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# Bak-Sneppen

Group 0

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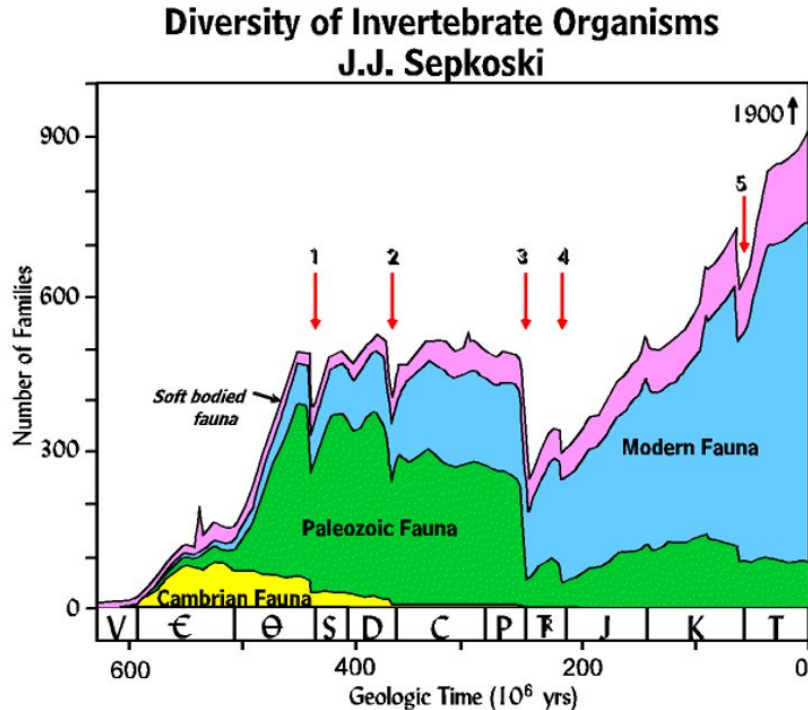
## **Research question:**

How do the dynamics change in the Bak-Sneppen model, when applying a 1D and 2D framework?

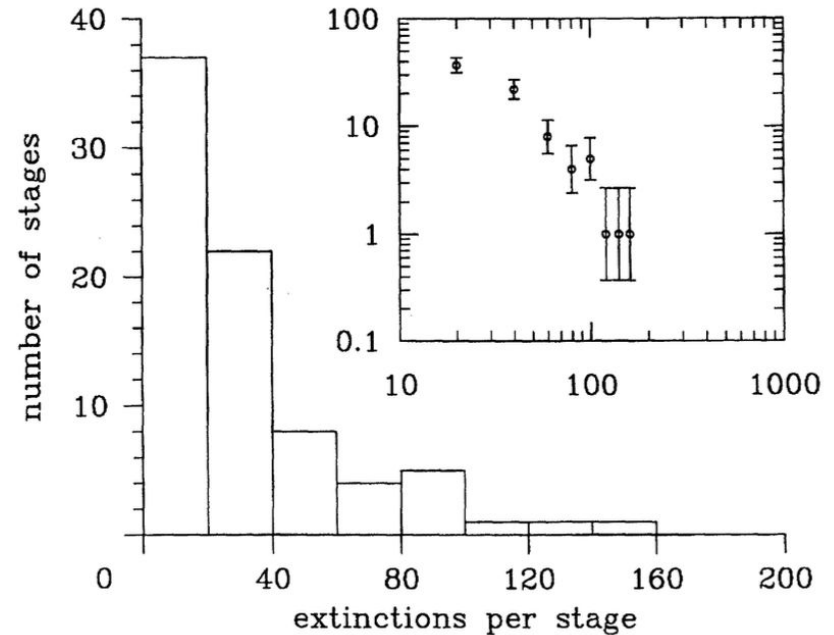
## **Hypotheses:**

1 mutation will have a bigger effect for the 2D model compared to the 1D model. If this increase is sufficiently large, the model could break as it is pushed out of its criticality state. This would happen when the power law exponent becomes  $> 2$ .

# Self-Organized Criticality



\*Figure from reference 4



\*Figure from reference 7

# Bak-Sneppen Model

Simulation:

- N species, 1D line with periodic boundary conditions.
- Random fitness (0 to 1) for each species from uniform distribution.
- At each time step, lowest fitness is mutated to a random fitness.
- Then mutating the fitness of the two neighbors, randomly as well.

VOLUME 71, NUMBER 24

PHYSICAL REVIEW LETTERS

13 DECEMBER 1993

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## Punctuated Equilibrium and Criticality in a Simple Model of Evolution

Per Bak

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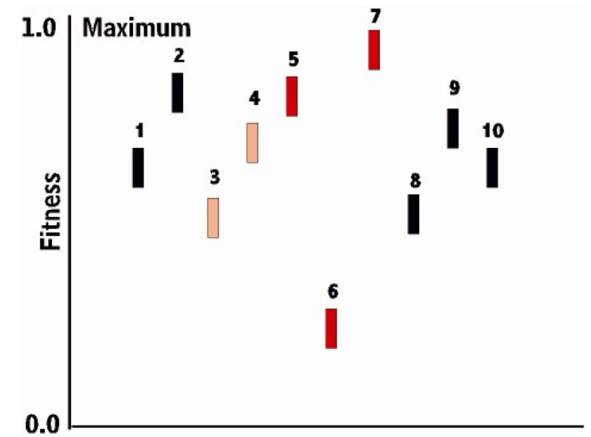
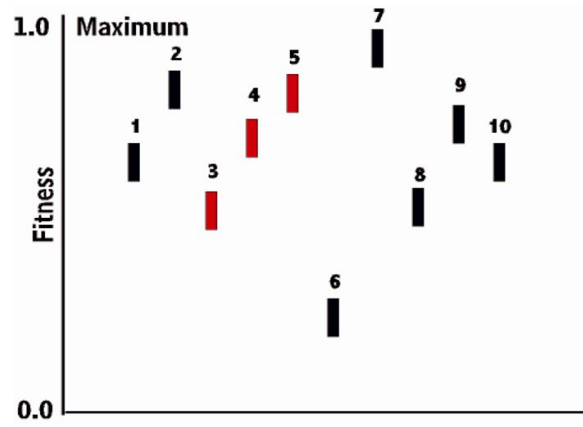
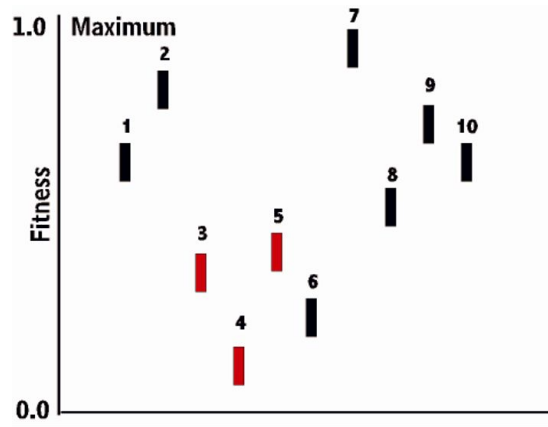
Kim Sneppen

*Niels Bohr Institute, Blegdamsvej 17, 2100 Copenhagen Ø, Denmark*

(Received 7 July 1993)

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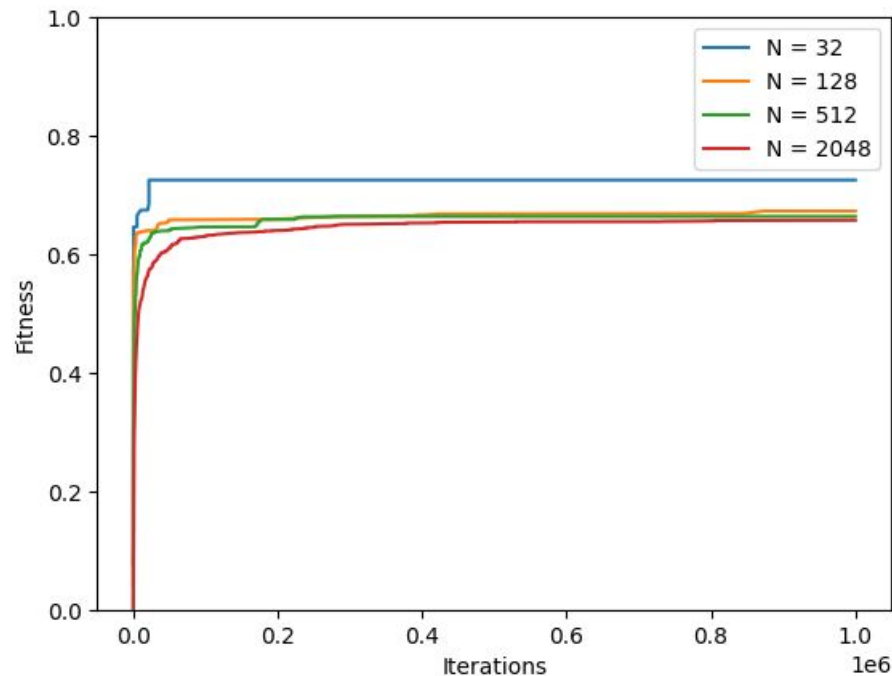
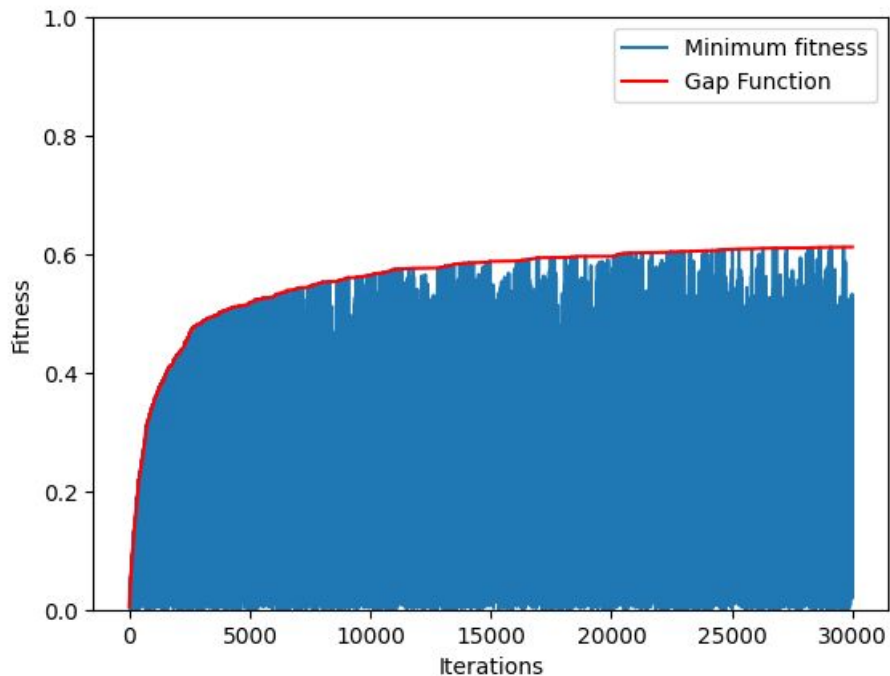
# Bak-Sneppen Model



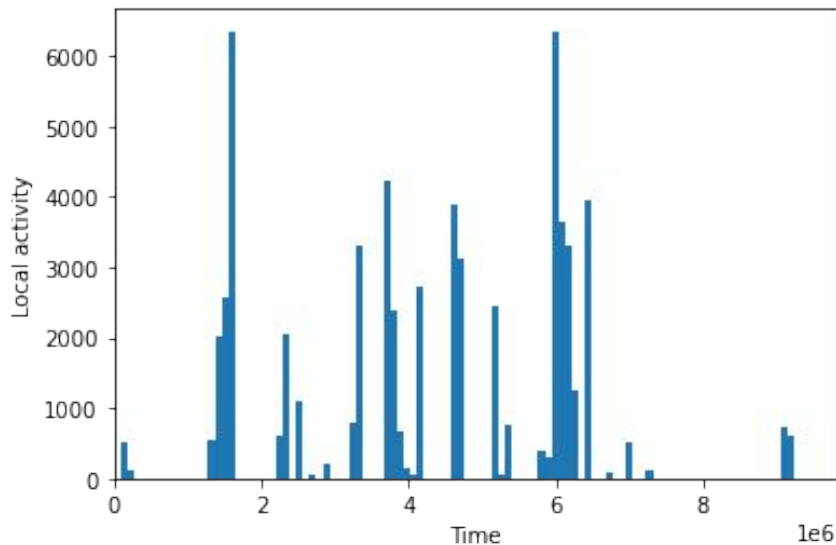
\*Figures from reference 4

# Gap function 1D

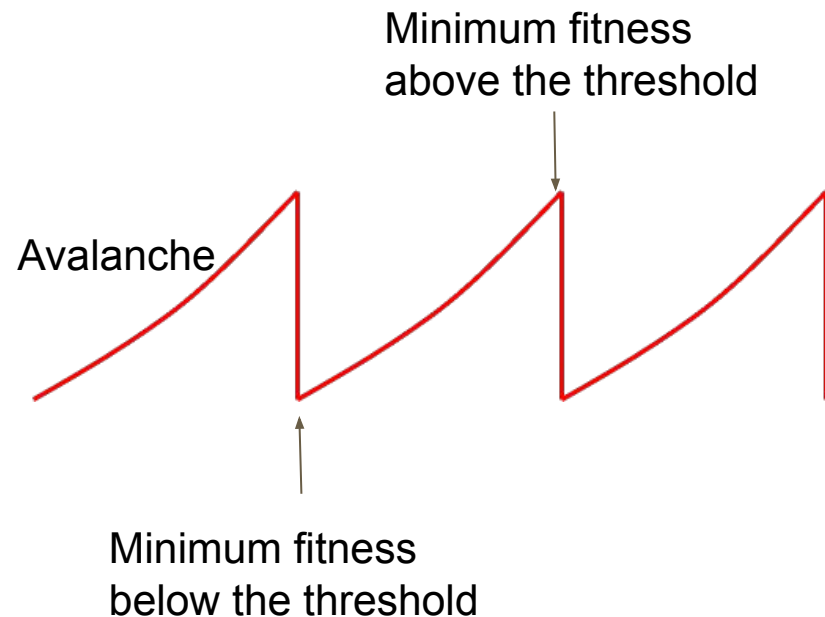
$f_c = 0.667$



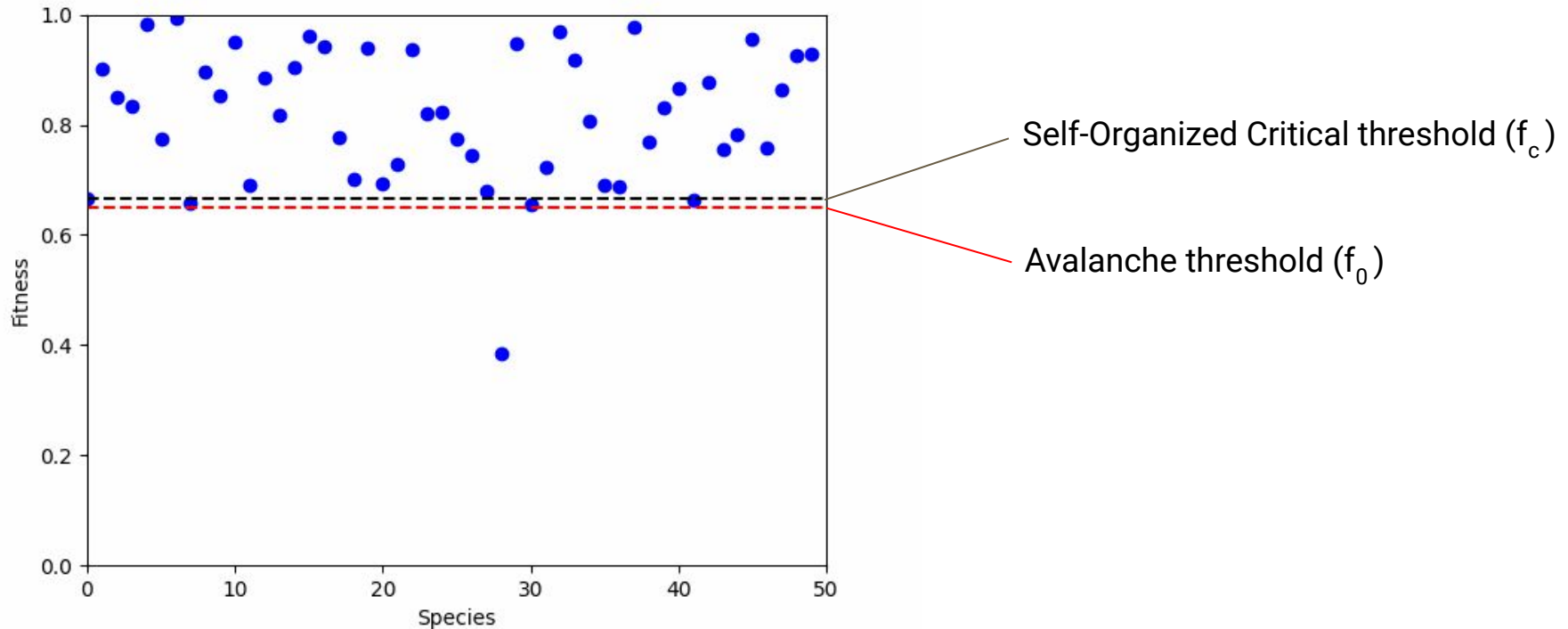
# 1D Bak-Sneppen Avalanches



Only 2% of species  
System already in Critical state



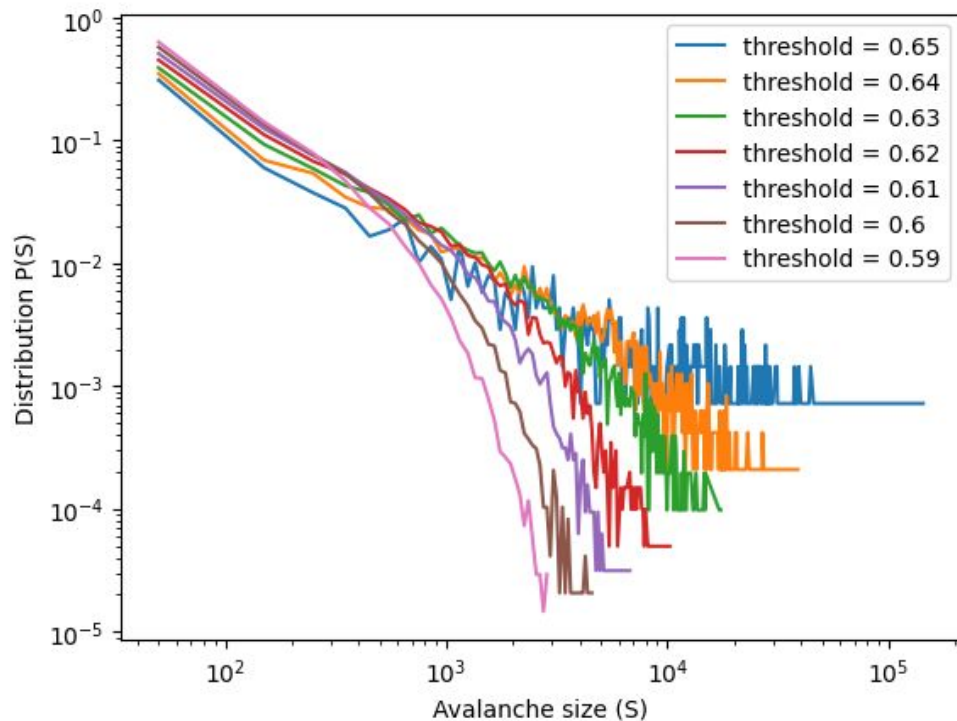
# Fitness changes in 1D model- animation





# Impact thresholds for 1D

Avalanche size distribution

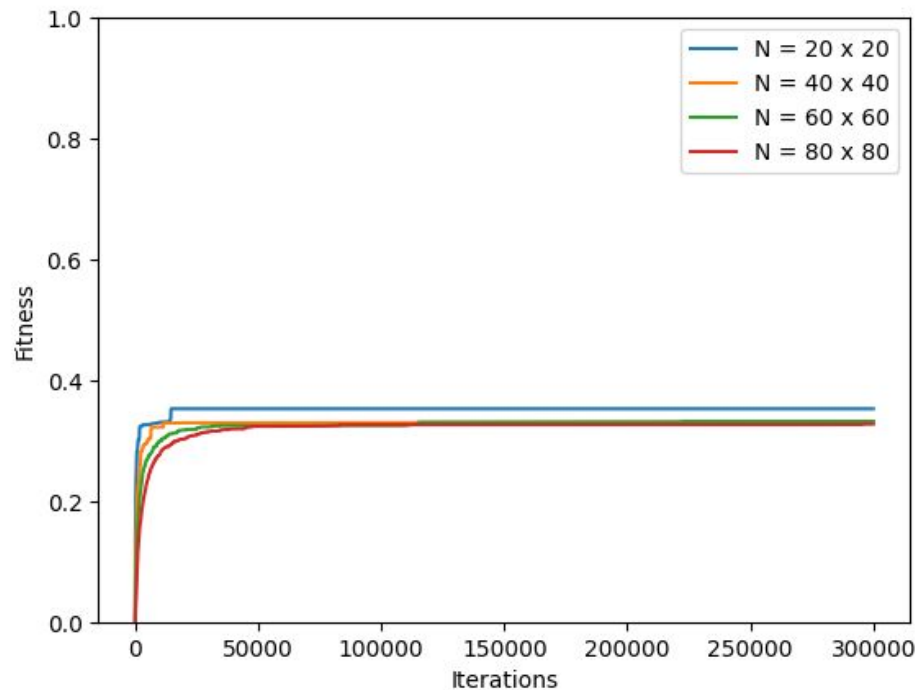
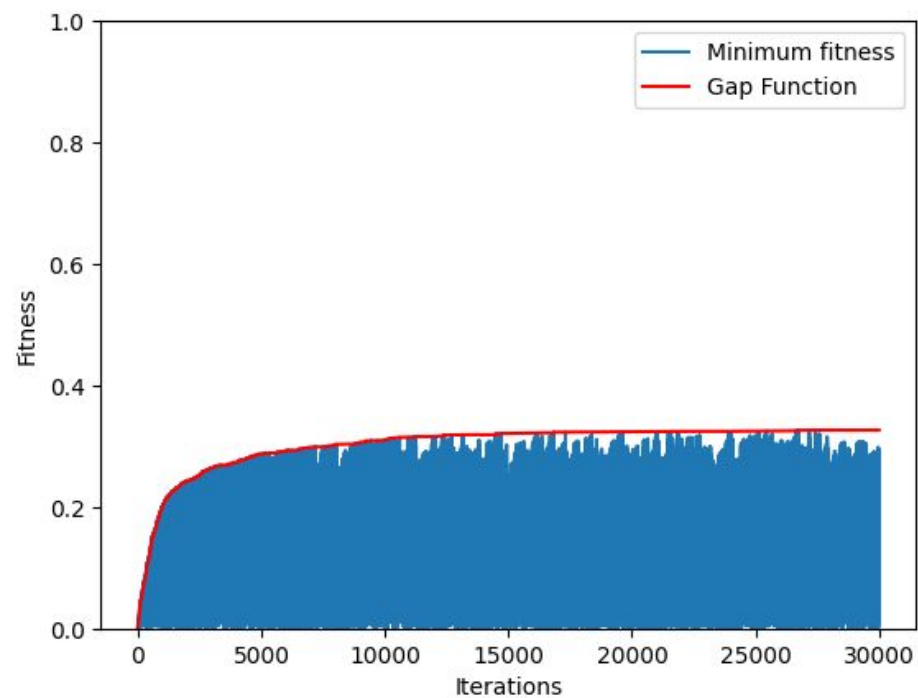


$$P(S, f_0) = S^{-\tau} g(S(f_c - f_0)^{1/\sigma})$$

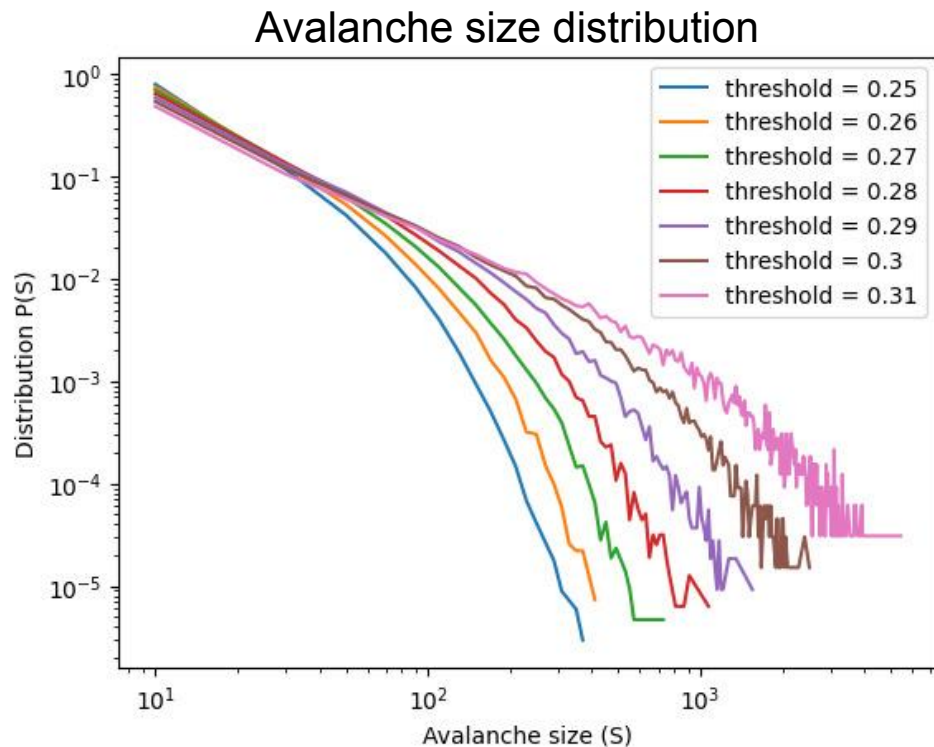
$$\text{cutoff } S_{co} = (f_c - f_0)^{-1/\sigma}$$

# Gap function 2D

$$f_c = 0.329$$



# Impact thresholds for 2D

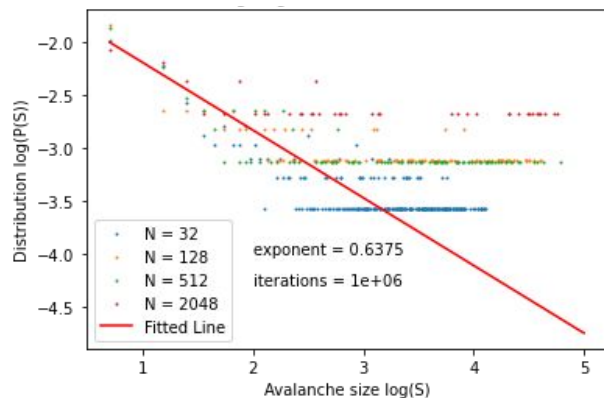


$$P(S, f_0) = S^{-\tau} g(S(f_c - f_0)^{1/\sigma})$$

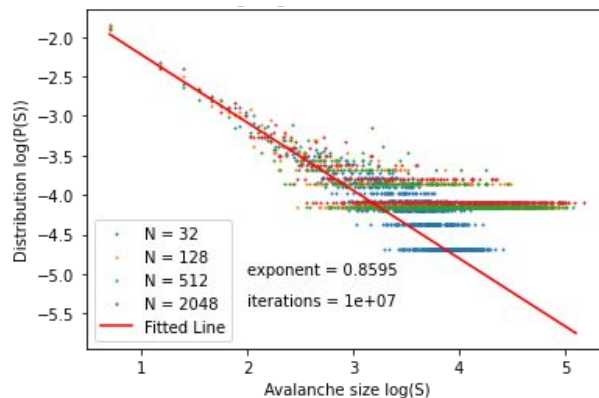
$$\text{cutoff } S_{co} = (f_c - f_0)^{-1/\sigma}$$

# Power law fit 1D

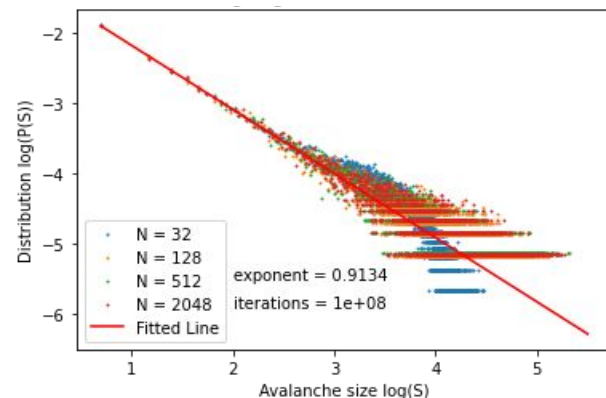
- Simulation avalanche threshold  $f_0 = 0.65$
- Critical threshold  $f_c = 0.667$
- Fitted exponent = 0.91
- Critical exponent  $\tau = 1.07$



$10^6$  iterations



$10^7$  iterations

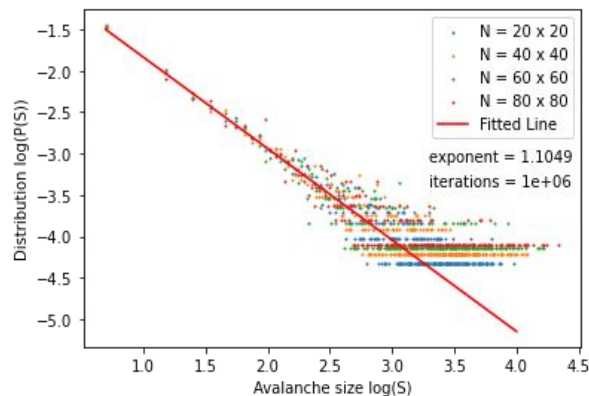


$10^8$  iterations

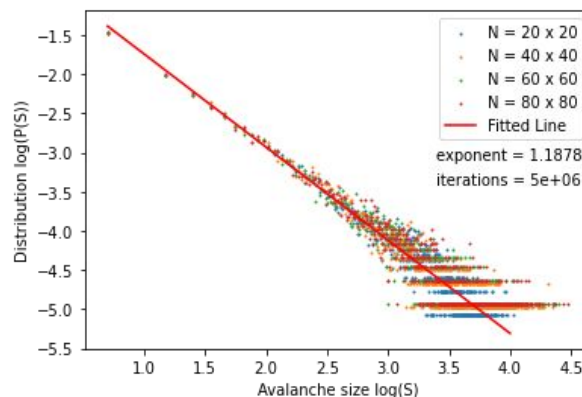
# Power law fit 2D

- Simulation threshold  $f_0 = 0.32$
- Critical threshold  $f_c = 0.329$
- Fitted exponent = 1.247
- Critical exponent  $\tau = 1.245$

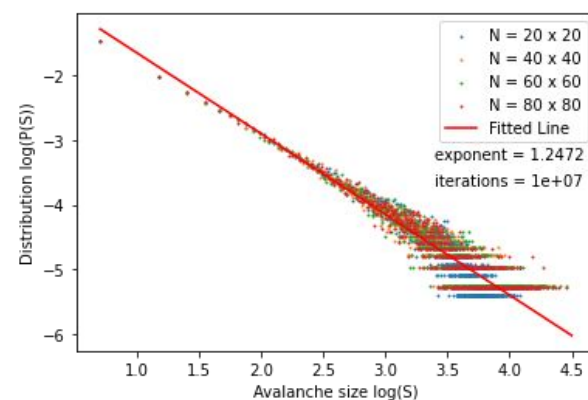
$10^6$  iterations



$5 \times 10^6$  iterations



$10^7$  iterations



# Results: Comparison of 1D and 2D

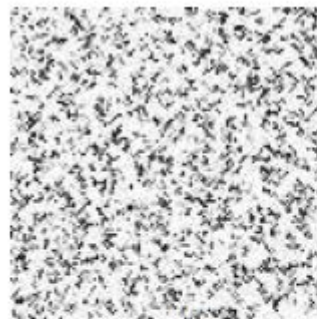
## Hypotheses:

1 mutation will have a bigger effect for the 2D model compared to the 1D model. If this increase is sufficiently large, the model could break as it is pushed out of its criticality state. This would happen when the power law exponent becomes  $> 2$ .

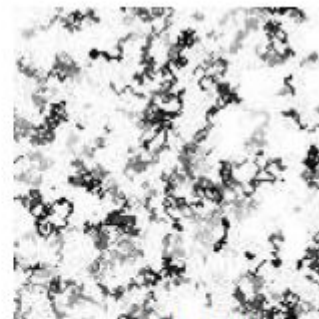
	Simulation Threshold	Critical Threshold	Simulation Exponent	Critical Exponent
1D	0.65	0.667	0.913	1.07
2D	0.32	0.329	1.247	1.245

# Growth Opportunities

- Implementing Migration
- Networks
- Increasing connections →  
when no longer SOC?



$t = 10$



$t = 10000$

**Figure 3.** Distribution of fitness values on the grid. Lighter grey areas correspond to particles with lower fitness.  $X \times Y$ :  $60 \times 60$ ;  $n = 1200$ .

\*Figures from reference 3.

**Questions?**



# References

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8. Paczuski, Maya, Sergei Maslov, and Per Bak. "Avalanche dynamics in evolution, growth, and depinning models." *Physical Review E* 53, no. 1 (1996): 414.
9. Wikipedia contributors. "Bak–Sneppen Model." *Wikipedia*, May 2023, [en.wikipedia.org/wiki/Bak%E2%80%93Sneppen\\_model](https://en.wikipedia.org/wiki/Bak%E2%80%93Sneppen_model).

# Appendix

# Adapting Bak-Sneppen to 2D Migration

Additions to Simulation:

- N species, 2D system with periodic boundary conditions.
- Von Neumann neighborhood mutations
- Moore neighborhood movement (migration)
- Leaves mark at previous location (migration)

## **Adapting the Bak-Sneppen Model to a Dynamic and Partially Connected Grid of Hierarchical Species**

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# Migration

- Implementing migration should result in clustering throughout the system
- We were not quite able to get full clustering
- This comes from not being able to find out the exact order in which to move the cells
- Small clusters did form, but only briefly so it's mostly random
- This could be because we could not get the periodic grid to work

