Analyzing patterns and critical transitions in spatially explicit populations with cubical homology

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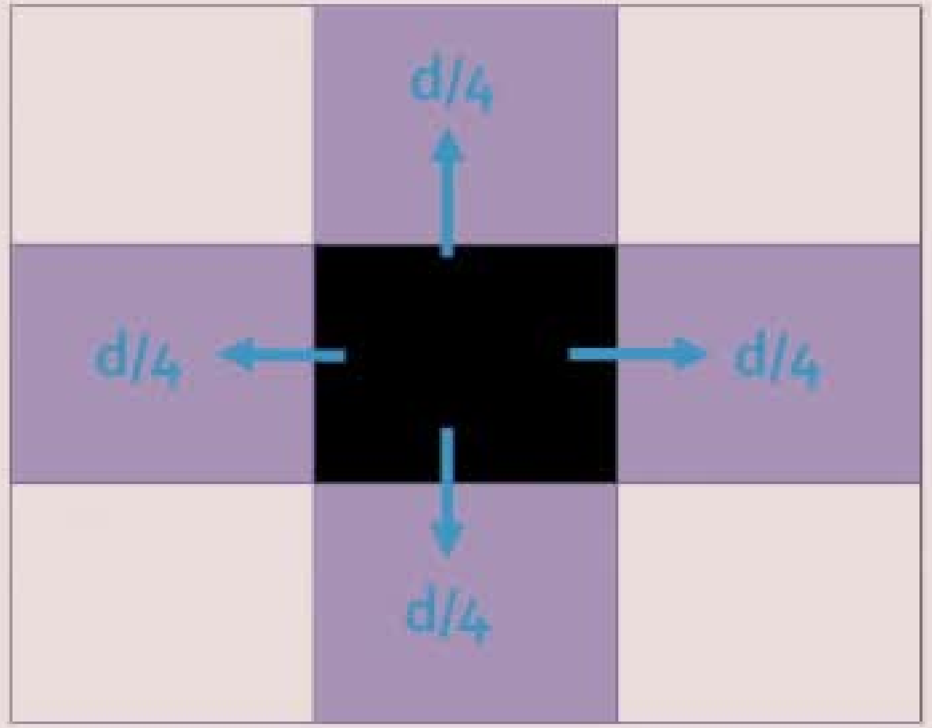
Population model

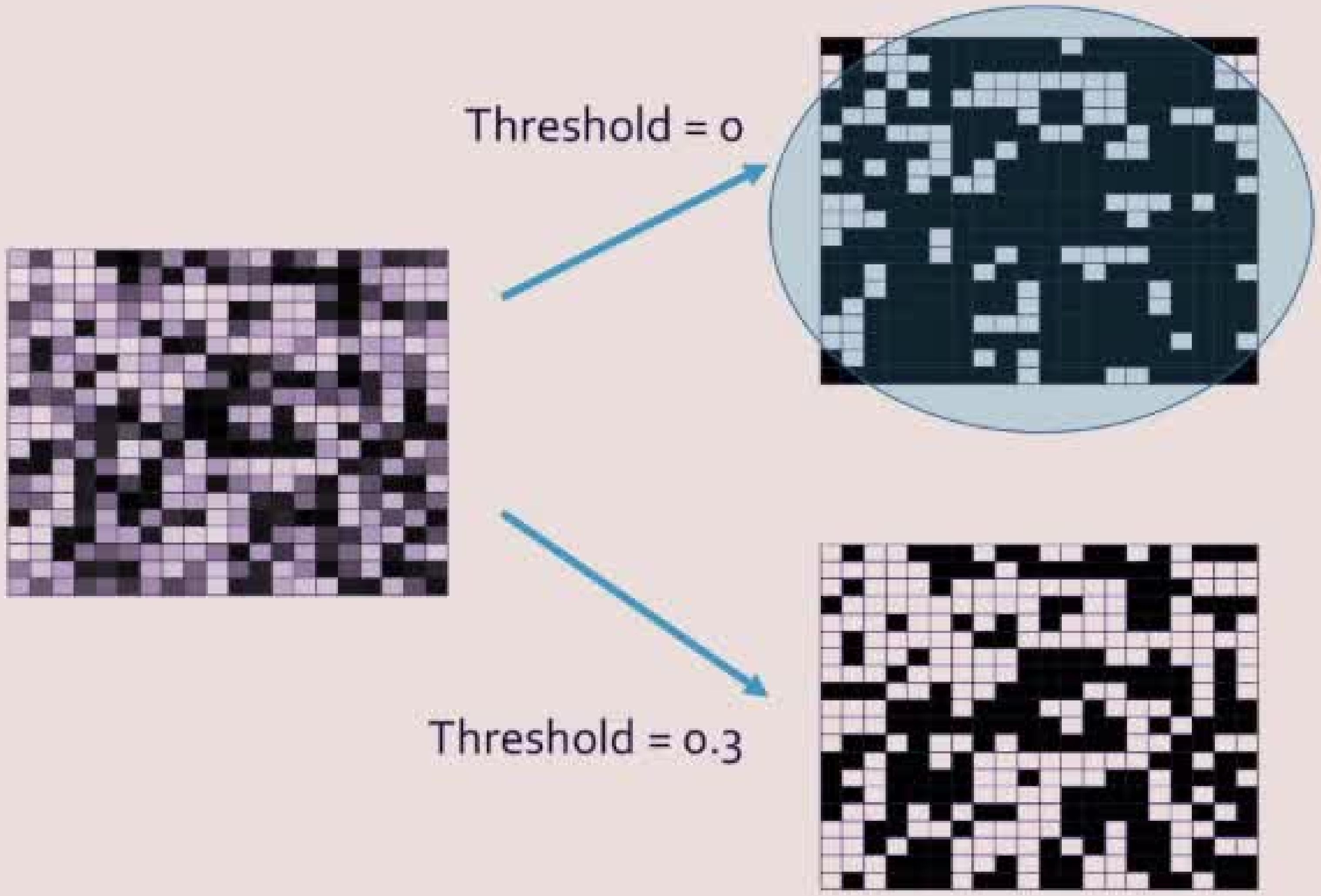
- **Dispersal phase**: coupled patch dispersal with absorbing boundaries

$$X_{n+1}(i,j) = (1-d)\bar{X}_n(i,j) + \frac{d}{4}\Big[\bar{X}_n(i-1,j) + \bar{X}_n(i+1,j) + \bar{X}_n(i,j+1) + \bar{X}_n(i,j-1)\Big]$$

d = fraction of the population dispersing to neighboring patches

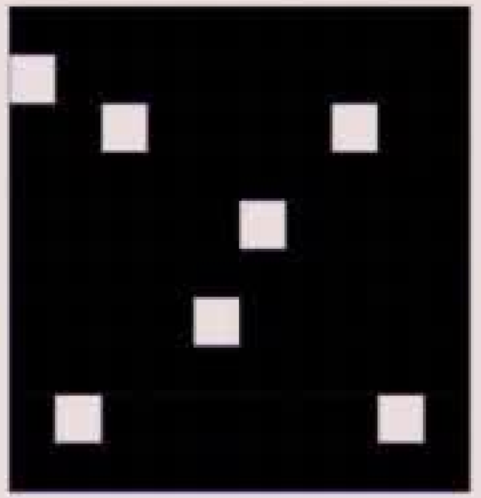


Global thresholding

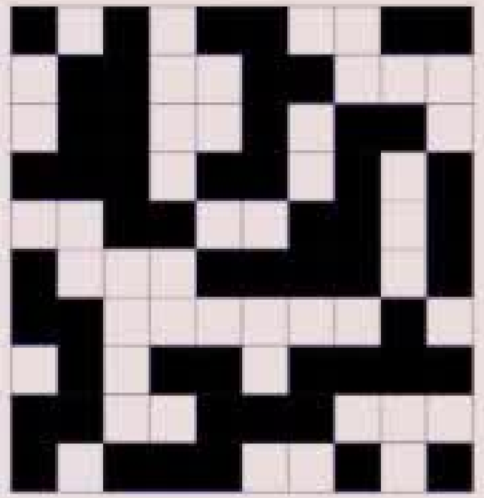


We employ cubical homology to quantitatively classify spatial patterns

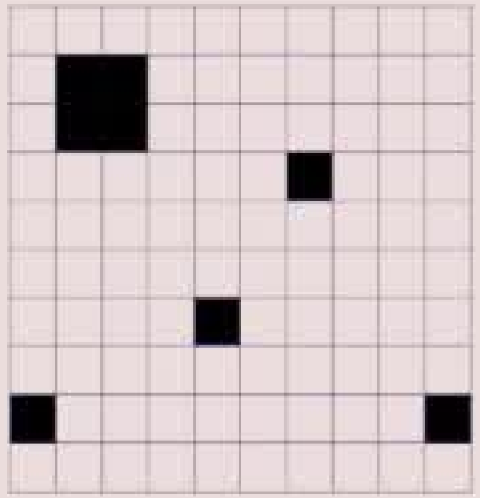
- We identify the first and second Betti numbers for spatial population time series ("connected components" and "holes")
- Also reducing dimensionality of problem



Example 1: Population on a 10x10 grid with 1 connected component and 6 holes ($\beta_0 = 1$ and $\beta_1 = 6$)

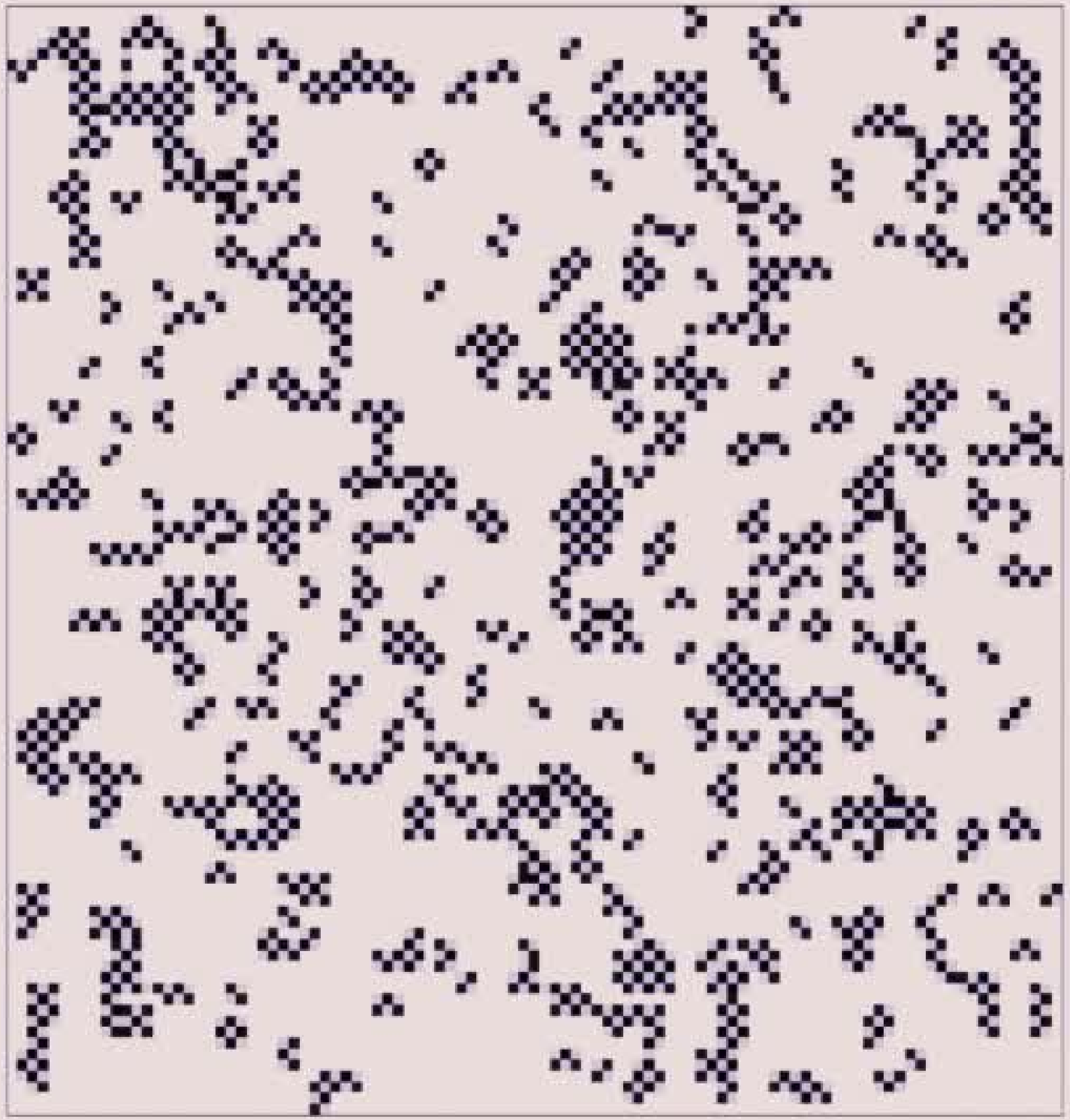


Example 2: Population on a 10x10 grid with 3 connected components and 3 holes ($\beta_0 = 3$ and $\beta_1 = 3$)

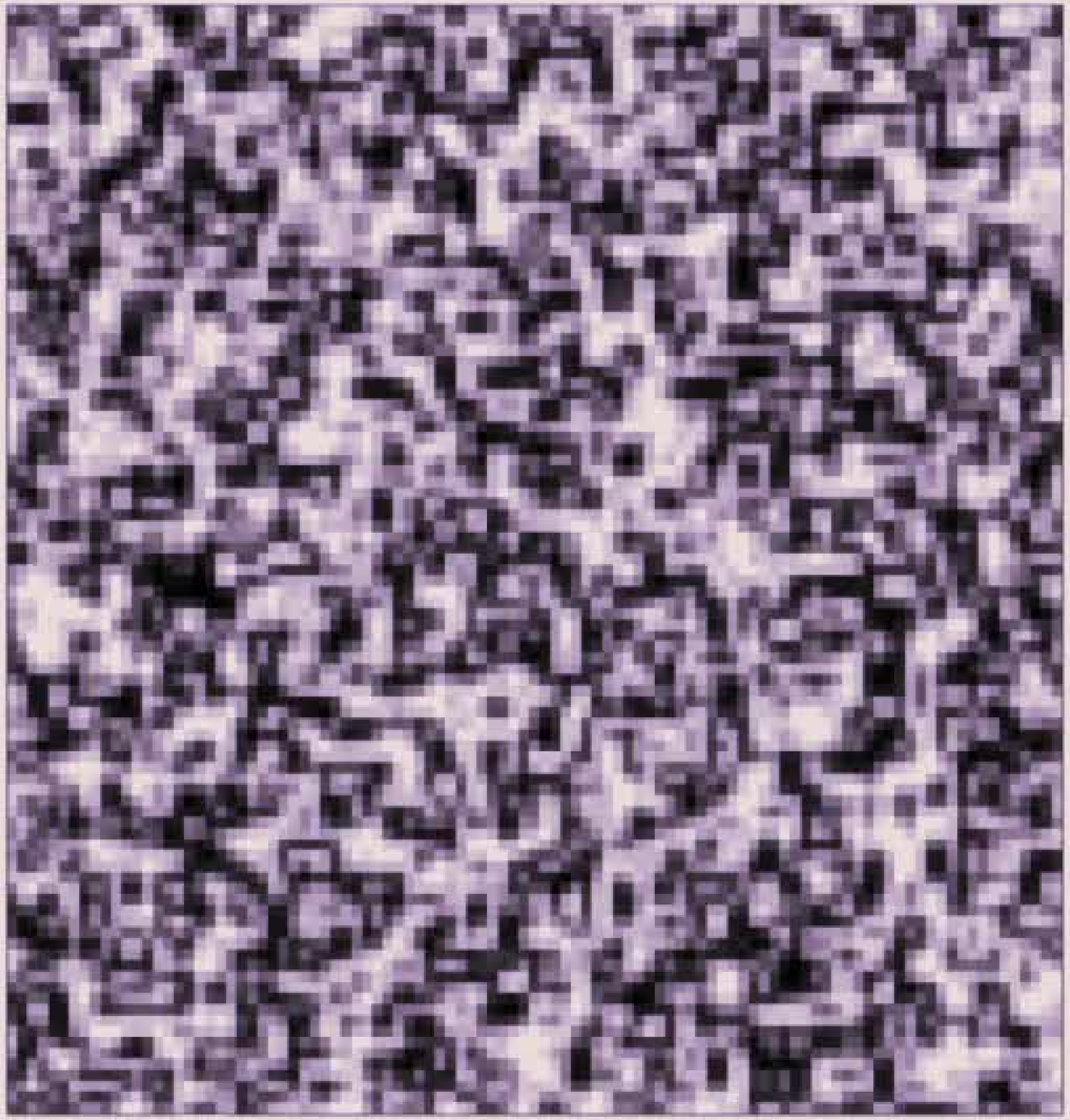


Example 3: Population on a 10x10 grid with 5 connected components and 0 holes ($\beta_0 = 5$ and $\beta_1 = 0$)

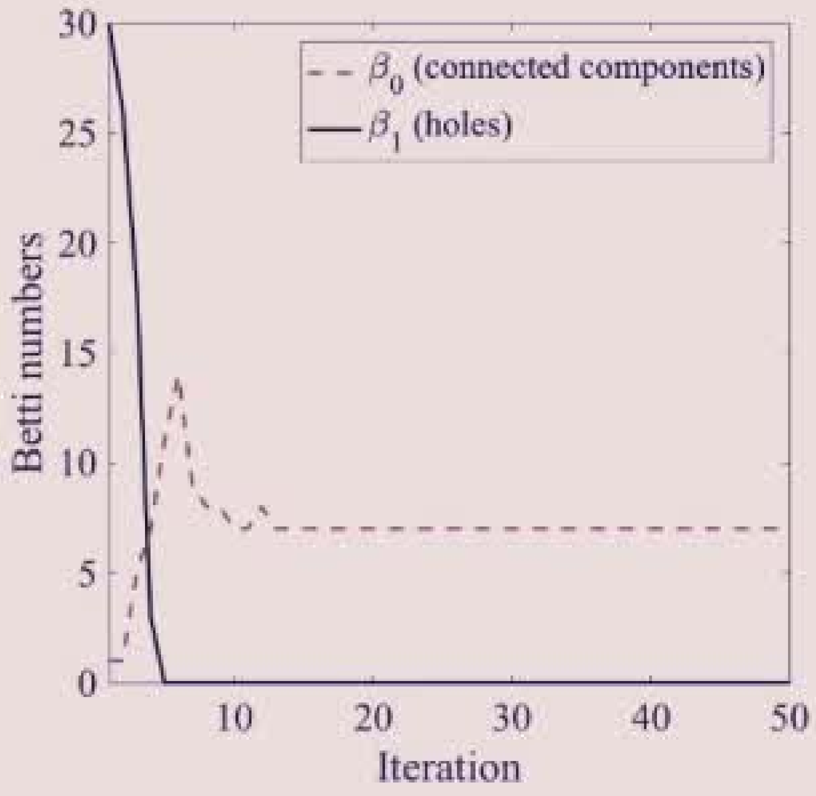
Population model



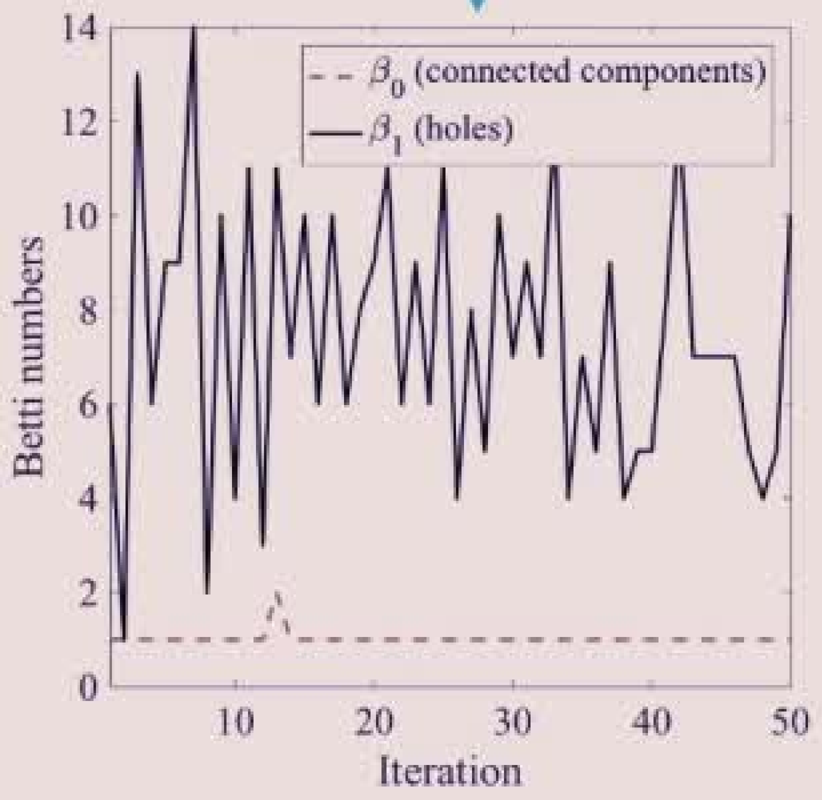
Population model



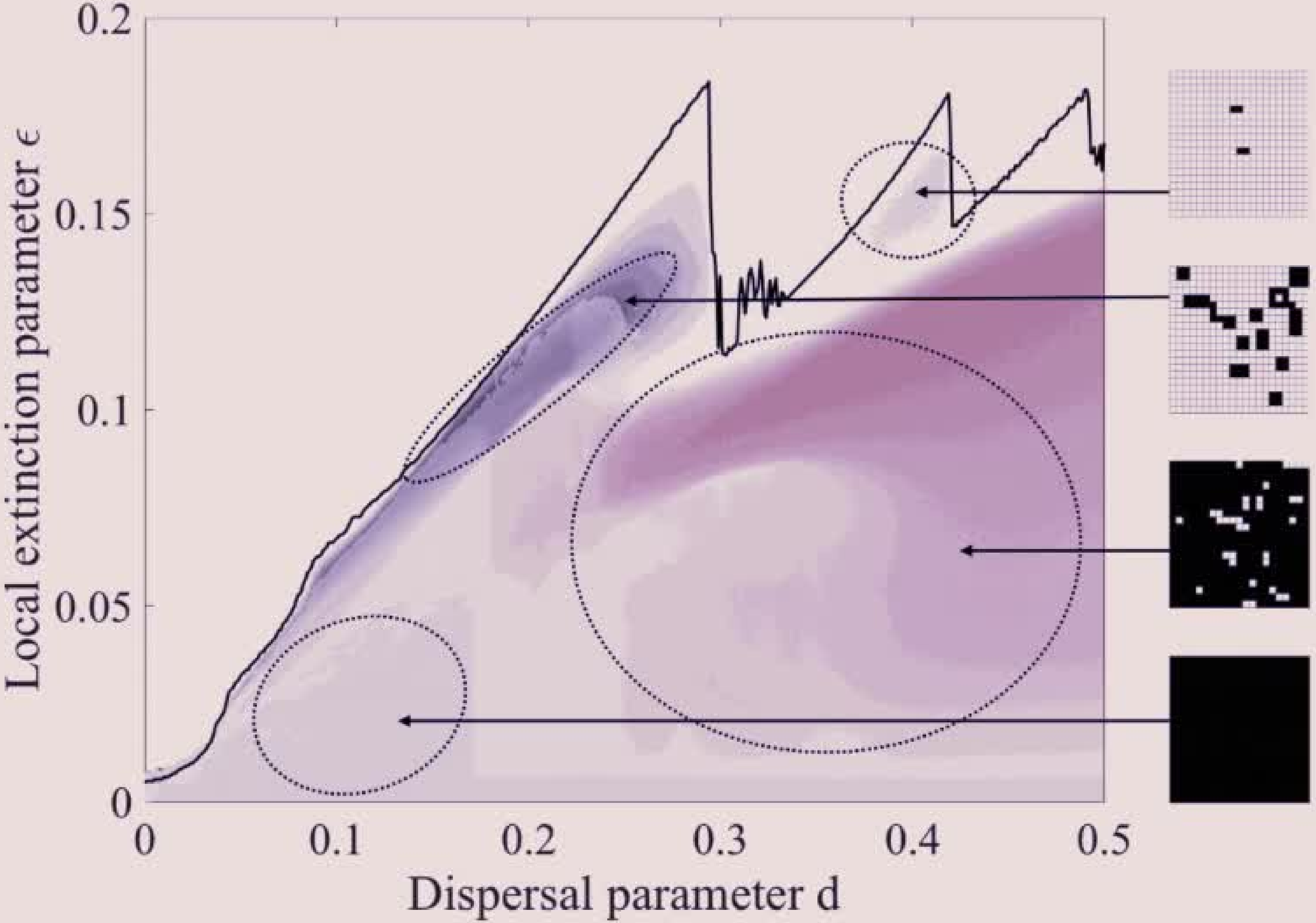
Population model



Large dispersal

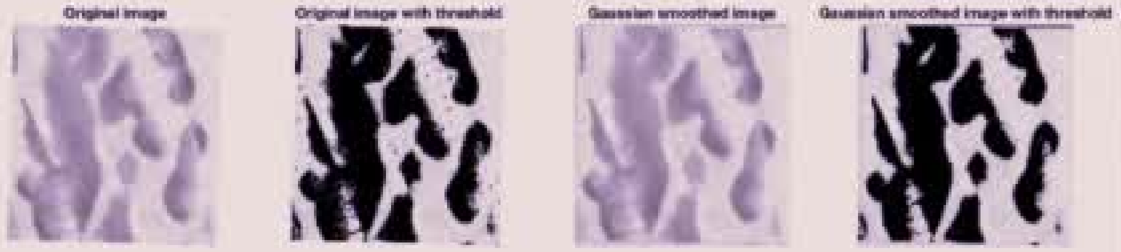


d = 0.5, r = 8, lattice 21 x 21


0.2
0.15
0.1
0.05
0
0
0.1
0.2
0.3
0.4
0.5
Local extinction parameter ϵ
Dispersal parameter d

Ongoing and future work

- Persistent homology:
  - Predicting critical dynamical transitions
  - Image processing
  - Model validation



Sonar image of oyster reefs distributed across a riverbed (obtained from David Bruce & Jay Lazar, NOAA Chesapeake Bay Office, NMFS)