

# Bootstrap Percolation in Random Geometric Graphs

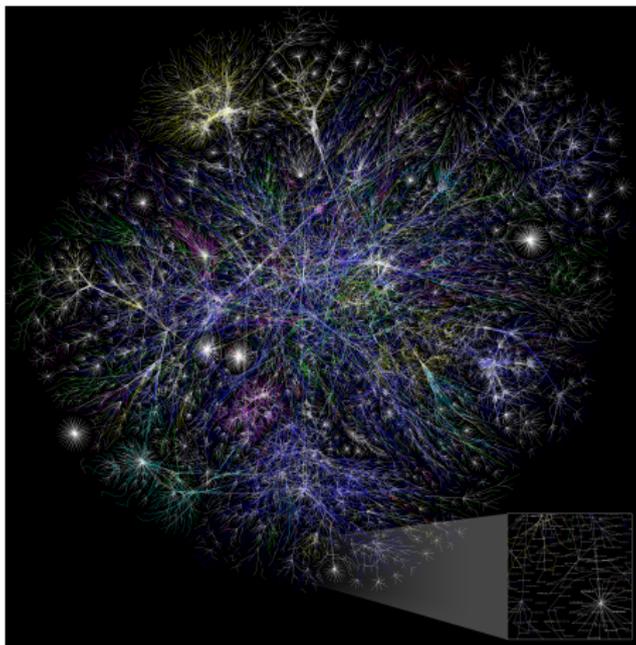
Amites Sarkar

Western Washington University

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Joint work with Victor Falgas-Ravry (Umeå University)

*Large networks* are everywhere.



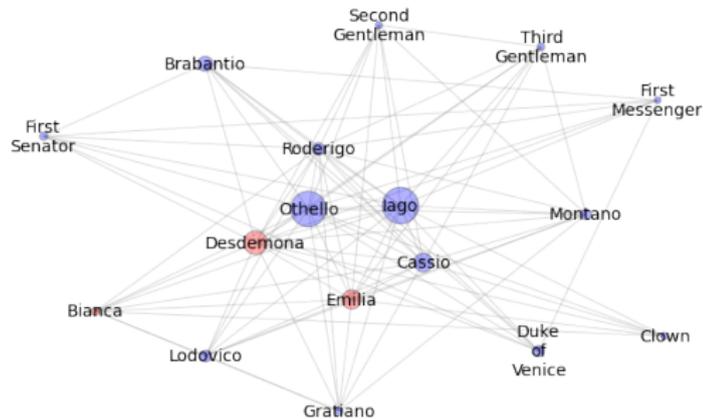
Internet

Credit: Matt Britt



And another:

Othello's Social Network



Credit: Shakespeare, Adam Palay

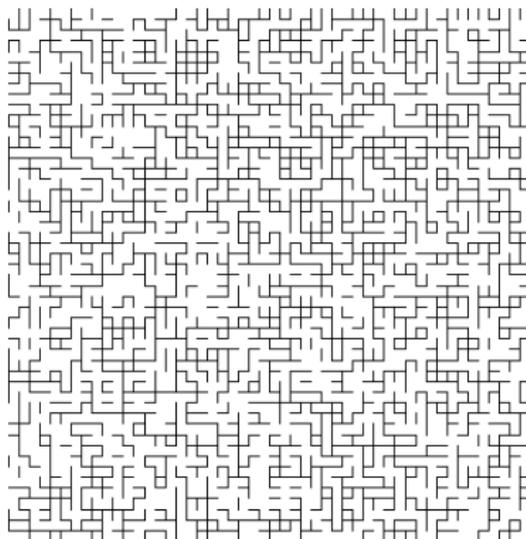
*Phase transitions* are also everywhere, especially in physics.

- Water boils at  $100^{\circ}\text{C}$ .
- The Curie temperature of iron is  $770^{\circ}\text{C}$ .
- An egg scrambles at  $70^{\circ}\text{C}$ .

Why?

A phase transition (math: *sharp threshold*) often has a large random network underneath it.

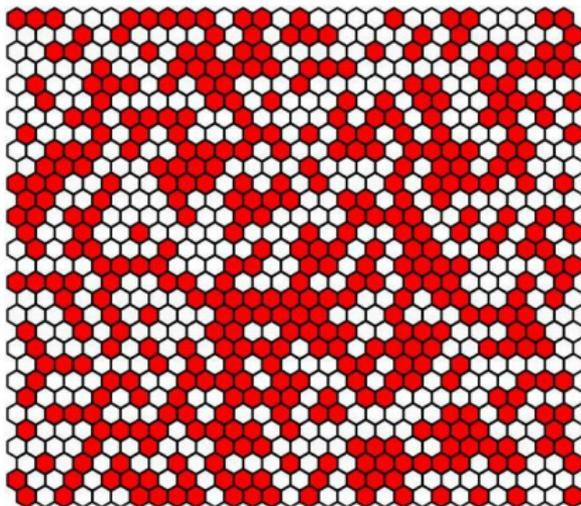
## Bond percolation in the square lattice (Broadbent and Hammersley 1957)



Edges (bonds) included independently with probability  $p$

Kesten (1980)  $p_c = \frac{1}{2}$

## Face percolation in the hexagonal lattice

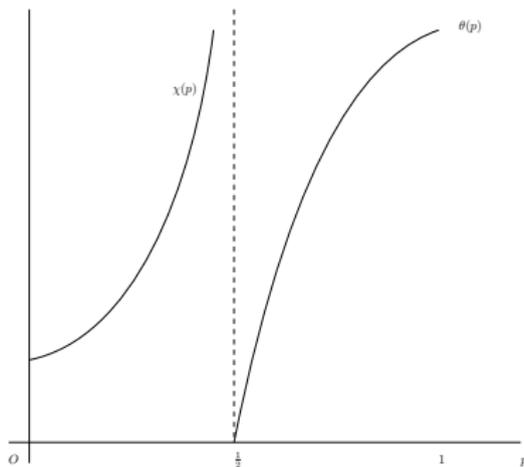


Kesten (1982)  $p_c = \frac{1}{2}$

Schramm, Smirnov, Lawler/Schramm/Werner, Smirnov/Werner  
(early 2000s)

$$\beta = \frac{5}{36}, \quad \gamma = \frac{43}{18}, \quad \delta = \frac{91}{5}, \quad \eta = \frac{5}{24}, \quad \nu = \frac{4}{3}$$

## $\beta$ and $\gamma$

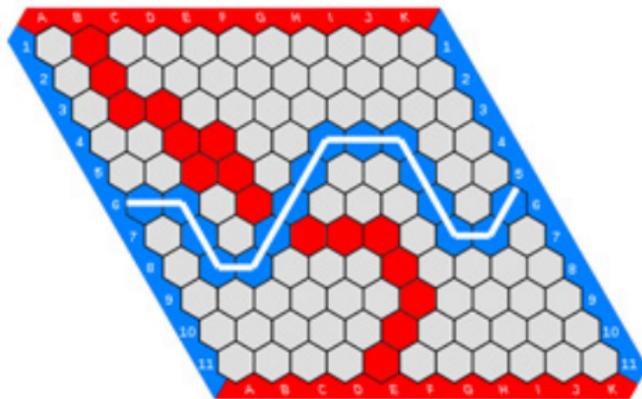


$C$  = connected cluster containing the origin

$$\theta(p) = \mathbb{P}_p(|C| = \infty) = (p - p_c)^{\beta+o(1)} \text{ as } p \downarrow p_c$$

$$\chi(p) = \mathbb{E}_p(|C|) = (p - p_c)^{-\gamma+o(1)} \text{ as } p \uparrow p_c$$

$$p_c = \frac{1}{2}$$



$$\mathbb{P}_{1/2}(R) = \mathbb{P}_{1/2}(B)$$

$$\mathbb{P}_{1/2}(R) + \mathbb{P}_{1/2}(B) = 1$$

$$\mathbb{P}_{1/2}(R) = \mathbb{P}_{1/2}(B) = \frac{1}{2}$$



Other models exhibiting phase transitions:

**random graphs**

**branching processes**

## Poisson processes - definition

- Tessellate  $\mathbb{R}^2$  with unit squares
- In each square  $S_i$ , independently, place  $X_i$  points uniformly at random, where  $X_i \sim \text{Po}(1)$ , i.e.,

$$\mathbb{P}(X_i = k) = \frac{1}{ek!}$$

- This has many more nice properties than one might expect

[A Poisson process is a limit as  $N \rightarrow \infty$  of the process obtained by placing  $N$  points uniformly at random in a box of area  $N$ .]

## Poisson processes - properties

$\mathcal{P} =$  **Poisson process** of intensity 1 in  $\mathbb{R}^2$



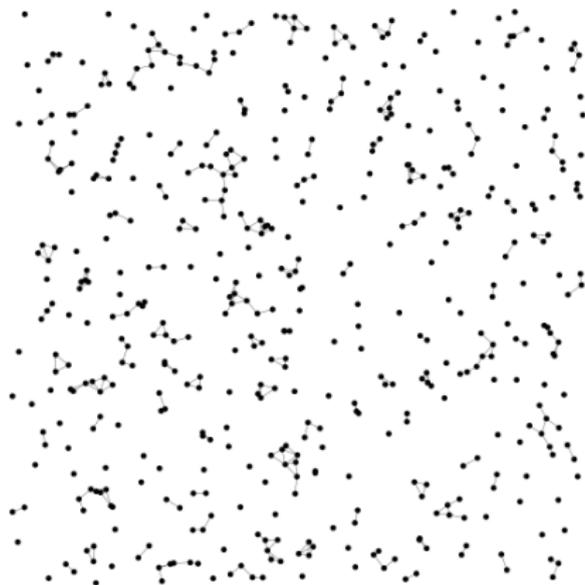
- Number of points  $X$  inside any region  $A$  is a random variable with the Poisson distribution of mean  $|A|$ , so that

$$\mathbb{P}(X = k) = \frac{e^{-|A|} |A|^k}{k!}$$

- Disjoint regions are independent

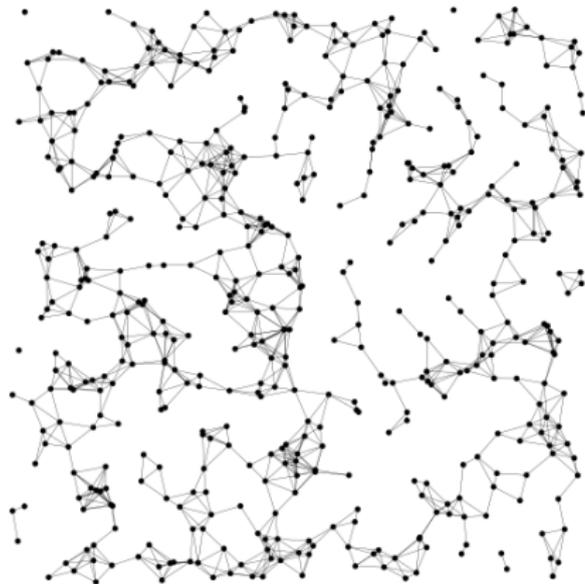
[A Poisson process is a limit as  $N \rightarrow \infty$  of the process obtained by placing  $N$  points uniformly at random in a box of area  $N$ .]

## Random geometric graphs (Gilbert 1961)



Vertices (nodes) are a Poisson process of intensity 1  
Edges join vertices at distance less than  $r$   
Gilbert's motivation: communications networks

## Percolation

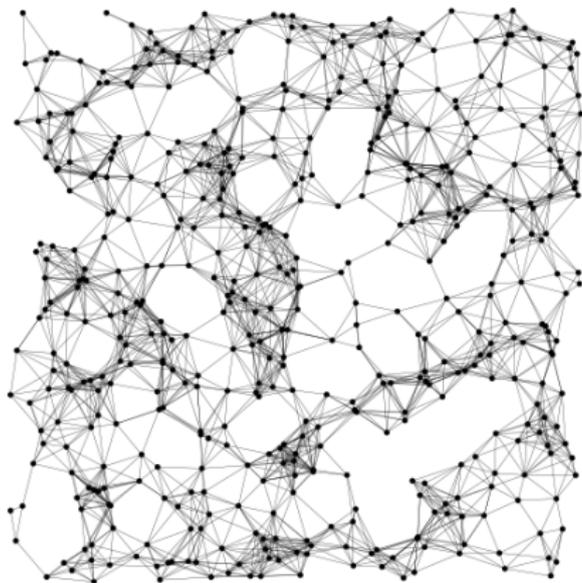


Hall (1985)  $0.833 < r_{\text{perc}} < 1.836$

Balister, Bollobás and Walters (2005)  $1.1978 < r_{\text{perc}} < 1.1989$

- semi-rigorous, high confidence result

## Connectivity



Penrose (1997)  $\pi r_{\text{conn}}^2(n) = \log n$

Obstruction to connectivity: isolated vertices

At the threshold,  $\mathbb{E}(\text{isolated vertices}) = 1$

## Disclaimers

Instead of using a square, we put the points in a **torus**, to avoid boundary effects.

Connectivity is only guaranteed **with high probability**, i.e., with probability tending to 1 as  $n \rightarrow \infty$ .

The same applies to (almost) every other definitive-sounding statement I'll make.

## The Bradonjić-Saniee model (2014)

Start with the Gilbert model, above the connectivity threshold

$$\pi r^2 = a \log n \text{ with } a > 1$$

Initially infect vertices independently with probability  $p$ : this is  $A_0$

Each vertex expects

$a \log n$  neighbors

$ap \log n$  infected neighbors

$A_t :=$  set of infected vertices at time  $t$

In each discrete time step ( $t = 1, 2, \dots$ )

For each  $v \notin A_t$  (i.e. each uninfected  $v$ )

If  $v$  has at least  $a\theta \log n$  infected neighbors

- $v$  becomes infected (and stays infected forever)

Repeat for each vertex  $v$  to get  $A_{t+1}$

Repeat for each  $t$  to get  $A_\infty$

What proportion  $|A_\infty|/n$  of the graph eventually becomes infected?

### Theorem (Bradonjić and Saniee 2014)

For  $x > 0$ , define

$$J(x) = \log x - 1 - 1/x$$

and write  $J_R^{-1}$  for the inverse of  $J$  on  $[1, \infty]$ . Then if

$$p < p' = \theta / J_r^{-1}(1/a\theta)$$

then no initially uninfected vertex becomes infected.

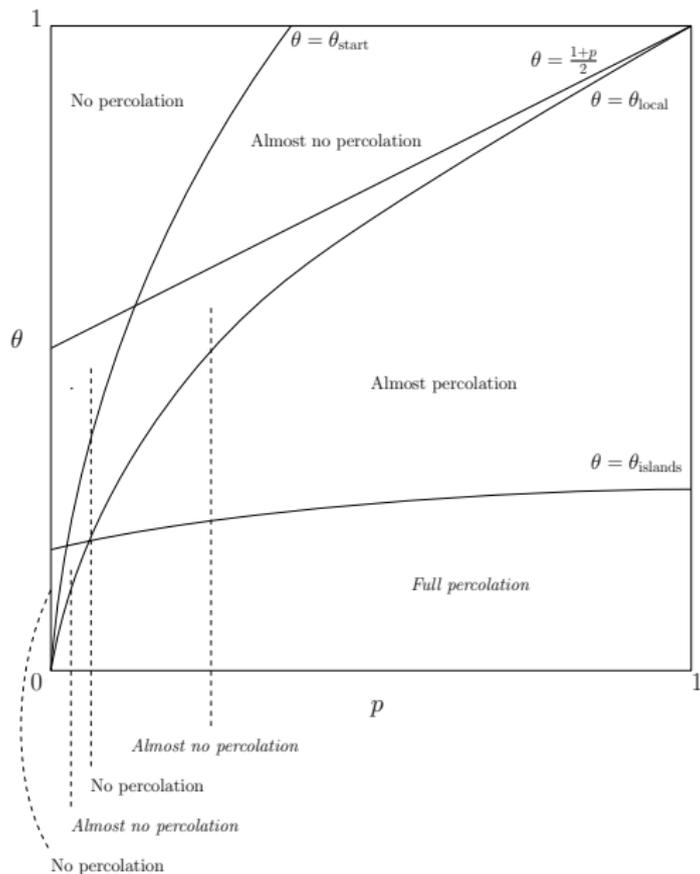
### Theorem (Bradonjić and Saniee 2014)

If

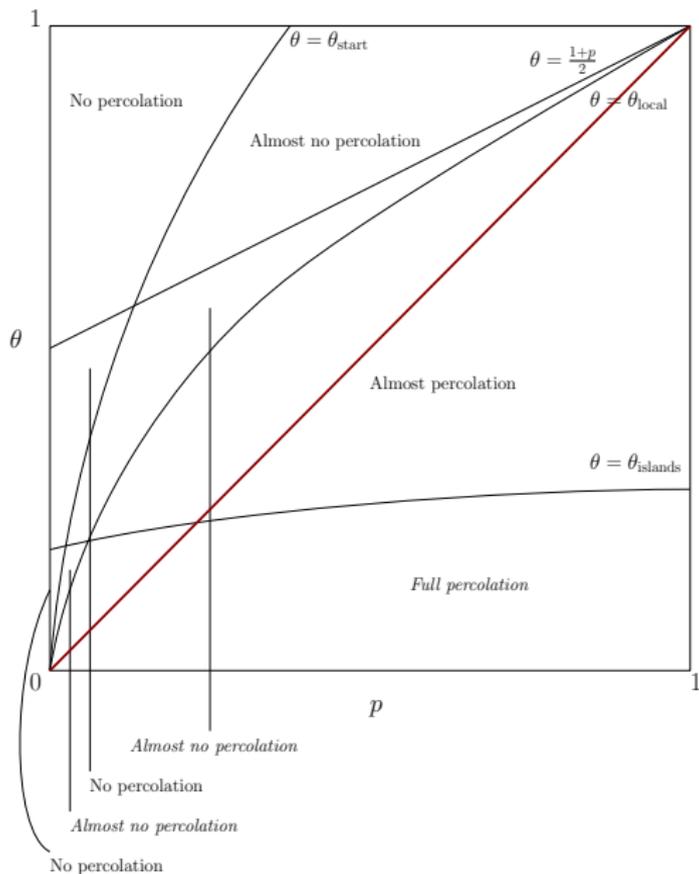
$$p > p'' = \min \left\{ \theta, \frac{5\pi\theta}{J_r^{-1}(1/a\theta)} \right\}$$

then every initially uninfected vertex becomes infected.

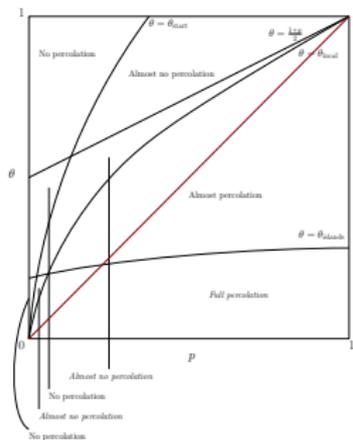
# Theorem (Falgas-Ravry and S 2022+)



## Basic orientation - the threshold $\theta = p$



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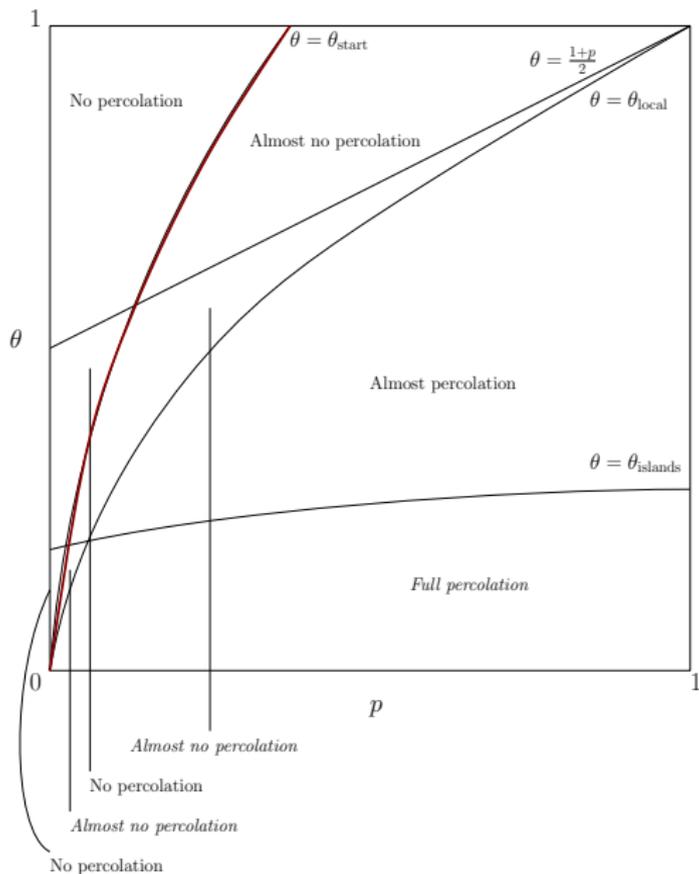


If  $\theta < p$ , almost everything becomes infected immediately.

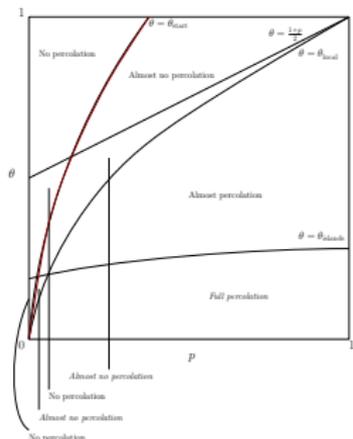
If  $\theta > p$ , almost no new infections occur initially.

But this turns out to be completely irrelevant.

# The starting threshold $\theta = \theta_{\text{start}}(p)$



## The starting threshold $\theta = \theta_{\text{start}}(p)$



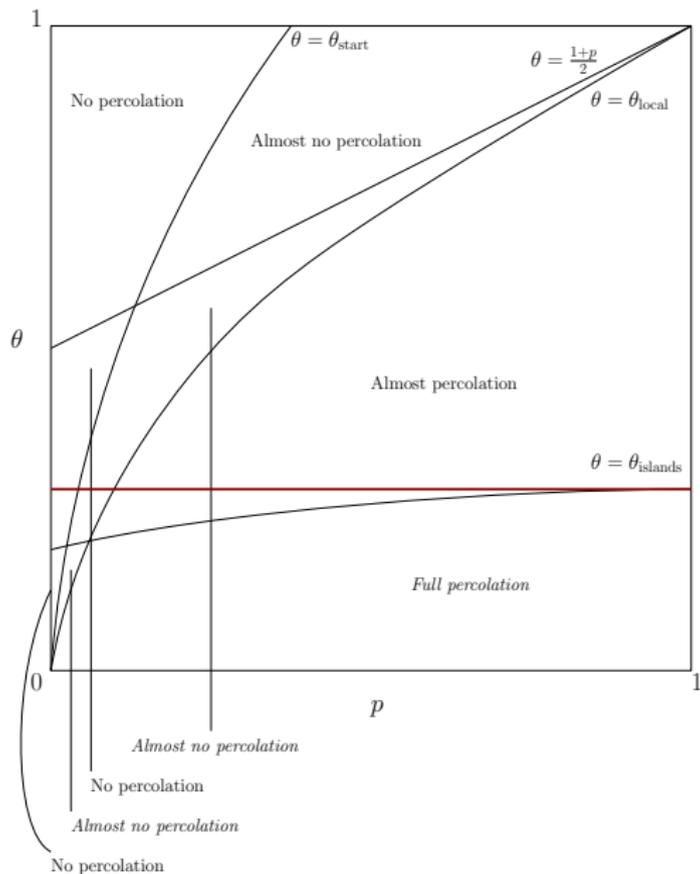
Sometimes, even when the threshold  $\theta$  is much greater than  $p$ , some uninfected vertices will see  $a\theta \log n$  infected neighbors, despite only expecting to see only  $ap \log n$ .

This will happen when

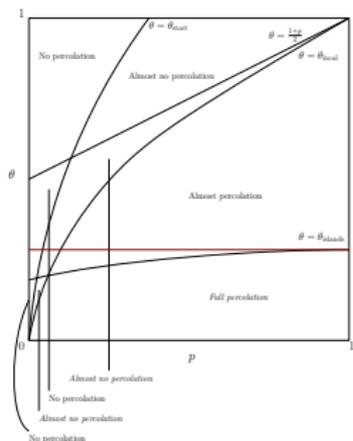
$$f_{\text{start}}(a, p, \theta) = a(p - \theta + \theta \log(\theta/p)) < 1.$$

In this case, the infection will start to spread, and grow to at least logarithmic size.

# The simple stopping threshold $\theta = \theta_{\text{stop}}$



## The simple stopping threshold $\theta = \theta_{\text{stop}}$



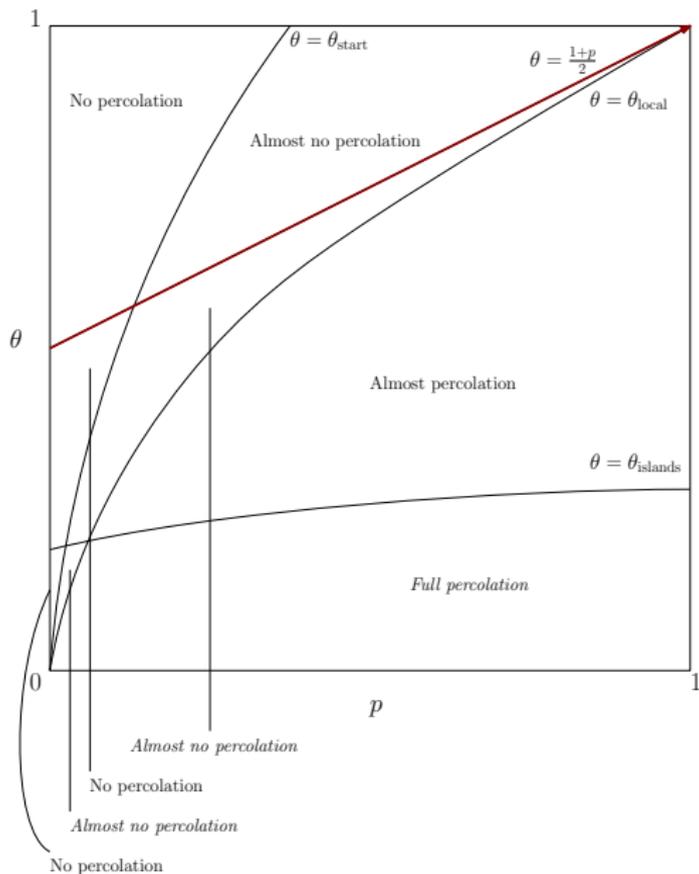
On the other hand, some initially uninfected vertices will not even have  $a\theta \log n$  neighbors, despite only expecting to see  $a \log n$ . These vertices can never become infected.

This will happen when

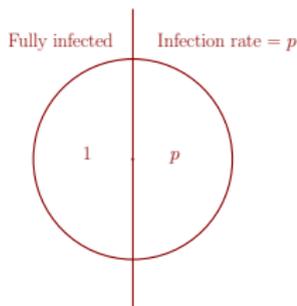
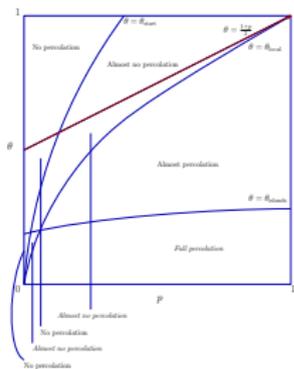
$$f_{\text{stop}}(a, \theta) = a(1 - \theta + \theta \log \theta) < 1.$$

This yields a simple necessary condition for full percolation.

# The growing threshold $\theta = \frac{1+p}{2}$



## The growing threshold $\theta = \frac{1+p}{2}$

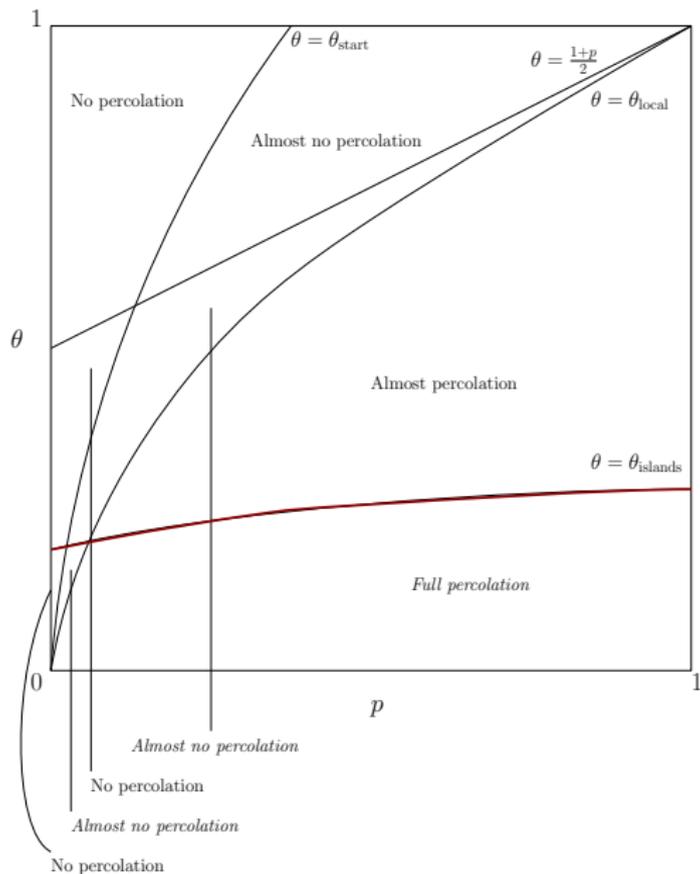


When infections have broken the logarithmic barrier, they will grow as long as

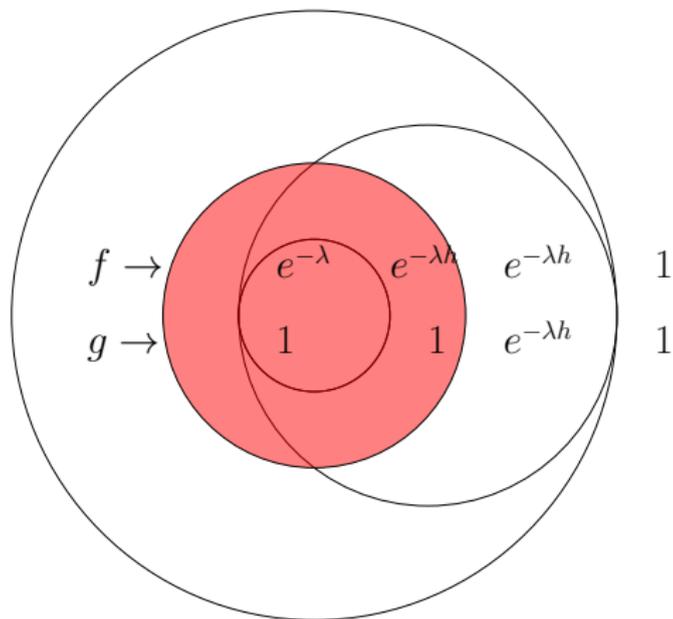
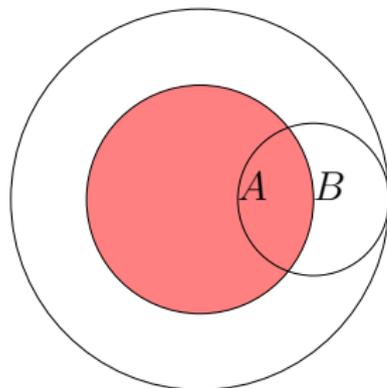
$$\theta < \frac{1+p}{2}$$

But they need to clear a lot of local hurdles first.

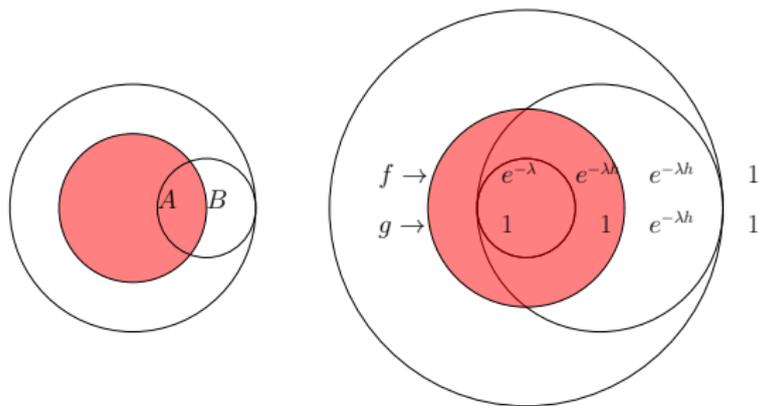
# The threshold for full percolation $\theta = \theta_{\text{islands}}(p)$



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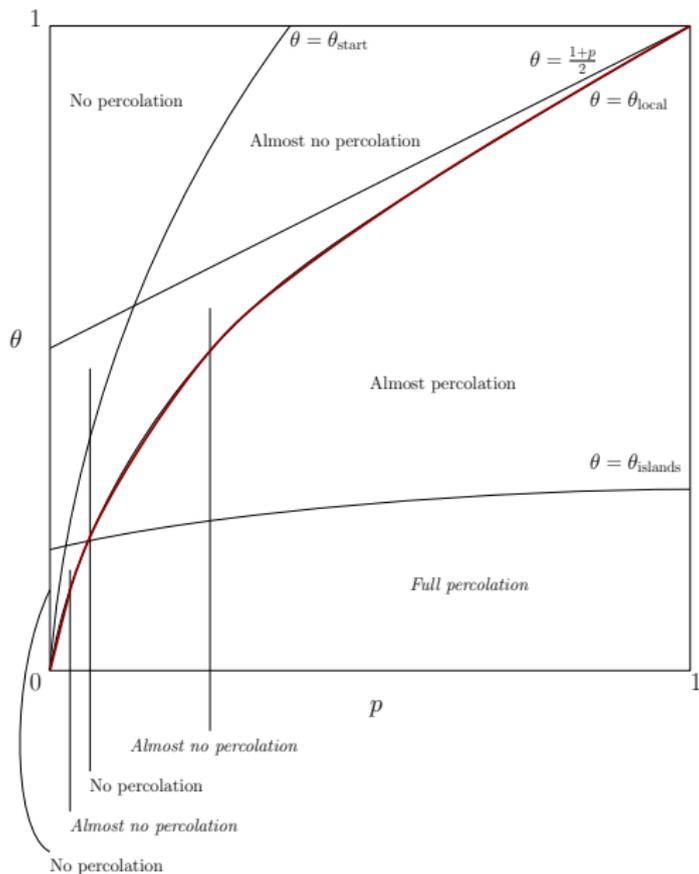


At the other end, there are small obstructions to full percolation, of radius  $\tau r$ . These can be optimized (for fixed  $\tau$ ) using Lagrange multipliers, and the Euler-Lagrange equations

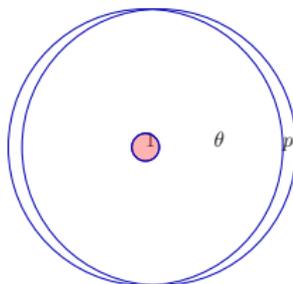
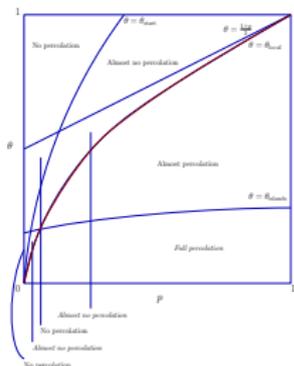
$$\frac{d}{dx} \frac{\partial F}{\partial y'} = \frac{\partial F}{\partial y}$$

We then optimize over  $\tau$ , to find the most likely obstruction.

# The local growth threshold $\theta = \theta_{\text{local}}(p)$



## The local growth threshold $\theta = \theta_{\text{local}}(p)$

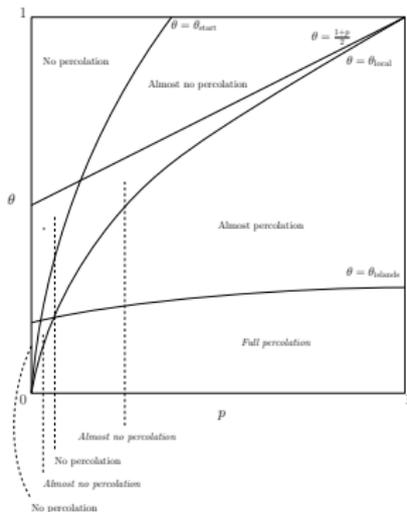


To break the logarithmic barrier, infections need to do more than just start.

They need to be able to expand beyond each radius  $\tau r$ .

This yields a Lagrange multiplier problem with **infinitely many conditions**.

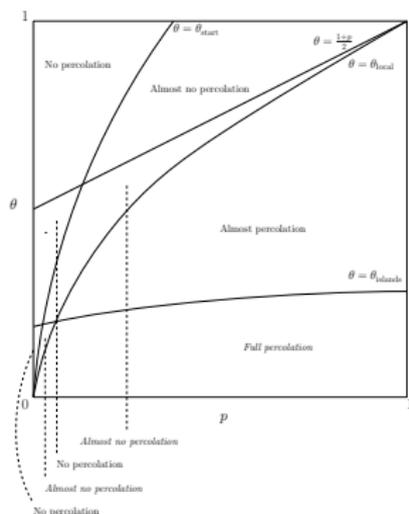
## What did we actually prove?



The local growth threshold is only a sufficient condition for local growth, and the islands threshold is only a necessary condition for full percolation.

Accordingly, these thresholds only provide a lower bound for local growth and an upper bound for full percolation.

## What did we actually prove?

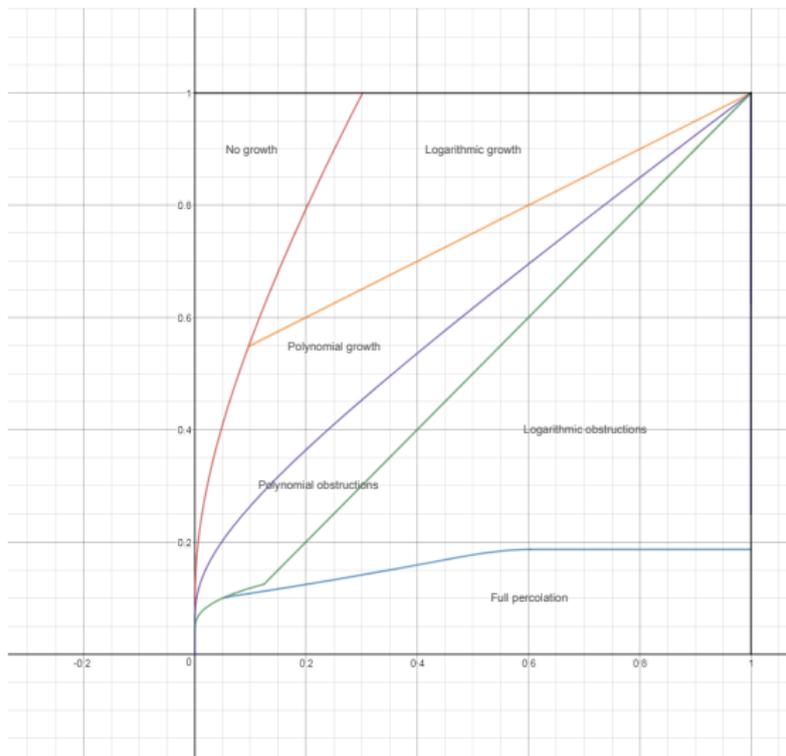


We did prove that the growing condition is the true threshold for local infections becoming global.

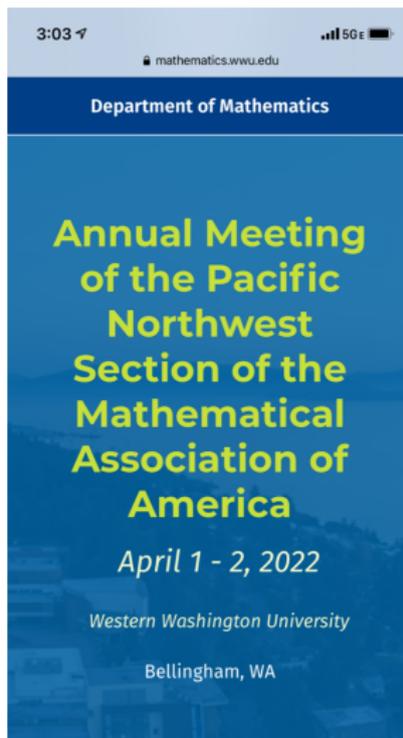
Some tools in the proof:

**tessellation arguments (fine and rough tilings)**  
**discrete isoperimetric inequalities**

# It's more complicated in one dimension



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Thank you for your attention!