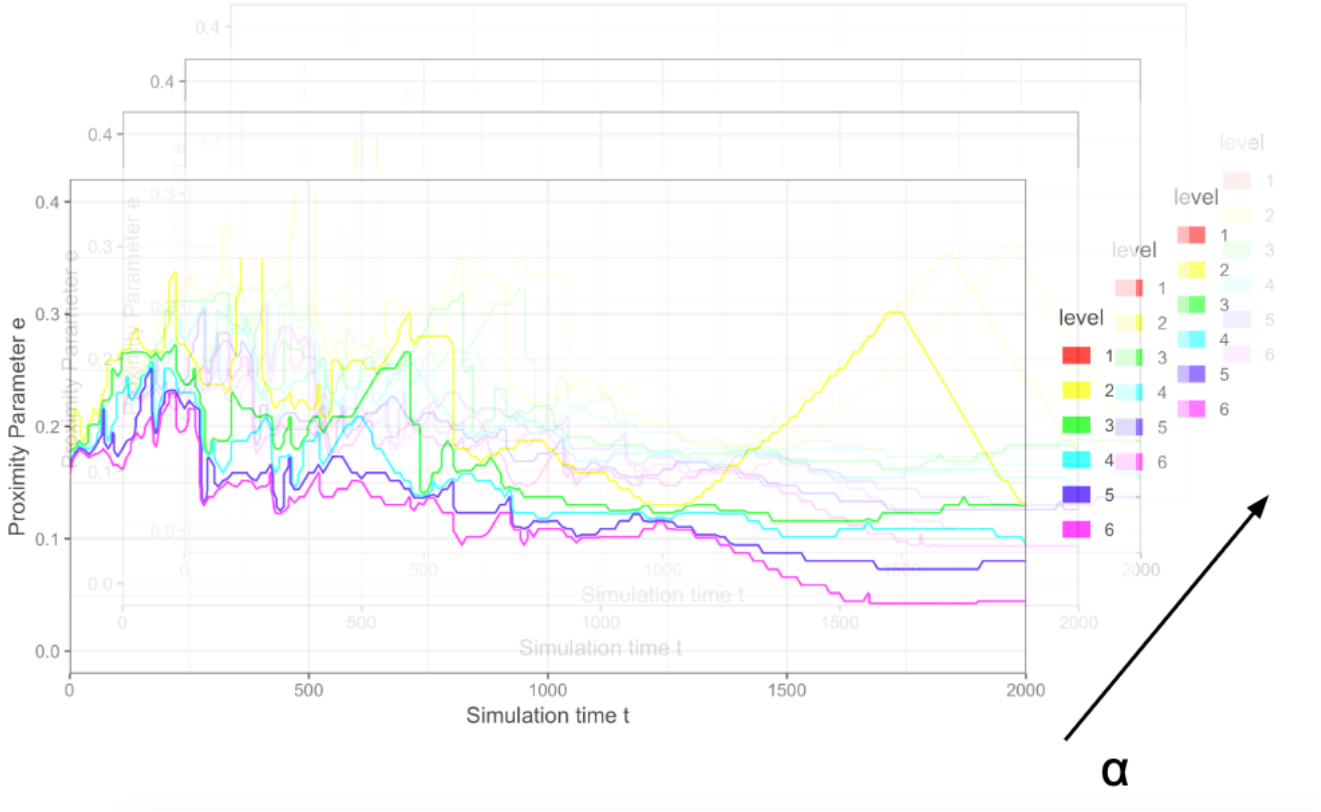
$$f(t, \varepsilon, \alpha) \leq f(t, \varepsilon, \alpha') \text{ for } \alpha \geq \alpha'.$$



CROCKER VIDEOS

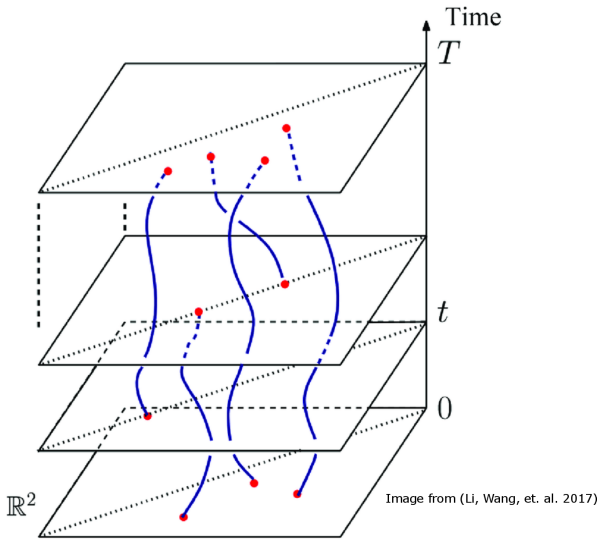
A crocker video is a non-increasing function,

$$f(t, \varepsilon, \alpha) \leq f(t, \varepsilon, \alpha') \text{ for } \alpha \geq \alpha'.$$



FEATURES OF CROCKER VIDEOS

- The crocker video is equivalent to the vineyard (Cohen-Steiner, Edelsbrunner, Morozov 2006) i.e. can obtain one from the other.



- The crocker video inherits some nice interpretability properties of the crocker plot.

- All times are represented in each frame α, whereas in a vineyard one only sees information about a single time.

- Crocker videos satisfy a stability property similar to the stability of vineyards.

CROCKER VIDEOS ARE STABLE

Theorem (Stability theorem for crocker videos)

If $\mathbf{X}$ *and* $\mathbf{Y}$ *are totally-bounded time-varying metric spaces, and if* $d_{\mathrm{GH}}^{\infty}(\mathbf{X}, \mathbf{Y}) \leq \delta/2$*, then the crocker videos for* $\mathbf{X}$ *and* $\mathbf{Y}$ *are close in the sense that for all* t*,* ε*, and* α*, we have*

- $f_{\mathbf{X}}(t, \varepsilon, \alpha + \delta) \leq f_{\mathbf{Y}}(t, \varepsilon, \alpha)$*, and*
- $f_{\mathbf{Y}}(t, \varepsilon, \alpha + \delta) \leq f_{\mathbf{X}}(t, \varepsilon, \alpha)$*.*

Here, by an abuse of notation, we let $f_{\mathbf{X}}$ *and* $f_{\mathbf{Y}}$ *denote* $f_{\mathrm{PH}(\mathrm{VR}(\mathbf{X}))}$ *and* $f_{\mathrm{PH}(\mathrm{VR}(\mathbf{Y}))}$*.*

(Adams, Topaz, Xian, Z. forthcoming) Capturing Dynamics of Time-Varying Systems with Topology

CONCLUSION

CONCLUSION

- Crocker plots (0-persistence crockers) are useful summaries of topological properties of time-varying systems.
  - Can be combined with machine learning and statistical tools
  - Provide means of identifying global behaviors, parameter identification, and model selection

- Crocker videos are stable.
  - If two time-varying metric spaces are “close", then their corresponding crocker videos will also be “close"

QUESTIONS?

Tom Halverson
M. Ulmer
Lu Xian
Henry Adams
Jesse Milzman
John Nardini
Kathleen Storey
Dhananjay Bhasker
Angelika Manhart
Chad Topaz

Lori Ziegelmeier
lziegel1@macalester.edu
Department of Mathematics, Statistics, and Computer Science

MACALESTER

MATHEMATICS RESEARCH COMMUNITIES

NSF

NSF:CDS&E-MSS-1854703

Join WinCompTop: email `WinCompTop+subscribe@googlegroups.com`