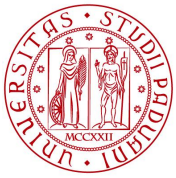

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Corso di Laurea Magistrale in Matematica

Bootstrap percolation in geometric inhomogeneous random graphs

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Contents

List of Figures

List of Symbols

$\Gamma(v)$	Set of neighbours of v
$v \leftrightarrow w$	v and w are connected
CC_G	Clustering coefficient of G
U	Uniform random variable
$\mathcal{C}_{\max}$	Connected component of maximum size
$\mathcal{C}_2$	Second largest connected component
η	Extinction probability of branching process
ζ	Survival probability of branching process
$\mathbb{G}(n,p)$	Erdős-Renyi random graph
$\mathbb{G}(n,\mathbf{K})$	Inhomogeneous random graph with kernel $\mathbf{K}$
$\mathbb{G}(n,\underline{w})$	Generalized random graph with weight sequence $\underline{w}$
$\mathbb{T}^d$	d-dimensional torus
$V_{\geq w}$	Set of vertices with weight larger than w
V_C	Set of vertices with position in C
V^t	Set of infected nodes at step t
$\mathrm{Poi}(\lambda)$	Poisson random variable with mean λ
$\mathrm{Be}(p)$	Bernoulli random variable with success probability p
$\mathrm{Bin}(n,p)$	Binomial random variable with n trials and success probability p
o	Landau small-o notation
$\mathcal{O}$	Landau big-O notation

Introduction

Graphs serve as essential tools for modeling a wide range of phenomena, from social interactions to biological networks. However, as the size and complexity of these systems grow, analyzing them becomes increasingly challenging. Random graphs have emerged as a powerful abstraction, enabling researchers to study large-scale networks by introducing randomness into graph structures. With the explosion of available data in today's digital age, random graph theory has gained more and more relevance for understanding complex systems.
The main focus of these studies aim to understand the common features shared by many networks and explore their implications for various kinds of dynamical processes evolving on them.

The Erdős-Rényi model stands as a cornerstone in random graph theory, providing a foundational framework characterized by its simplicity and elegance. This model, where edges between vertices are independently included with a certain probability, has paved the way for more sophisticated variations, such as inhomogeneous random graphs, which accommodate the heterogeneity observed in real-world networks, leading to scale-free structures characterized by power-law degree distributions.

Real-world networks frequently demonstrate high connectivity, leading to the emergence of a prominent structural feature known as the giant component. This component represents the largest portion of nodes that happens to be interconnected; requiring that this component covers the majority of the graph, or more precisely a positive fraction of its vertex set, is a needed assumption for the study of any process performed on it, and one of the main problem when dealing with a random graph model is thus to establish the conditions that guarantee its existence.
High connectivity in real-world networks often accompanies the so-called 'small-world' property, characterized by polylogarithmic distances between nodes. One prominent example of this typical phenomenon is the Erdős number, which illustrates how even within the vast scientific community, a

relatively small number of collaborations - represented as edges in the publication network - is often sufficient to connect an author to Paul Erdős. Erdős, being a highly connected node, effectively reduces the distances between seemingly remote authors to a logarithmic scale.

Another key feature, struggled to be captured by classical random graph models, is large clustering coefficient. The formulation of preferential attachment models, like those proposed by Watts and Strogatz, addressed the absence of this characteristic, which was a shared missing attribute due the assumption of independence of the edges, as well as in inhomogeneous random graphs.
However, recent advancements such as hyperbolic random graphs and geometric inhomogeneous random graphs offer promising avenues for bridging this gap, enabling more accurate representations with the incorporation of all these features.
In random graphs, geometry serves not only as a representation of spatial attributes but also as a broader concept reflecting proximity between nodes. This proximity can encompass various dimensions, such as shared interests, geographical proximity, common affiliations, or frequent interactions. Whether nodes are physically close or share similar characteristics, the underlying geometry captures the essence of their connectivity, facilitating the formation of edges based on various types of proximity or similarity.

It is through the concept of thresholds that researchers formulate the absence or emergence of these properties: these are functions depending on the parameters of the model (in particular the network size) that set an asymptotic boundary to the certain (probabilistically) occurrences of these events.

Among the processes that has been studied on graphs, lattices or general network structures, bootstrap percolation is probably one of the most relevant. Recent studies have explored this process within geometric models, shedding light on its applicability and implications.
Bootstrap percolation is a deterministic process of activation or infection that spreads through a given realization of a graph, starting from a set of initially active nodes. At each step, inactive vertices with at least $r \geq 2$ active neighbors become active themselves. This process continues until no more vertices can become active, resulting in a set of active vertices that grows monotonically. It has gained attention for its effectiveness in modeling various phenomena, ranging from the diffusion of a disease or information to neuronal activity, from the spread of defaults in banking systems to the jamming transition of materials. Originally developed in the context of magnetic systems, bootstrap percolation offers a simplified yet powerful approach to understanding network resilience.

Its dynamics has been extensively studied on different types of graphs, ranging from deterministic to random graphs. In deterministic scenarios, researchers investigate optimal initial sets, while in random scenarios, initial sets are chosen randomly, and the general aim is to investigate the dependence of the initial set of activation on the final activated set.
In the same way as the study of 'statical' properties of standalone random graphs, the behavior of this process, its outcome and velocity are tried to be contained within thresholds: as happens, for example, in the emergence of the giant component, the process will be shown to face a sharp transition with respect to a specific function, from a situation in which, basically, no vertex becomes infected (excepts the initial ones) to one in which almost all the vertices will be infected (where the meaning of 'almost all the vertices' will be made clear already in the analysis of the largest connected component).
However, differently from what has been observed in the percolation of the previous models such as Erdős-Rényi or Chung-Lu, there is also a 'gray' area, coinciding with the threshold function itself, in which both scenarios are possible with positive probability.

Outline of the thesis

In this thesis, we will give an introduction to the theory of random graph, trying to give a uniform and smooth presentation of the key concepts and ideas both behind construction and proof of the prescribed characteristics. The theory is vast, with different models enclosing different purposes and features: we will focus the dissertation starting from the Erdős-Rényi model, generalizing and enriching it to finally achieve the geometric model, which incorporates all the desired characteristics, focusing in particular on the giant component feature. On this model we will present the study of bootstrap percolation and describe the main results, before simulating and testing numerically their validity.

In chapter one, we introduce definitions and key concepts of the theory of random graphs, present the cornerstone model of Erdős-Rényi, and analyze it using in particular Branching processes, through which the existence of the giant component is shown.

In chapter two, we extend the model of Erdős-Rényi to the Inhomogeneous random graph model and study the existence of the giant component through multi-type branching processes. We focus then on the generalized random graph or Chung-Lu model.

In chapter three, we present the geometric inhomogeneous random graph model as an extension of the Chung-Lu model, analyze its characteristics

and prove the existence of the giant component for the threshold case of the model.

In chapter four, we define bootstrap percolation and summarize some known results concerning the evolution of the process on the models of the first two chapters. The rest of the chapter is devoted to its analysis on the geometric model.

Finally, in chapter five, a numerical simulation of the process on the geometric model is performed. The results presented are tested numerically for increasing number of nodes.

Acknowledgments

There are too many people I would like to thank for their presence and support during this long period of my master's degree, so I will thank two individuals. First, my supervisor Alessandra Bianchi, for introducing me to the fascinating theory of random graphs, encouraging me in my studies, motivating me with various insights into different topics and applications and helping me in the understanding of difficult concepts. Last but not least, I thank myself for not giving up, for persevering in the goal of concluding a long journey that began well but was disrupted by a pandemic and made challenging by finding a full-time job.

Chapter 1

Random graphs

1.1 Preliminaries

A graph is a pair $G = (V, E)$, where V is the set of vertices and E is the set of edges, where an edge is identified by a pair of vertices. We will identify the vertex set with natural number; denote with $[n] = \{1, 2, \ldots, n\}$ and $\mathcal{G}_n = \{G = (V, E)\colon V = [n]\}$ the set of graphs with n vertices.

- Two vertices v, w are neighbours if the edge $(v, w) \in E$, and we will then write $v \sim w$. The number of neighbours of v is called degree of v and denoted as $d_G(V) = \#\{w \in V : w \sim v\}$.

- A path γ from v to w is a sequence $v = v_0, v_1, \ldots, v_k = w$ such that $v_j \sim v_{j+1}, \forall j$. It can be viewed as a sequene of edges $e_1, \ldots, e_k$ where $e_i = (v_{i-1}, v_i)$. Its length is by definition the number of edges apperaing in the sequence and denoted by $|\gamma| = \#\text{edges}$.

- Two vertices v, w are connected if there exists a path connecting them, and we will write $v \leftrightarrow w$.
  We define the Cluster or connected component of a vertex $v \in V$ as $\mathcal{C}(v) = \{w \in V : v \leftrightarrow w\}$.

- We can define a distance on V setting $\mathrm{d}_G(v, w) = \min_{\gamma : v \leftrightarrow w} |\gamma|$ with the convention $\min \varnothing = \infty$.

- The diameter of a graph G is defined as $\mathrm{diam}(G) = \max_{v,w \in V} \mathrm{d}(v, w)$

- The largest component of G (which may be not unique) is defined as $\mathcal{C}_{\max} = \max_{v \in V} |\mathcal{C}(v)|$

- denote with $\mathcal{K}_n$ the complete graph with n vertices and $\mathcal{E}_n$ its edge set.

A rooted graph is a pair (G_n, ρ_n), with $G_n \in \mathcal{G}_n$ and $\rho_n \in [n]$ a fixed vertex. Let (G, ρ) an infinite size rooted graph.

Definition 1.1.1. A sequence $(G_n, \rho_n)_{n\in\mathbb{N}}$ converges locally to (G, ρ) if

$$\forall r \geq 1, \quad \lim_{n\to\infty} B_r^{G_n}(\rho_n) \cong B_r^G(\rho)$$

where an isomorphism between graphs is a bijection that preserves the property of vertices of being neighbourhood, and we denoted with $B_r^G(\rho)$ the ball in G of radius r centered in ρ, i.e. the subgraph of G spanned by the vertices at a distance $< r$ from ρ.
We can ask equivalently that

$$\forall H^* = (H, \rho), \forall r \geq 1 \quad \lim_{n\to\infty} B_r^{G_n}(\rho_n) \cong H^* \iff B_r^G(\rho) \cong H^*$$

Asymptotic notations: let $f(x), g(x)$ be non negative functions. We say that

- $f(x) = \mathcal{O}(g(x))$ iff
$$\limsup_{x\to\infty} \frac{f(x)}{g(x)} < \infty;$$
in particular $f = \mathcal{O}(1)$ means that f is bounded, $f = \mathcal{O}(n)$ that it is at most linear.
- $f(x) = o(g(x))$ iff
$$\lim_{x\to\infty} \frac{f(x)}{g(x)} = 0;$$
in particular, $f = o(1)$ means that $f \to 0$ and $f = o(n)$ that it is sublinear.
- $f(x) = \Omega(g(x))$ iff $g = \mathcal{O}(f)$;
- $f(x) = \omega(g(x))$ iff $g = o(f)$
- $f(x) = \Theta(g(x))$ iff $f(x) = \mathcal{O}(g(x)) \cap \Omega(g(x))$
- $f(x) \sim g(x)$ iff
$$\lim_{x\to\infty} \frac{f(x)}{g(x)} = 1$$

We say that a property (represented through some event $A = A_n$ depending on n, the graph size) holds with high probability (abbreviated whp) if $\mathbb{P}(A_n) = 1 - o(1)$, meaning that with n increasing the probability that A_n is true tends to 1.

1.2 Random Graphs

We endow $\mathcal{G}_n$ with the σ-algebra given by the power set, together with a probability distribution $\mathbb{P}_n$.

Definition 1.2.1. A random graph is an element of $\mathcal{G}_n$, chosen with probability $\mathbb{P}_n$, and denoted as $\mathbb{G}_n$.

Let $U = U^{(n)} \sim \text{Uniform}([n])$ the uniform random variable on the set $[n]$. Denote the proportion of vertices with degree k in $\mathbb{G}_n$ with P_k,

$$P_k := \frac{1}{n}\sum_{i=1}^{n} \mathbb{1}_{\{\mathrm{d}_{\mathbb{G}}(i)=k\}} = \mathbb{P}(\mathrm{d}_{\mathbb{G}_n}(U) = k). \tag{1.1}$$

When modelling the so called 'real world networks', we want our model to have some key properties that are often empirically observed in them. Real worlds networks are typically really large, so we will be interested in studying the behaviour of $\mathbb{G}_n$ as $n \to \infty$, i.e. we will consider sequences of random graphs with increasing number of vertices.
The main properties that we want our random graphs to possess are the following (here the definitions are given for deterministic sequences; in the context of sequences of random graphs the convergence should be intended as almost everywhere, in distribution or in probability, with eventually more hypothesis concerning convergence of the mean or second moment, thus in general using the notions of convergence of random variables, according to the situation):

- Sparsity: A graph sequence $(G_n)_{n\geq 1}$ is sparse if

$$\lim_{n\to\infty} P_k^{(n)} = p_k, \qquad k \in \mathbb{N} \tag{1.2}$$

  for some $(p_k)_{k\geq 0}$ probability distribution with finite mean μ, so in particular $\sum_{k\geq 0} p_k = 1$.
  Equivalently, we will ask that the random variable $\mathrm{d}(U)$ converges in distribution to a random variable D with density $(p_k)_k$.
  Observe that from this hypothesis it follows that

$$|E(\mathbb{G}_n)| = \frac{1}{2}\sum_{i\in[n]} \mathrm{d}_{\mathbb{G}_n}(i) = \frac{n}{2}\sum_{k\in\mathbb{N}} k \cdot P_k \approx \frac{n}{2}\mu \tag{1.3}$$

  so $|E(G)| \sim \mathcal{O}(n)$, from which the term 'sparse'.

- Scale-free property: A graph sequence $(G_n)_{n\geq 1}$ is scale-free with exponent τ if it is sparse and

$$\lim_{k\to\infty} \frac{\log(1-F(k))}{\log(\frac{1}{k})} = \tau - 1 \tag{1.4}$$

where $F(k) = \sum_{j\leq k} p_j$ is the distribution function of the random variable $D = \mathrm{d}(U)$, which then follows a power-law distribution; roughly speaking, it means that $\mathbb{P}(D \geq k) \sim ck^{-(\tau-1)}$, i.e. the limiting distribution has power-law tails.
Equivalently, we can ask the density $(p_k)_k$ to satisfy

$$\lim_{k\to\infty} \frac{\log(p_k)}{\log(\frac{1}{k})} = \tau \tag{1.5}$$

Observe that in this case we have

$$\mathbb{E}(D) = \sum_{k\geq 0} kp_k \approx \sum_{k\geq 0} \frac{c}{k^{\tau-1}}$$
$$\mathrm{Var}(D) \approx \sum_{k\geq 0} k^2 p_k \approx \sum_{k\geq 0} \frac{c}{k^{\tau-2}}$$

What is observed in real world networks is bounded average degree and a high level of variability in the nodes degree, meaning finite mean and infinite variance of D; this leads to set typically the parameter τ in the interval $(2, 3)$.

- High Connectivity: A graph sequence $(G_n)_{n\geq 1}$ is highly connected if

$$\liminf_{n\to\infty} \quad \frac{|\mathcal{C}_{\max}|}{n} > 0 \tag{1.6}$$

and in this case $\mathcal{C}_{\max}$ is called 'giant component'.

- Small-world: a graph sequence $(G_n)_{n\geq 1}$ has the small world property if the typical distance between vertices is small compared to n.
Formally, considering $U_1, U_2 \sim \mathrm{Uniform}([n])$, it means that

$$\exists K > 0 : \quad \lim_{n\to\infty} \mathbb{P}(\mathrm{d}(U_1, U_2) < K \log n) = 1 \tag{1.7}$$

It has the ultra small world property if the same condition holds with $\log\log n$ instead of $\log n$.

Another important concept in the study of random graphs is that of clustering, which focus on the tendency of neighbours of a node to be neighbours themselves, thus creating subsets of nodes that are highly connected within themselves, called clusters. Formally, let

$$W_G = \sum_{1\leq i,j,k\leq n} \mathbb{1}_{\{ij,jk\in E\}} \tag{1.8}$$

be twice the number of wedges in the graph G (since every wedge ij, jk is the same as kj, ji so it's counted twice), and let

$$\Delta_G = \sum_{1\leq i,j,k\leq n} \mathbb{1}_{\{ij,jk,ki\in E\}} \tag{1.9}$$

be six times the number of triangles in G. The clustering coefficient CC_G of G is defined as the ratio between triangles and wedges in G, thus it measures the proportion of wedges for which the closing edge is also present.

Definition 1.2.2. A graph sequence $(G_n)_{n\geq 1}$ is highly clustered when

$$\liminf_{n\to\infty} CC_{G_n} > 0 \tag{1.10}$$

We can generalize the notion of local convergence of graph, given in the deterministic setting, to the random one:

Definition 1.2.3. A sequence of random graphs $(\mathbb{G}_n)_{n\in\mathbb{N}}$ converges locally in probability to the the graph$(\mathbb{G}, \rho)$ (which can be either deterministic or random) if

$$\forall r \geq 1, \forall H^* \text{rooted graph}, \qquad P(B_r^{\mathbb{G}_n}(U) \cong H^*) \xrightarrow{\mathbb{P}} \tilde{\mathbb{P}}(B_r^{\mathbb{G}}(\rho) \cong H^*)$$

Note that $P(\cdot)$ is the probability related to the uniform distribution, so that the left hand side is indeed a random variable in $[0, 1]$, the convergence in probability $\mathbb{P}$ is related to the $\mathbb{G}_n$ and $\tilde{\mathbb{P}}$ is relative to $\mathbb{G}$.

1.3 Branching processes

In this section we introduce and show the main properties of the branching processes, the simplest models for the evolution of a population in time. The results presented here will be used later to prove threshold results for the Erdős-Rényi model.

Assume that every individual in the population has the same offspring distribution X and that they are indipendent of each other. Call $p_i = \mathbb{P}(X = i)$ the probability that an individual gives birth to i children. Let Z_n the number of individuals in the nth generation and set $Z_0 = 1$. Denoting with $X_{n,i}$ the number children of individual i of the generation n, Z_n then statisfies

$$Z_n = \sum_{i=1}^{Z_{n-1}} X_{n-1,i} \tag{1.11}$$

where $(X_{n,i})_{n,i\geq 0}$ is a doubly infinite array of i.i.d. random variables. Define the extinction probability as

$$\eta = \mathbb{P}(\exists n : Z_n = 0) \tag{1.12}$$

and the random variable T as

$$T = \sum_{n=0}^{\infty} Z_n \tag{1.13}$$

representing the total progeny of the branching process. Call $\psi_n(s) = \mathbb{E}(s^{Z_n})$, $\psi_T(s) = \mathbb{E}(s^T)$ and $\psi_X(s) = \mathbb{E}(s^X)$ the probability generating functions of Z_n, T and X respectively.

Theorem 1.3.1. *For a branching process with i.i.d. offspring distribution X,*

- *η is the minimal solution of the equation*

$$\psi(s) = s \tag{1.14}$$

  and in particular

  1. *if $\mathbb{E}(X) < 1$ then $\eta = 1$ and we are in the subcritical regime*
  2. *if $\mathbb{E}(X) > 1$ then $\eta < 1$ and we are in the supercritical regime*
  3. *if $\mathbb{E}(X) = 1$ and $\mathbb{P}(X = 1) < 1$, then nothing can be said about η a priori and we are in the critical regime*

- *ψ_T satisfies*

$$\psi_T(s) = s \cdot \psi_X(\psi_T(s)) \tag{1.15}$$

Proof. Observe first that ψ_n satisfies

$$\psi_{n+1}(s) = \psi_n(\psi(s)) = \psi(\psi_n(s)), \tag{1.16}$$

indeed, conditioning at the first generation

$$\psi_{n+1}(s) = \mathbb{E}(s^{Z_{n+1}}) = \mathbb{E}(\mathbb{E}(s^{Z_{n+1}}|Z_1)) = \mathbb{E}(\mathbb{E}(s^{Z_n^{(1)}+\dots Z_n^{(Z_1)}}))$$
$$= \mathbb{E}(\prod^{Z_1} \mathbb{E}(s^{Z_n})) = \mathbb{E}(\psi_n(s)^{Z_1}) = \psi(\psi_n(s))$$

As a consequence, taking $s = 0$ and passing to the limit in 1.16, we get that η is indeed solution of equation 1.14.
To see that is the minimal one, we study the function ψ in the domain $[0, 1]$: we have that $\psi(0) = p_0$, $\psi(1) = 1$ and moreover it is strictly increasing and convex in $(0, 1)$:

$$\psi'(s) = \sum_{k\geq 0} k s^{k-1} p_k > 0$$
$$\psi''(s) = \sum_{k\geq 0} k(k1) s^{k-2} p_k > 0,$$

so $\psi([0, 1]) = [0, 1]$. We have now two cases:

- if $\lim_{s\to 1^-} \psi'(s) \leq 1$, then it means that equation 1.14 has only one solution in $s = 1 = \eta$
- if $\lim_{s\to 1^-} \psi'(s) > 1$, then equation 1.14 has two solutions, one in $s = 1$ and another < 1; to prove that η is the smaller one, we proceed by induction on the generation: if z is solution of $z = \psi(z)$, for $n = 1$ then

  $$z = \psi(z) = \mathbb{E}(z^{Z_1}) = \mathbb{E}(z^X) = p_0 + \sum_{j\geq 1} z^j p_j \geq p_0 = \mathbb{P}(Z_1 = 0),$$

  while for $n + 1$

  $$z \geq \psi(\mathbb{P}(Z_n = 0)) = \psi(\psi_n(0)) = \psi_{n+1}(0) = \mathbb{P}(Z_{n+1} = 0) \qquad (1.17)$$

  where the inequality follows by monotonicity of ψ and induction hypothesis. Taking the limit in (1.17) we get that $\eta \leq z$ whenever $z = \psi(z)$.

To prove equation (1.15), we do as done for ψ_n, conditioning to the first generation, observing that the total progenies $T^{(1)}, \dots, T^{(Z_1)}$ are i.i.d. random variables with the same distribution as T:

$$\psi_T(s) = \mathbb{E}(s^T) = \mathbb{E}(\mathbb{E}(s^T|Z_1)) = \mathbb{E}(\mathbb{E}(s^{1+\sum T^{(i)}}|Z_1)) = s\mathbb{E}(\mathbb{E}((s^T)^{Z_1}|Z_1))$$
$$= s\mathbb{E}(\mathbb{E}((s^T)^{Z_1})) = s\mathbb{E}(\mathbb{E}(s^T)^X) = s\mathbb{E}((\psi(s))^X) = s\psi_X(\psi_T(s))$$

□

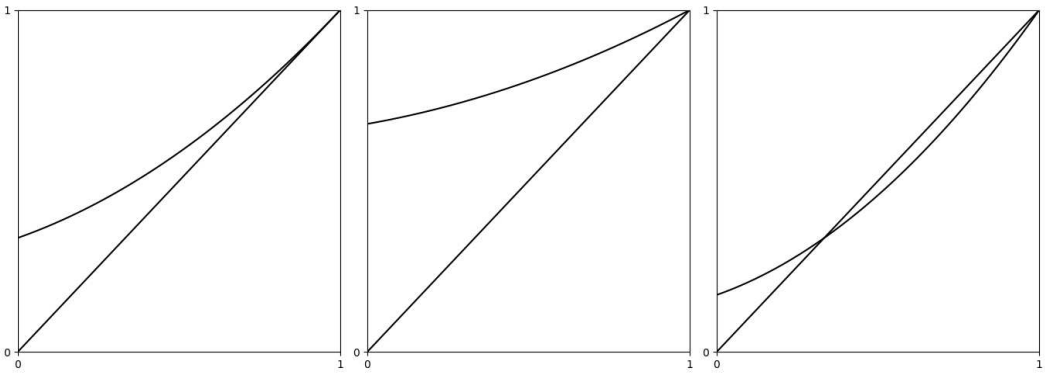

Figure 1.1: Solution of $s = \psi(s)$ for $\mathbb{E}(X) = 1$,$\mathbb{E}(X) < 1$,$\mathbb{E}(X) > 1$ respectively

Duality principle

Let X and X' be the offspring distribution of two branching processes BP(p), BP(p') respectively, with η the extinction probability for the branching process X. We say that $p = (p_k)_{k\geq 0}$ and $p' = (p'_k)_{k\geq 0}$ are a conjugate pair if

$$p'_k = \eta^{k-1} p_k, \quad \forall k \in \mathbb{N} \tag{1.18}$$

Theorem 1.3.2. *The distribution of BP(p) conditioned on extinction is equal to the distribution of BP(p').*

In the particular case of a Poisson branching processes BP_λ, with $\lambda > 1$, where the offspring distribution is given by

$$p_k = e^{-\lambda} \frac{\lambda^k}{k!}, \tag{1.19}$$

we have that $p'_k = e^{-\lambda\eta} \frac{(\lambda\eta)^k}{k!}$, i.e. a Poisson branching process with parameter λ conditioned on extinction is again Poisson with parameter $\lambda\eta := \mu_\lambda$. Using 1.3.1, which in the Poisson case takes the form

$$\eta = e^{\lambda(\eta-1)} \tag{1.20}$$

we obtain that μ and λ are conjugate pair if and only if they satisfy

$$\mu e^{-\mu} = \lambda e^{-\lambda}. \tag{1.21}$$

and so $\mu = \mu_\lambda < 1$.

Exploration

Exploring the tree associated to a branching process gives us a random walk perspective of them and will be useful to link with random graphs; consider a branching tree P with a total progeny T, together with the following procedure:

- each vertex can be labeled with L (live), N (neutral) or D (dead).
- At step 0, the root of the tree is labeled as live, while all the other $T-1$ vertices are labeled as neutral
- at each step $n \geq 0$, choose a live vertex, label it from Live to Dead and all of its offspring vertices from Neutral to Live
- let $S_n = |\{\text{live vertices at step } n\}|$, $K_n = |\{\text{dead vertices at step } n\}|$ and $N_n = |\{\text{neutral vertices at step } n\}|$; clearly $S_n + K_n + N_n = T$, $\forall n$
- from the definition it follows that

$$S_0 = 1 \tag{1.22}$$
$$S_n = S_{n-1} + X_n - 1 = X_1 + \dots X_n - (n-1) \tag{1.23}$$

  where X_n is the offspring distribution of the vertex chosen at step n, with $(X_j)_{j\in\mathbb{N}}$ are i.i.d. $\sim X$.

It follows that $(S_n)_{n\in\mathbb{N}}$ is a random walk with increments $(X_n - 1)_{n\in\mathbb{N}}$ and, denoting with T'_{-k} the random variable

$$T'_{-k} = \inf\{n : S_n = -k\},$$

T'_0 has the same distribution of the random variable T; this allows us to see T as a stopping time for the random walk S_n and to apply theorem 6.1.1 to get

$$\mathbb{P}(T = N) = \mathbb{P}_1(T'_0 = N-1) = \mathbb{P}_0(T'_{-1} = N) = \frac{1}{N}\mathbb{P}(X_1 + \dots + X_N = N-1) \tag{1.24}$$

where $\mathbb{P}_k(\cdot) = \mathbb{P}(\cdot | S_0 = k)$.

1.4 Erdős-Rényi model

In this section we will present and discuss the simplest model and one of the first to appear in the literature, considered the foundation of random graphs

theory, introduced by Erdős and Rényi.
In their model, each edge between any two vertices has a fixed probability $p \in [0,1]$ to appear in the graph, independently from the other edges. This leads to consider independent Bernoulli random variables with parameter p for each of the possible $\binom{n}{2}$ edges of a graph with n vertices, and thus on $\mathcal{G}_n$ the measure

$$\mathbb{P}_{n,p}(G) := p^{|E(G)|} \cdot (1-p)^{\binom{n}{2}-|E(G)|} \tag{1.25}$$

In order to analyze the main properties of the model, we introduce some definition:

Definition 1.4.1. An event $A \subset \mathcal{G}_n$ is increasing if it satisfies

$$\text{if } G \in A \Rightarrow G \cup \{e\} \in A, \quad \forall e \in \mathcal{E}_n. \tag{1.26}$$

A real random variable $X : \mathcal{G}_n \to \mathbb{R}$ is increasing if the event $\{X \geq x\}$ is increasing for every x.

It is easy to see, using coupling (see 6.1.4 in the appendix) that $\mathbb{P}_{n,p_1}(A) \leq \mathbb{P}_{n,p_2}(A)$ for every increasing event A, whenever $p_1 \leq p_2$.

Most of the properties can be expressed in terms of increasing or decreasing events, and in this case, in the limit $n \to \infty$, the graph exhibits a transition with respect to the parameter p:

Definition 1.4.2. A threshold in $\mathbb{G}(n,p)$ for an increasing event A is a function $p_c = p_c(n)$ such that

$$\lim_{n\to\infty} \mathbb{P}_{n,p}(A) = \begin{cases} 0 & \text{if } p \ll p_c \\ 1 & \text{if } p \gg p_c \end{cases} \tag{1.27}$$

where $p \ll p_c$ stands for $\frac{p}{p_c} \to 0$.

Despite its simplicity, the Erdos Renyi random graph has a big variety of substructures arising for different thresholds.
First observe that, for $p(n) \ll \frac{1}{n^2}$ the graph has no edges w.h.p. as $n \to \infty$, i.e. $\frac{1}{n^2}$ is a threshold for the event $A = \{\mathbb{G}_{n,p} \text{ has at least one edge}\}$. Indeed, if X is the random variable counting the edges, precisely

$$X(G) := |E(G)| = \sum_{e \in \mathcal{E}} \mathbb{1}_{\{e \in E\}} \qquad G \in \mathbb{G}_n,$$

then X is sum of $\binom{n}{2}$ independent Bernoulli random variables with parameters $p(n)$. Thus

$$\mathbb{P}_{n,p}(A) = \mathbb{P}_{n,p}(X \geq 1) \leq \mathbb{E}(X) = \binom{n}{2} \cdot p(n) \to 0 \quad \text{if} \quad p(n) \ll \frac{1}{n^2}.$$

On the other hand,

$$\mathbb{P}_{n,p}(A^c) = \mathbb{P}_{n,p}(X = 0) \leq \frac{Var(X)}{\mathbb{E}(X)^2} \approx \frac{1-p}{\binom{n}{2} \cdot p} \to 0 \quad \text{if} \quad p(n) \gg \frac{1}{n^2}.$$

There are other important thresholds connected to different subgraphs containment, we highlight the following transitions:

Theorem 1.4.3. *For the Erdos-Renyi random graph $\mathbb{G}(n,p)$, with $p = p(n)$, the following thresholds hold:*

- *for $p(n) = \bar{p} \in (0,1)$, we are in the dense regime, with $\mathbb{E}(E(\mathbb{G}(n,p))) \sim cn^2$ and $diam(\mathbb{G}(n,p)) \to 2$;*
- *for $p \sim \frac{\lambda}{n}$, with $\lambda > 0$, we have that $\mathbb{E}(E(\mathbb{G}(n,p))) \sim cn$ and we are then in sparse regime*
- *for $p(n) = \frac{\log(n)+c_n}{n}$, we have that*

$$\lim_{n\to\infty} \mathbb{P}(\mathbb{G}(n,p) \text{ is connected}) = \begin{cases} 0 & \text{if } c_n \to -\infty \\ e^{-e^{-c}} & \text{if } c_n \to c \\ 1 & \text{if } c_n \to \infty \end{cases}$$

Sparse Regime

We restrict now to the sparse regime, considering only p of the form $p(n) = \frac{\lambda}{n}$, and deduce results on the size of connected components and small world property. From the definition we can immediately observe that it is not scale-free: indeed each vertex $i \in [n]$ has degree distribution

$$\mathrm{d}(i) \sim \mathrm{Bin}(n-1, \frac{\lambda}{n}) \xrightarrow{d} \mathrm{Poi}(\lambda) \tag{1.28}$$

where the convergence follow from lemma 6.1.3; thus

$$\mathbb{P}_{n,p}(\mathrm{d}(i) = k) = \binom{n}{k} p^k (1-p)^{n-k} \approx e^{-\lambda} \frac{\lambda^k}{k!}. \tag{1.29}$$

Exploration of the giant component

In order to build a link with branching processes and use results of the previous section, we define in the following a procedure to perform exploration of the connected components in $\mathbb{G}(n,p)$, with $p = \frac{\lambda}{n}$.
Choose a vertex $j \in [n]$:

- at step 0 j is live, while all other vertices are in status neutral
- at every step $k \geq 1$, choose a live vertex i. Every neighbour l of i will change or keep its status to live if it's neutral or live and keep its status to dead if it's already dead; i will become dead and all other vertices will keep their status.

Denote with S_k, D_k and N_k the number of live, dead and neutral vertices respectively. Observe that $D_k = k$, so $S_k + N_k = n - k$. It follows from this procedure that

$$|\mathcal{C}(j)| = \min\{k : S_k = 0\} := T \tag{1.30}$$

Let X_i be the number of vertices becoming live at step i, so that

$$S_0 = 1, \qquad S_k = S_{k-1} + X_k - 1 = \sum_{i=1}^{k} X_i - (k-1), \tag{1.31}$$

thus $(S_k)_{0 \leq k \leq T}$ is a random walk with increment $(X_i - 1)$. The difference with the branching process' random walk defined in (1.22) is in that the increments are not i.i.d., but their distribution varies at each step, indeed

$$X_i \sim \text{Bin}(N_{i-1}, p). \tag{1.32}$$

Since $N_0 = n - 1$, by recursion and applying Lemma 6.1.2

$$N_i \sim \text{Bin}(n-1, (1-p)^i) \tag{1.33}$$

from which it follows that

$$S_i \sim \text{Bin}(n-1, 1-(1-p)^i) - i + 1. \tag{1.34}$$

Theorem 1.4.4. *For the random graph ER(n,p), with $p = \frac{\lambda}{n}$, it holds that*

1. *if $\lambda < 1$, then*

$$\frac{|\mathcal{C}_{max}|}{\log n} \xrightarrow{d,\mathbb{P}} c_\lambda := I_\lambda(1)^{-1} = (1 - \lambda - \log \lambda)^{-1} \tag{1.35}$$

2. *if $\lambda > 1$, then*

$$(a) \quad \frac{\mathcal{C}_{max}}{n} \xrightarrow{\mathbb{P}} \zeta \tag{1.36}$$

$$(b) \quad \frac{\mathcal{C}_2}{n} \xrightarrow{\mathbb{P}} 0 \tag{1.37}$$

where $\zeta = 1 - \eta$ is solution of Poisson branching process' survival equation (1.20). The first case is called subcritical regime, while the second one is called supercritical. Observe that the last equation of the supercritical scenario tells us that the giant component is unique.

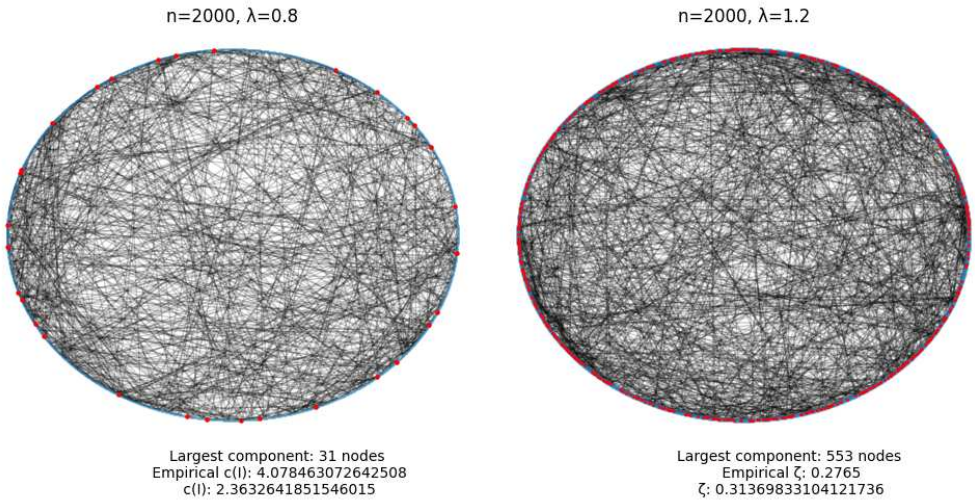

Figure 1.2: Largest component in Erdős Renyi graph $G(n,p)$, with $n = 2000$. The vertices in the largest component are drawn in red while the others are in blue. On the left, the parameter $\lambda = 0.8$ is subcritical and the realization of the graph indeed displays a largest component of size 31 which is of the order of $\log n$. On the right, $\lambda = 1.2$ is supercritical and the largest component has size 533, with a empirical fraction of ζ nodes similar to the theoretical ζ.

Proof. We will prove upper and lower bound on the probabilities:

1. Proving convergence in the subcritical regime amounts to show that both the following convergence holds:

$$\begin{aligned} (i) \quad & \mathbb{P}(|\mathcal{C}_{\max}| \geq c \log n) \to 0, \quad \forall c > c_\lambda \\ (ii) \quad & \mathbb{P}(|\mathcal{C}_{\max}| \leq c' \log n) \to 0, \quad \forall c' < c_\lambda \end{aligned}$$

   We will show the lower bound (i) : let $C > c_\lambda$, let $(S_k)_{k=1\dots T}$ the exploration process of $\mathcal{C}(j)$.
   For $k = k(n) = o(n)$, it holds that

$$\begin{aligned} & \mathbb{P}_{n,p}(|\mathcal{C}(j)| > k) = \mathbb{P}_{n,p}(T > k) = \mathbb{P}_{n,p}(S_k \geq 1) \\ = \quad & \mathbb{P}(\mathrm{Bin}(n-1, 1-(1-p)^k) \geq k) \approx \mathbb{P}(\mathrm{Poi}(k\lambda) \geq k) \leq e^{-kI_\lambda(1)} \end{aligned}$$

   where the approximation follows from $1-(1-p)^k \approx kp$ and apllying 6.1.3, while in the last inequality Chernoff has been used. Substituting $k(n) = c \log n$, one gets the upper bound $n^{-cI_\lambda(1)}$ which is $o(n^{-1})$ for $c > c_\lambda$. Then

$$\mathbb{P}_{n,p}(|\mathcal{C}_{\max}| \geq c \log n) \leq \sum_{j \in [n]} \mathbb{P}_{n,p}(|\mathcal{C}(j)| > c \log n) = o(1)$$

2. To prove convergence in (a), first we show that $\mathbb{P}_{n,p}(|\mathcal{C}_{\max}| = o(n)) \to 0$ as $n \to \infty$, then prove upper and lower bound for $\frac{\mathcal{C}_{\max}}{n}$.
Let $k = k(n) = o(n)$ and $k(n) \to \infty$. It holds that

$$\mathbb{P}_{n,p}(|\mathcal{C}_{\max}| \leq k) = \mathbb{P}_{n,p}(\bigcap_{j\in[n]} \{|\mathcal{C}(j)| \leq k\}) \leq \mathbb{P}_{n,p}(|\mathcal{C}(j)| \leq k)$$
$$= \mathbb{P}_{n,p}(T \leq k) = \mathbb{P}_{n,p}(S_k \leq 0) = \mathbb{P}_{n,p}(\mathrm{Bin}(n-1, 1-(1-p)^k < k)$$
$$\approx \mathbb{P}(\mathrm{Poi}(\lambda k) < k) \leq e^{-I_\lambda(1)k} \to 0, \quad \text{as } n \to \infty$$

where the approximation follows from $1-(1-p)^k \approx kp$ and the last inequality from Chernoff's Bound with $\lambda < 1$.
To prove upper and lower bound, let $k(n) = cn$, with $c > 0$.

$$\mathbb{P}_{n,p}(|\mathcal{C}_(j)| \leq k) = \mathbb{P}_{n,p}(T \leq k) = \mathbb{P}(S_k \leq 0)$$
$$= \mathbb{P}(\mathrm{Bin}(n-1, 1-(1-p)^k < k) \approx \mathbb{P}(\mathrm{Bin}(n, 1-e^{-\lambda c} < cn)$$

where the last approximation follows from $1-(1-p)^k = 1-(1-\frac{\lambda}{n})^{cn} \approx 1-e^{\lambda c}$.
Observe now that, by (1.20), $1-e^{-\lambda c} > c \iff c < \zeta_\lambda$. When $c < 1-e^{-\lambda c}$, we have by (6.1) that

$$\mathbb{P}_{n,p}(|\mathcal{C}(j)| \leq cn) \leq e^{-nI_{\mathrm{Bin}}(c)} \to 0$$

and so for every $c < \zeta_\lambda$ it holds that $\mathbb{P}(|\mathcal{C}_{\max}| \leq cn) \to 0$.
When $c > 1-e^{-\lambda c}$, again by (6.1), we have that

$$\mathbb{P}_{n,p}(|\mathcal{C}(j)| \leq cn) = 1 - \mathbb{P}_{n,p}(|\mathcal{C}(j)| > cn) \geq 1 - e^{-I_{\mathrm{Bin}}(c)n} \to 1$$

and so for all $c > \zeta_\lambda$ it holds that

$$\mathbb{P}_{n,p}(|\mathcal{C}_{\max}| > cn) \leq n\mathbb{P}_{n,p}(|\mathcal{C}(j)| > cn) \leq ne^{-I_{\mathrm{Bin}}(c)n} \to 0.$$

To prove uniqueness in (b), we iterate the exploration procedure, at each step removing from the graph the component explored. When removing a component $\mathcal{C}(j)$ that is not giant, the remaining graph is of size $n - o(n) \approx n$, so we proceed with iteration until we encounter the giant component, which should eventually happen by its existence proven in (a). In this case the remaining graph will have distribution

$$\mathbb{G}(n - n\zeta_\lambda, \frac{\lambda}{n}) = \mathbb{G}(n\eta_\lambda, \frac{\lambda}{n}) = \mathbb{G}(m, \frac{\mu_\lambda}{m})$$

where $\eta_\lambda = 1 - \zeta_\lambda$ and we called $m := \eta_\lambda n$ and $\mu_\lambda = \lambda\eta_\lambda < 1$ is the Poisson dual of η_λ. Then $\mathbb{G}(m, \frac{\mu_\lambda}{m})$ is an ER random graph in the sparse regime, thus its maximal component is of order $\mathcal{O}(n)$.

□

We state now a convergence theorem for the ER random graph that will be used to prove small world property

Theorem 1.4.5. *For $\lambda > 1$, $\mathbb{G}(n, \frac{\lambda}{n})$ converges locally in probability to the Poisson Branching process BP(Poi(λ)).*

This further connection between ER and BP(Poi(λ)) allows us to prove the following

Theorem 1.4.6. *Let U_1, U_2 independent uniform random variables on $[n]$. Conditionally on the event $\{U_1 \leftrightarrow U_2\}$, it holds that*

$$\frac{dist_{\mathbb{G}(n,p)}(U_1, U_2)}{\log n} \xrightarrow{\mathbb{P}} \frac{1}{\log \lambda}$$

Chapter 2

Inhomogeneous random graphs

The most direct generalization of random graph, starting from the baseline model of Erdős-Renyi, is built by keeping the independence of edges but allowing a different probability distribution between them. There are different ways to do so, i.e. to define the probability of existence of any edge. The most general approach is to consider vertices of the graph to be of different types and to define the edge probability between two vertices to be dependent on those types. For the most general definition, where the set of types can be either finite or infinite (countable or uncountable), see [7]. Nevertheless the models that can be built from a finite set of types is already rich and various and we will initially focus on this particular case.
Then, for the infinite case we will restrict our study to the so called Generalized Random Graphs, a particular case of the IRG that can be formulated through weight assignment to each node of the graph.
We will denote vectors with underline bar and matrix in bold.

Definition 2.0.1. An Inhomogeneous random graph (IRG) is defined by a finite set of types T, a probability measure μ on T and a function

$$t : V = [n] \to T$$

such that

$$\mu(s) = \frac{|\{i \in [n] : t(i) = s\}|}{n}, \quad \forall s \in T,$$

together with a symmetric non negative matrix $\mathbf{K} = (K_{s,t})_{s,t \in T}$, called kernel, such that

$$\forall i, j \in V, \quad \mathbb{P}(i \sim j) = \mathbb{P}(t(i), t(j)) = K_{t(i),t(j)}.$$

The corresponding random graph, which is determined by the kernel $\mathbf{K}$ and the vector $\underline{\mu} = (\mu(1), \ldots, \mu(|T|))$, will be denoted with $\mathbb{G}(n, \mathbf{K})$ and its corresponding probability with $\mathbb{P}_{n,\mathbf{K}}$.

We will assume in the following that the kernel is irreducible, meaning that it is not possible to split the type set into two proper subsets $T_1 \sqcup T_2$ such that $k_{ij} = 0$ for every pair $i \in T_1, j \in T_2$.

Assumption 2.0.2. We will assume from now on, as done for the ER model, that the edge probabilities scale as $\frac{1}{n}$, i.e.

$$\mathbb{P}(t(i), t(j)) = \frac{K_{t(i)t(j)}}{n}.$$

Then it follows that, for $i \in [n]$ with $t(i) = t$,

$$\begin{aligned} d(i) = \sum_{s\in T} \sum_{\substack{j\in[n] \\ t(j)=s}} \mathbb{1}_{\{i\sim j\}} &\overset{d}{=} \sum_{s\in T} \sum_{a=1}^{\mu(s)n} Be(\frac{K(s,t)}{n}) \\ &\overset{d}{=} \sum_{s\in T} Bin(\mu(s)n, \frac{K(s,t)}{n}) \approx Poi(\lambda(t)), \end{aligned}$$

where $\lambda(t) = \sum_{s\in T} K(s,t)\mu(s) = (\mathbf{K} \cdot \underline{\mu})_t$.

Definition 2.0.3. Let ϕ a probability density function on $\mathbb{R}^+$. A random variable X is distributed as a Mixed Poisson distribution with density ϕ if its probability density is

$$\mathbb{P}(X = k) = \int_0^\infty \frac{\lambda^k}{k!} e^{-\lambda} \phi(\lambda) d\lambda$$

The vertex degree sequence in $\mathbb{G}(n, \mathbf{K})$ is then ruled by Mixed Poisson distribution with density μ:

$$\mathbb{P}_{n,\mathbf{K}}(d(U) = r) = \sum_{t\in T} \sum_{\substack{i\in[n] \\ t(i)=t}} \frac{1}{n} e^{-\lambda(t)} \frac{\lambda(t)^r}{r!} = \sum_{t\in T} \mu(t) e^{-\lambda(t)} \frac{\lambda(t)^r}{r!}$$

which can be rewritten as $d_{\mathbb{G}_{n,\mathbf{K}}}(U) \overset{d}{=} \mathrm{Poi}(W)$, with $\mathbb{P}(W = \lambda(t)) = \mu(t)$.

2.1 Multi-type Branching processes

In order to extend the existing correlation between random graphs and branching processes to the inhomogeneous settings, we need to generalize and allow the progeny to be of different type. We restrict for the moment to

the finite type case and first introduce some notation.
Let $T \in \mathbb{N}_0$, $[T]$ the set of types and denote with $p_{\underline{i}}^{(s)}$ the probability that an individual of type s gives birth to an offspring $\underline{i}$, where $\underline{i} = (i_1, \dots, i_T)$, i.e. i_t individual of type t, for each type t in $[T]$, and with $\underline{p}_{\underline{i}} = (p_{\underline{i}}^{(1)}, \dots, p_{\underline{i}}^{(T)})$.
Let $Z_{k,r}^{(s)}$ be the number of individual of type r in generation k starting from an individual of type s, so that we can denote with

$$\underline{Z}_k^{(s)} = (Z_{k,1}^{(s)}, \dots, Z_{k,T}^{(s)})$$

the vector of k-th generation. Let

$$\zeta^{(s)} = \mathbb{P}(\underline{Z}_k^{(s)} \neq \underline{0}, \forall k \geq 0)$$

and $\underline{\zeta} = (\zeta^{(1)}, \dots, \zeta^{(T)})$.

Assume that the offspring of different individuals are mutually independent and also that children of different type of a single individual are generated independently, i.e. $Z_{1,r}^{(t)} \perp\!\!\!\perp Z_{1,s}^{(t)}$, for all t, r and s. This implies that the probability distribution of a single individual split as the product of the probability distribution of different types:

$$p_{\underline{i}}^{(s)} = \prod_{t \in [T]} p_{i_t}^{(s,t)},$$

where $p_{i_t}^{(s,t)}$ is the probability that an individual of type s generates i_t individuals of type t.
Finally, for $\underline{z} \in [0,1]^T$, denote the joint probability generating functions of the offspring distribution of an individual of type s with

$$G^{(s)}(\underline{z}) = \sum_{\underline{i} \in \mathbb{N}^T} p_{\underline{i}}^{(s)} \prod_{t \in [T]} z_t^{i_t},$$

by $G_k^{(s)}(\underline{z})$ the one of $\underline{Z}_k^{(s)}$ and the corresponding vectors by $\underline{G}(\underline{z})$ and $\underline{G}_k(\underline{z})$. By independence, splitting by type in the product of expectation and applying separately 1.16, one can prove that

$$\underline{G}_{k+1}(\underline{z}) = \underline{G}(\underline{G}_k(\underline{z}))$$

Now since $\underline{G}_k(\underline{0}) = (\mathbb{P}(\underline{Z}_k^{(s)} = \underline{0}))_{s \in [T]}$, passing to the limit we have

$$\underline{1} - \lim_{k \to \infty} \underline{G}^k(\underline{0}) = \underline{\zeta},$$

and so, reasoning as in the 1 type case, one can show that $\underline{\zeta}$ is the largest solution (in lexicographic order) of the equation

$$\underline{\zeta} = \underline{1} - \underline{G}(\underline{1} - \underline{\zeta}). \tag{2.1}$$

To emphasize analogy with IRGs, call $\lambda_{sr} := \mathbb{E}(Z_{1,r}^{(s)})$ and write $\lambda_{sr} = K(s,r)\mu(r)$ (this can always be done in different ways).
Let $\mathbf{T} = (\lambda_{sr})_{s,r\in[T]}$ the matrix of expected offspring.

Definition 2.1.1. We say that the multi-type branching process is singular if $\underline{G}$ is linear in $\underline{z}$, i.e. if there exist a matrix $\mathbf{M}$ such that $\underline{G}(\underline{z}) = \mathbf{M}\underline{z}$. In this case every individual has a.s. one offspring of a given type and the branching process reduce to a Markov chain between types and a.s. survives.
We say that the branching process is positively regular if there exist a positive integer l such that $(\mathbf{T}^l)_{sr} > 0$ for every s, r.

Theorem 2.1.2. *Assume that the branching process is not singular and positively regular. Then $\underline{\zeta} \neq \underline{0}$ if and only if $\|\mathbf{T}\| > 1$.*

Proof (sketch). Let $l \geq 1$ such that $(\mathbf{T}^l)_{sr} > 0$ for every $s, r \in [T]$. Then by the Perron-Frobenius theorem, there exists a unique largest eigenvalue $\alpha = \|\mathbf{T}^l\|$, with eigenvector $\underline{x}$; thus also

$$\mathbf{T}^l\mathbf{T}\underline{x} = \mathbf{T}\mathbf{T}^l\underline{x} = \mathbf{T}\alpha\underline{x} = \alpha\mathbf{T}\underline{x},$$

i.e. x is eigenvector of $\mathbf{T}$, too, with

$$\alpha = \sup_{\|\underline{x}\|\leq 1} \mathbf{T}\underline{x}.$$

Now, since $\mathbb{E}(\underline{Z}_{k+1}^{(s)}|\underline{Z}_k = \underline{y}) = \mathbf{T}\underline{y}$, taking $\underline{y} = \underline{e}^{(s)}$ the s-th basis vector (the ancestor of the progeny tree), we have that

$$\mathbb{E}(\underline{Z}_k^{(s)}) = \mathbf{T}^k\underline{e}^{(s)}.$$

Then, when $\|\mathbf{T}\| < 1$, it holds that

$$\mathbb{P}(|\underline{Z}_k^{(s)}| \geq 1) \leq \mathbb{E}(|\underline{Z}_k^{(s)}|) \leq \|\mathbf{T}\|^k\|\underline{e}^{(s)}\| = \|\mathbf{T}\|^k$$

hence the branching process dies out a.s.
On the other hand, observe that $M_k := \underline{x} \cdot \underline{Z}_k^{(s)}\|\mathbf{T}\|^{-k}$ is a non-negative martingale, which then converges to some M_∞ by the Martingale convergence theorem. Since $\mathbb{E}(M_0) > 0$, it follows that $|\underline{Z}_k^{(s)}|$ grows exponentially with positive probability, which means that the survival probability is positive. □

These three different behaviours depending on the value of $\|\mathbf{T}\|$ are called, in line with the single type case, supercritical ($\|\mathbf{T}\| > 1$), critical ($\|\mathbf{T}\| = 1$) and subcritical ($\|\mathbf{T}\| < 1$).

Assume now that the branching process is Poisson, meaning that $Z_{1,r}^{(s)}$ are independent Possion random variables, with mean λ_{sr}. In this case,

$$G^{(s)}(\underline{z}) = \prod_{t\in[T]} e^{\lambda_{st}(z_t-1)} = e^{\mathbf{T}(\underline{z}-\underline{1})} \tag{2.2}$$

and thus the survival equation becomes $\underline{\zeta} = \underline{1} - e^{-\mathbf{T}\underline{\zeta}}$, where the exponential is meant component-wise.

2.2 Consequences on multi-type ER

Consider now the IRG defined before.

Assumption 2.2.1. From now on we will assume that $p_{i_t}^{(s,t)} \overset{d}{=} \mathrm{Poi}(\lambda(s,t))$, and call $\mathbf{\Lambda} = (\lambda(s,t))_{s,t\in[T]}$.

The local structure of the IRG with finitely many types, that is how edges arise in the neighbourhood of a vertex, is explained in the following theorem, which is a direct generalization of theorem 1.4.5:

Theorem 2.2.2. *The random graph $\mathbb{G}(n,\mathbf{K})$, with $K_{st}(n) \sim k_{st}/n$, converges in probability to the multi-type Poisson branching process with the root type distribution $\underline{\mu}$ and vertex type offspring distribution Poi$(\lambda(t,s))$ independent for each $v \in [n]$, where $\lambda(s,t) = K_{st}\mu_t$*

As in the ER model, in the supercritical regime the largest connected component arises, having the same size of the whole graph:

Theorem 2.2.3. *For the random graph $\mathbb{G}(n,\mathbf{K})$ it holds that*

$$\frac{\mathcal{C}_{max}}{n} \xrightarrow{\mathbb{P}} \zeta_{\mathbf{K}}$$
$$\frac{\mathcal{C}_2}{n} \xrightarrow{\mathbb{P}} 0$$

where $\zeta_{\mathbf{K}} = \underline{\zeta}\cdot\underline{\mu}$, so by theorem 2.1.2the giant component arises precisely when $\|T_{\mathbf{K}}\| > 1$, and in that case it is unique.

In the subcritical case a small-world property holds for IRG too:

Theorem 2.2.4. *Let U_1, U_2 independent uniform random variables over $[n]$. Then for the inhomogeneous random graph $\mathbb{G}(n,\mathbf{K})$, with $\mathbf{K}$ irreducible, it holds that, conditionally on $\{U_1 \leftrightarrow U_2\}$*

$$\frac{dist_{\mathbb{G}(n,p)}(U_1,U_2)}{\log n} \xrightarrow{\mathbb{P}} \frac{1}{\log\|T_{\mathbf{K}}\|}$$

2.3 Generalized Random Graphs and Chung-Lu model

One particular case of Inhomogeneous random graphs are the so called Generalized Random Graphs (GRG). In this framework, a weight (that can in general be deterministic or random) is assigned to each node of the graphs and edges between nodes appear with some probability depending on weights.

Definition 2.3.1. Let $\underline{w} = (w_i)_{i\in[n]}$ the set of weights assigned to each vertex $i \in [n]$, with $w_i \geq 0$, and define the edge probability between two vertices $i \neq j$ as

$$p_{ij}^{GRG} = \phi(w_i, w_j) = \frac{w_i w_j}{l_n + w_i w_j}, \qquad l_n = \sum_{i\in[n]} w_i. \tag{2.3}$$

The resulting random graph is called Generalized random graph with weights $\underline{w}$ (GRG($\underline{w}$)) and denoted with $\mathbb{G}(n, \underline{w})$ with law $\mathbb{P}_{n,\underline{w}}$.

In general there are different choices for the function ϕ; we will focus the study to the case $\phi(w_i, w_j) = \min\{\frac{w_i w_j}{l_n}, 1\}$ making the assumption

$$\max_{i\in[n]} w_i^2 < l_n$$

so that we can avoid the minimum in the definition and work in the so called Chung-Lu model,where

$$p_{ij} = \frac{w_i w_j}{l_n}. \tag{2.4}$$

Observe that associating a different type to each vertex and calibrating the kernel values depending on the weights, one can formulate equivalently the GRG in the IRG settings with countable infinite many types: explicitly, choose $T = [0, 1]$ as set of types and assign to each vertex $i \in [n]$ the type $t(i) = \frac{i}{n}$, set the edge probability regulated by a kernel with

$$p_{ij} = \frac{K(\frac{i}{n}, \frac{j}{n})}{n + K(\frac{i}{n}, \frac{j}{n})}$$

and $K(\frac{i}{n}, \frac{j}{n}) = \frac{w_i w_j n}{l_n}$, for $n \to \infty$.

Definition 2.3.2. Define the empirical distribution function to be the distribution function of the weight of a vertex chosen uniformly at random $W_n := w_U$,

$$F_n(x) = \frac{1}{n} \sum_{i\in[n]} \mathbb{1}_{\{w_i \leq x\}} \tag{2.5}$$

which can be itself random in the case of random weights, where the source of randomness comes both from the uniform random variable U on $[n]$ and the weights distribution $\underline{w}$.

In the Chung-Lu model the weight of a vertex coincides asymptotically with its expected degree, indeed

$$\mathbb{E}(d(i)) = \sum_{j\in[n]} \mathbb{E}(\mathbb{1}_{\{i\sim j\}}) = \sum_j \frac{w_i w_j}{l_n} = \frac{w_i}{l_n}\sum_j w_j = w_i;$$

in the analogy with the IRG seen above, this coincide with saying that $K(\frac{i}{n},\frac{j}{n}) = \frac{w_i w_j}{\mathbb{E}(W_n)}$, and the model goes in fact also by the name "random graph with prescribed expected degrees".

In order to have convergence of the degree sequence in $\mathrm{GRG}(\underline{w})$ we will require that there exist a random variable W with distribution F such that the following regularity conditions hold:

Weak convergence. In case of deterministic weights

$$(a) \quad W_n \xrightarrow{d} W \tag{2.6}$$

while in case of random weights

$$(a*) \quad \mathbb{P}_n(W_n \le x) \xrightarrow{\mathbb{P}} \mathbb{P}(W \le x) = F(x) \tag{2.7}$$

where $\mathbb{P}_n$ denotes the conditional probability given the weights.
This is equivalent to ask, by the definition of convergence in distribution, that for every x continuity point of F,

$$\mathbb{P}(W_n \le x) \to \mathbb{P}(W \le x)$$

where again convergence is meant in probability in the case of random weights.

Convergence of first and second moments. In case of deterministic weights

$$(b) \quad \lim_{n\to\infty} \mathbb{E}(W_n) = \mathbb{E}(W) \tag{2.8}$$

$$(c) \quad \lim_{n\to\infty} \mathbb{E}(W_n^2) = \mathbb{E}(W^2) \tag{2.9}$$

while in case of random weights

$$(b*) \quad \mathbb{E}(W_n) \xrightarrow{\mathbb{P}} \mathbb{E}(W) \tag{2.10}$$

$$(c*) \quad \mathbb{E}(W_n^2) \xrightarrow{\mathbb{P}} \mathbb{E}(W^2) \tag{2.11}$$

where $\mathbb{E}_n$ again denotes the expected value given the weights.

Observe that, if w_i are i.i.d random variables, these conditions are automatically verified by the law of large numbers. With this hypothesis, the first consequence is that GRG is sparse, precisely

$$\mathbb{E}(|E(\mathbb{G}(n, \underline{w}))|) \to \frac{\mathbb{E}(W)n}{2}$$

As for IRG with finite number of types, one would expect that the degrees a vertex chosen uniformly at random has a mixed Poisson distribution, and indeed in the limit it will converge toward it:

Theorem 2.3.3. *In the GRG model $\mathbb{G}(n, \underline{w})$, let $U \sim$ Uniform$([n])$; then*

$$d(U) \xrightarrow{d} D$$

where $\mathbb{P}(D = k) = \mathbb{E}(e^{-W}\frac{W^k}{k!})$.

It follows that we can calibrate the weights to make the model scale-free: indeed, if we ask that

$$\mathbb{P}(W \geq x) \approx c \cdot x^{-(\tau-1)}, \quad \text{as } x \to \infty \tag{2.12}$$

then also D follows a power law distribution, since $\mathbb{P}(D \geq x) \approx \mathbb{P}(W \geq x)$.

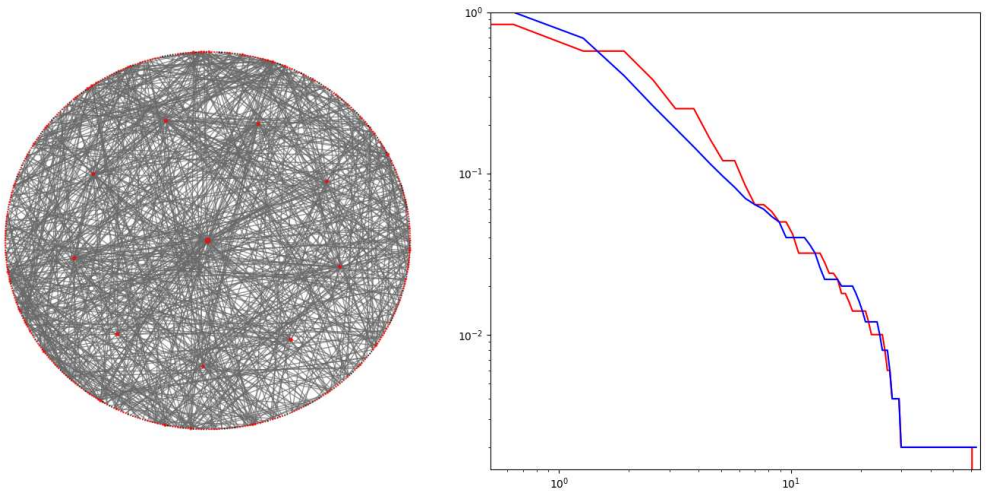

Figure 2.1: On the left a Generalized Random graph (Chung-Lu) with power-law exponent $\tau = 2.5$ consisting of 500 nodes. Node sizes and distance from the center are according to the weights, in red those in the giant components. On the right, log-log plot of the weight (blue) and degree (red) sequences.

The role played in ER by the parameter λ and in IRG by the norm (or max eigenvalue) of the matrix of expected offspring $\|T_{\mathbf{K}}\|$ is, in the GRG

settings, replaced by the ratio $\nu = \frac{\mathbb{E}(W^2)}{\mathbb{E}(W)}$. The reason behind this is that, in the general IRG setting (with an arbitrary separable metric space of types $\mathcal{S}$ with measure μ), the kernel K is a general continuous function $\mathcal{S}^2 \to \mathbb{R}^+$, with norm

$$\|T_K\| := \sup_{0<\|f\|\leq 1} \{\|T_K f\|\},$$

where $T_K f(x) := \int_{\mathcal{S}} K(x,y) f(y) \mu(dy)$.
In this general settings, for the Chung-Lu model with weight distribution F, the kernel is defined as

$$K(x,y) = \frac{\psi(x)\psi(y)}{\mathbb{E}(W)}$$

where $\psi(x) := (1-F)^{-1}(x)$. In this case

$$T_K f = \frac{\int \psi(x)\psi(y) f(y) \mu(dy)}{\mathbb{E}(W)}$$

and the supremum is reached precisely in $f = \frac{\psi}{\int \psi} = \frac{\psi}{\mathbb{E}(W)}$ so that

$$\|T_K\| = \frac{\int \psi(x)\psi(y)\psi(y)\mu(dy)}{\mathbb{E}(W)^2} = \frac{\mathbb{E}(W)\mathbb{E}(W^2)}{\mathbb{E}(W)} = \frac{\mathbb{E}(W^2)}{\mathbb{E}(W)}.$$

We state now an analogous treshold result for generalized random graphs, where again the critical value of this ratio is 1:

Theorem 2.3.4. *In the GRG($\underline{w}$) model, under the hypothesis 2.6 and 2.8, with $\nu = \frac{\mathbb{E}(W^2)}{\mathbb{E}(W)}$, let $\zeta_{\underline{w}}$ be the survival probability of a multi type Poisson branching process with infinite type set $\underline{w}$. Then it holds that:*

1 for $\nu > 1$, the giant component appears and is unique:

$$\frac{\mathcal{C}_{\max}}{n} \xrightarrow{\mathbb{P}} \zeta_{\underline{w}}, \qquad \frac{\mathcal{C}_2}{n} \xrightarrow{\mathbb{P}} 0$$

while for $\nu \leq 1$, we are in the subcritical regime and

$$\frac{\mathcal{C}_{max}}{n} \xrightarrow{\mathbb{P}} 0$$

2 for $\nu > 1$, conditionally on the event $\{U_1 \leftrightarrow U_2\}$, it holds that

$$\frac{dist_{\mathbb{G}(n,p)}(U_1, U_2)}{\log n} \xrightarrow{\mathbb{P}} \frac{1}{\log \nu}, \tag{2.13}$$

so the small-world property holds in the supercritical regime.
In particular, when $\mathbb{E}(W^2) = \infty$*, thus* $\nu = \infty$ *and the left hand side of (2.13) converges to* 0*, if we assume (2.12) with* $2 < \tau < 3$*, we have an ultra small world behaviour:*

$$\frac{dist_{\mathbb{G}(n,p)}(U_1, U_2)}{\log\log n} \xrightarrow{\mathbb{P}} \frac{2}{|\log(\tau - 2)|} \tag{2.14}$$

Chapter 3

Geometric Inhomogeneous Random Graphs

In the previous chapter we assigned different types or weights to nodes in the random graphs, allowing for heterogeneity in order to make them more adaptable to represent real world networks. One feature that can usually have relevance in them and which we did not consider so far is the geometric one, that means if and how the nodes are located in some underlying space, and in that case how this space and its geometry are defined. One important consequence of embedding the random graph in a metric space is the increase of clusters, which makes them more realistic in many contexts. In this chapter we present what are known as Geometric Inhomogeneous Random Graphs (GIRG), and then specialize in the most studied one, where the underline space is a Torus.

3.1 Introducing geometry: small world and hyperbolic model

The first model to appear in the literature which considered the presence of an underlying metric space was the so called 'small-world model' [13], where the graph is some sort of interpolation between a deterministic and a random graph, the idea being to start from a given graph with nodes placed on a one dimensional lattice with a fixed number of edges per node that connects neighbours (in the underlying metric), and then 'rewire' with probability p each edge, creating shortcuts in the graph, i.e. edges connecting nodes that are far in the geometric sense. The increasing number of shortcuts (which depends on how one chooses p) brings after a certain threshold the desired small-world property, while preserving a sufficiently high level of clustering.

The model was then improved, considering multidimensional lattice together with the adjoints of shortcuts instead of rewiring.
However, in all these models, a quantitative feature of the metric was not taken into account still, indeed only the underlying topology and the property of being neighbour in the lattice was considered.
Subsequently, an underlying metric space where edge probabilities depend explicitly by the distance between node was considered in the so called 'Hyperbolic random graph', introduced firstly in [2].
In this model, each node is placed u.a.r. in the angular coordinate θ inside the hyperbolic disk of radius R D_R and at a distance from the origin r with density regulated by a parameter α

$$f(r) = \frac{\alpha \sinh \alpha R}{\cosh \alpha R - 1} \approx \alpha e^{\alpha(R-r)} \sim e^{\alpha r}$$

The probability of two nodes $i, j \in D_R$, depending on their hyperbolic distance, is usually defined as

$$\mathbb{P}(i \sim j) = \frac{1}{1 + e^{\frac{1}{2T}(\mathrm{d}(i,j) - \chi)}}$$

where T is a parameter which, in the limit $T \to 0$, gives us the so called threshold hyperbolic model, where the connection rule is the simplest one, i.e. the indicator function on the nodes distance:

$$\mathbb{P}(i \sim j) = \mathbb{1}_{\{d(i,j) < \chi\}}$$

where $\chi < 2R$ is some parameter and for $i = (r, \theta)$ and $j = (r', \theta')$,

$$\cosh(d(i,j)) = \cosh r \cosh r' - \sinh r \sinh r' \cos(\Delta\theta),$$

with $\Delta\theta = (\theta - \theta') \mod \pi$.
The model is proven to have power law degrees and be highly clustered, this last property following directly from the triangle inequality of the hyperbolic geometry.

3.2 Geometric model

Aware of the importance of geometry in the structure of graphs to reflect in a more realistic way real world networks, numerous models have been proposed, most of all possessing the property of being highly clustered. In general, what is needed to build such models is an underlying metric space together with a weight assigned to each nodes (and hence in each position,

balancing the mass distribution in the space where the graphs lies). This leads to a more general definition of what comes with the name of Geometric Inhomogeneous Random Graphs (GIRG) [3], for which we will restrict our dissertation to the case in which the underlying space is a torus:

Definition 3.2.1. Fix a dimension $d \geq 1$ and consider as ground space the d-dimensional torus $\mathbb{T}^d = \mathbb{R}^d/\mathbb{Z}^d$, (interpretable also as the d-dimensional cube $[0,1]^d$ where opposite boundaries are identified), together with the infinity distance

$$\|\underline{x} - \underline{y}\| = \max_{1 \leq i \leq d} |x_i - y_i|_C, \quad \underline{x}, \underline{y} \in \mathbb{T}^d$$

where $|x_i - y_i|_C = \min\{|x_i - y_i|, 1 - |x_i - y_i|\}$.

For each vertex $v \in [n]$ there is associated, in addition to a weight w_v as in the Chung-Lu model, a position $x_v \in \mathbb{T}^d$ chosen uniformly at random and independently between nodes. The edge probability between two vertices u, v will depend now both on weights and positions:

$$p_{uv} = \Theta \cdot \min\left\{ \frac{1}{\|x_u - x_v\|^{\alpha d}} \cdot \left(\frac{w_u w_v}{l_n} \right)^{\alpha}, 1 \right\}. \tag{3.1}$$

In the limit case $\alpha = \infty$, require additionally that

$$p_{uv} = \begin{cases} \Theta(1), & \text{if } \|x_u - x_v\| \leq \mathcal{O}\left(\left(\frac{w_u w_v}{l_n} \right)^{\frac{1}{d}} \right) \\ 0, & \text{if } \|x_u - x_v\| \geq \Omega\left(\left(\frac{w_u w_v}{l_n} \right)^{\frac{1}{d}} \right) \end{cases} \tag{3.2}$$

where the constants hidden by $\mathcal{O}$ and Ω do not have to match, so that there can be an interval $\left[c_1 \cdot \left(\frac{w_u w_v}{l_n} \right)^{1/d}, c_2 \cdot \left(\frac{w_u w_v}{l_n} \right)^{1/d} \right]$ for $\|x_u - x_v\|$ in which p_{uv} is arbitrary.

A vertex v will be denoted by its position-weight coordinates: $v = (x_v, w_v)$. It will be assumed that weights w_i are i.i.d following power-law distribution, in particular we ask that

$$1 - F_n(x) = \mathbb{P}(W_n \geq x) = \frac{1}{n} \sum_{i \in [n]} \mathbb{1}_{\{w_i \geq x\}} \sim x^{1-\beta} \tag{3.3}$$

for some $\beta > 2$ and that the minimum weight is constant, meaning

$$w_{\min} := \min_{v \in [n]} w_v = \Omega(1)$$

The resulting random graph $\mathbb{G}(n, d, \alpha, \beta, \underline{w}, \underline{x})$ has free parameters $d, \alpha \in (1, \infty]$, β and the average weight $\mathbb{E}(W)$ (at which $\mathbb{E}(W_n)$ converges by hypothesis, as seen for the CL model in case of i.i.d. weights). In the following it will be assumed, as commonly done, $2 < \beta < 3$.

It can be shown [4] that the model is whp scale-free, having degree sequence

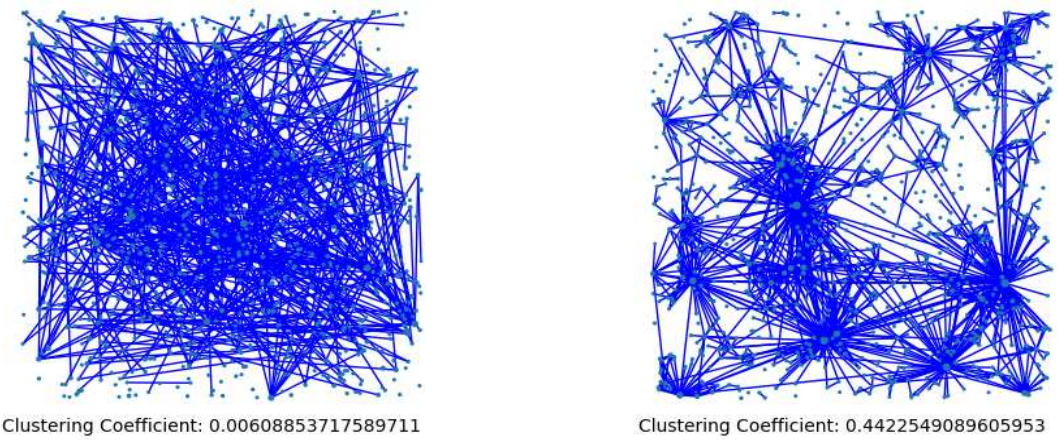

Figure 3.1: Chung-Lu (left) and geometric random graph (right) with the same power law on the weights, in particular $\tau = 2.5$. The introduction of geometry in the formula ruling the edge probabilities cause the clustering coefficient to be significantly different between the two models, as one can see even already here with $n = 1000$ nodes

following a power law, which is not surprising since we asked the same for the weights, as in the CL model. Even more foreseeable is that, as shown in the following lemma, marginal edge probabilities fixing one position are approximately Chung-Lu probabilities:

Lemma 3.2.2. *Let $x_v \in \mathbb{T}^d$ and $w_v \geq w_{\min}$ being fixed. Then for $v = (x_v, w_v)$, it holds that $\mathbb{E}(\mathrm{d}(v)) = \Theta(w_v)$ and for $u = (x_u, w_u)$ with fixed weight and random position, the probability that v, u are neighbours is*

$$\mathbb{P}(u \sim v | x_v, w_v, w_u) = \Theta(\min\{1, \frac{w_v w_u}{l_n}\}) \tag{3.4}$$

In the geometric model, it is useful to have a bound on the number of neighbours of a given vertex whose positions lie in a prescribed region. The following lemma, which will be crucial in the study of the percolation on this random graph, gives a bound for balls:

Lemma 3.2.3. *Let $m = \min\{\alpha, \beta - 1\}$, let $B = \bar{B}_r(0) \subset \mathbb{T}^d$ the closed ball of radius r centered at 0 with volume $\nu = n\mathrm{Vol}(B)$. Then, for any constant $C > 0$ and any vertex with given weight and position $v = (x_v, w_v)$, denoting with $\mu_v =: \mathbb{E}(|\Gamma(v) \cap B)|)$, it holds that*

$$\mu_v = \mathcal{O}(\nu) \cdot \begin{cases} \min\left\{\frac{w_v}{\nu}, 1\right\} & \text{if } \|x_v\| \leq Cr \\ \min\left\{\left(\frac{w_v}{\|x_v\|^d n}\right)^m, 1\right\} & \text{if } \|x_v\| \geq Cr \end{cases}$$

As done for the previous models presented, we highlight in the next theorem the main features concerning connection, size and distances in the geometric model, and present later a proof of the first fact for the threshold geometric model.

Theorem 3.2.4. *Let G the GIRG described above, then it will holds that:*

1. whp $|\mathcal{C}_{\max}| \in \Theta(n), \quad |\mathcal{C}_2| \in \mathcal{O}(\log n)$
2. whp $\mathrm{diam}(\mathcal{C}_{\max}) \sim (\log(n))^{\mathcal{O}(1)}$
3. *Conditionally on the event $\{U_1 \leftrightarrow U_2\}$, we are (as in CL model with infinite variance of the weights) in an ultra small-world:*

$$\frac{\mathrm{dist}(U_1, U_2)}{\log\log n} \xrightarrow{\mathbb{P}} \frac{2 \pm o(1)}{|\log(\beta - 2)|}$$

   and, moreover, the convergence is also in expectation.

4. whp $CC_G = \Theta(1)$

3.3 Giant component in the threshold GIRG

We present the proof of the existence of of the giant component in the threshold model [5], i.e. when $\alpha = \infty$ and the edge probability is the indicator function on the relation between weight and position:

$$p_{uv} = \begin{cases} 1 & \text{if } \|x_u - x_v\| \leq \left(\frac{\lambda w_u w_v}{n}\right)^{\frac{1}{d}} \\ 0 & \text{if } \|x_u - x_v\| > \left(\frac{\lambda w_u w_v}{n}\right)^{\frac{1}{d}} \end{cases} \tag{3.5}$$

The parameters d, τ, λ are constant not depending on n. We also assume that the nodes positions is sampled via a Poisson point process (instead of a uniform distribution of positions in the torus), which has the advantage that the number of vertices in disjoint regions is independent. This approach will be used also in the next section for the formulation of the percolation process on a GIRG.

Proof of 1. The strategy is the following: first observe that, with these assumptions, the subgraph induced by $V_{\geq\sqrt{\frac{n}{\lambda}}}$ is a clique, i.e. it's complete, call it the core of G. The proof amount to show then that every non-core vertex has a path into the core with non-vanishing probability, thus leading to a linear number (in expectation) of vertices in the component 'generated' by the core. Once this is proven, a Chernoff bound will be applied to show concentration around the mean; for this we subdivide the ground space in disjoint cells and show that a constant fraction of this cells possess a path to the core that remains within the cells (and thus are pairwise independent): for this the key point will be then to choose the correct size of the cells, i.e. small enough to have independence of the path and big enough to have a sufficiently large probability of this path to exists.

Step 1.
Define $V_l := V_{\geq e^{l/2}} \cap V_{\leq e^{l+1/2}}$ to be the l-th layer. Then it holds that

$$\mathbb{P}(v \in V_l) = \Theta(\mathbb{P}(w_v \geq e^{l/2})) = \Theta(e^{-l(\tau-1)/2}). \tag{3.6}$$

Call a sequence $(v_0, \dots, v_k)$ a layer path if, for every i, $\{v_i, v_{i+1}\} \in E(G)$ and if $v_i \in V_l$ then $v_{i+1} \in V_{l+1}$.

Lemma 3.3.1. *For every v not in the core, $\mathbb{P}$(there exists a layer path from v to the core) $= \Omega(1)$.*

Proof. Let $u \in V_l$. Then for a $u' \in V_{l+1}$ we have $w_u, w_{u'} \geq w = e^{l/2}$, and the edge $\{u, u'\}$ exists if

$$\text{dist}(u, u') \leq \left(\frac{\lambda w^2}{n}\right)^{\frac{1}{d}} = \lambda^{\frac{1}{d}} \left(\frac{e^l}{n}\right)^{\frac{1}{d}} := \Delta_l. \tag{3.7}$$

By independence between weights and positions, the probability that such u' exists is then

$$\mathbb{P}(u' \in V_{l+1})\mathbb{P}(\text{dist}(u, u') \leq \Delta_l) = \Theta(e^{-l(\tau-1)/2}\Theta(\Delta_l^d) = \Theta(\frac{e^{l(3-\tau)/2}}{n}). \tag{3.8}$$

Consider the random variable that counts the number of such vertices $X_l := |\{u' : u' \in V_{l+1}, \text{dist}(u, u') \leq \Delta_l\}|$. It has mean $\Theta\left(e^{l(3-\tau)/2}\right)$ and, since it is Poisson distributed,

$$\mathbb{P}(X_l > 0) = 1 - \mathbb{P}(X_l = 0) = 1 - e^{-\mathbb{E}(X_l)} = 1 - \exp(-\Theta(e^{l(3-\tau)/2})) > 0$$

Consider now the events $A_l = \{X_l > 0\}$ for $l = 0, \dots, \lceil \log(n/\lambda) \rceil$, where the latter is the core layer.

We have that the existence of a layer path from any vertex in layer 0 to the core layer has probability

$$\mathbb{P}\left(\bigcap_{l=0}^{\lceil \log(n/\lambda)\rceil} A_l\right) = \mathbb{P}\left(\bigcap_{l=0}^{c-1} A_l\right) \cdot \mathbb{P}\left(\bigcap_{l=c}^{\lceil \log(n/\lambda)\rceil} A_l\right)$$
$$= \mathbb{P}\left(\bigcap_{l=0}^{c-1} A_l\right) \cdot \left(1 - \mathbb{P}\left(\bigcup_{l=c}^{\lceil \log(n/\lambda)\rceil} A_l^c\right)\right) \geq \mathbb{P}\left(\bigcap_{l=0}^{c-1} A_l\right) \cdot \left(1 - \sum_{l=c}^{\lceil \log(n/\lambda)\rceil} (1 - \mathbb{P}(A_l)\right)$$
$$= \mathbb{P}\left(\bigcap_{l=0}^{c-1} A_l\right) \cdot \left(1 - \sum_{l=c}^{\lceil \log(n/\lambda)\rceil} \exp(-\Theta(e^{l(3-\tau)/2})\right) \geq K \cdot (1-\epsilon) > 0$$

since the series in the second term converges and so we can lower bound this quantity by a constant positive factor (being the product of a constant number c of positive terms) times a factor bigger than $1-\epsilon$, for every $\epsilon > 0$. Thus the existence of a layer path has non vanishing probability for every non-core vertex (clearly the constant c determined for layer 0 makes the inequality holding for any higher layer) and we proved our claim. □

The consequence of this is that

$$\mathbb{E}(|\mathcal{C}_{\max}|) \geq \mathbb{E}(|\{v : v \text{has a layer path to the core}|) = \Theta(n) \tag{3.9}$$

and we want to apply a concentration inequality to $|\mathcal{C}_{\max}|$ around its mean.

Step 2.
In order to do that, we will divide the ground space in different subregion and construct paths to the core that are enough independent (restricted to a single cell) and at the same time enough likeable to exist.
For a weight w and a region of the underlying metric space C, denote with

$$V_{\geq w,C} := \{v : x_v \in C, w_v \geq w\}$$

Lemma 3.3.2. *Let C a d-dimensional cube of side length Δ, called cell, and divide $\mathbb{T}^d$ in Δ-cells. Then*

$$\mathbb{P}(G(V_{\geq w,C}) \text{ is connected}) \geq 1 - \frac{(2\Delta)^d}{\lambda w^2} \exp(-\frac{\lambda w^{3-\tau}}{2^d})n \tag{3.10}$$

Proof. Subdivide each cell into subcells C_w of size $\Delta_w = \frac{1}{2}\left(\frac{\lambda w^2}{n}\right)^{1/d}$, so that any two vertices of weight greater than w in adjacent subcells are adjacent

themselves. Again, weight and position are independent features, and point positions follows a Poisson distribution, so for a random vertex v

$$\mathbb{P}(x_v \in C_w, w_v \geq w) = \Delta_w^d \cdot w^{-(\tau-1)} = \frac{\lambda w^{3-\tau}}{2^d n}$$

and thus

$$\mathbb{E}(|V_{\geq w, C_w}|) = \mathbb{P}(|V_{\geq w, C_w}| = 0) = \frac{\lambda w^{3-\tau}}{2^d}.$$

Now since there are $R = (\lfloor \frac{\Delta}{\Delta_w} \rfloor)^d$ subcells C_w fully contained in each cell C, the probability that the subgraph induced by $V_{\geq w,C}$ is connected is greater or equal to the probability that each of this subcells $C_w^1, \ldots, C_w^R$ contains at least one heavy vertex, which is

$$\mathbb{P}(|V_{\geq w, C_w^i}| > 0, \quad \forall i = 1, \ldots, R) = \left(\mathbb{P}(|V_{\geq w, C_w^i}| = 0)\right)^R \tag{3.11}$$

$$\geq 1 - R \cdot \mathbb{P}(|V_{\geq w, C_w^i}| = 0) = 1 - (\lfloor \frac{\Delta}{\Delta_w} \rfloor)^d \cdot e^{-\frac{\lambda w^{3-\tau}}{2^d}} \tag{3.12}$$

$$\geq 1 - \Delta^d \cdot \frac{2^d n}{\lambda w^2} \cdot e^{-\frac{\lambda w^{3-\tau}}{2^d}} = 1 - \frac{(2\Delta)^d}{\lambda w^2} \exp(-\frac{\lambda w^{3-\tau}}{2^d}) n. \tag{3.13}$$

□

We call a cell 'good' if a linear number of its vertices has a path within the cell that connect them to the core. The following lemma will show that cells are good independently and with non-vanishing probability, so we are basically in a situation of an independent Bernoulli coin flip for each cell and in the hypothesis of Chernoff inequality to be applied.

Lemma 3.3.3. *Let $\hat{w}$ weight, C cell or size Δ with $\mu = \Delta^d n = \mathbb{E}(|\{v : x_v \in C\}|)$. Assume that*

1. $\mu \geq \hat{w}^{\tau-1}$
2. $\mu \in \omega\left((\log n)^{\frac{2}{3-\tau}} (\log\log n)^d\right)$
3. $\hat{w} \in \omega\left((\log n)^{\frac{1}{3-\tau}}\right)$

Then with non vanishing probability the graph induced by V_C contains a vertex of weight $\geq \hat{w}$ whose connected component has size $\Theta(\mu)$.

Proof. (i) Observe first that, since the random variable $|C_{\geq \hat{w},C}|$ is Poisson distributed and by the first hypothesis it has mean

$$\mathbb{E}(|C_{\geq \hat{w},C}|) = \mu \hat{w}^{1-\tau} \geq 1, \tag{3.14}$$

it holds that $\mathbb{P}(|C_{\geq \hat{w},C}| \geq 1) = \Omega(1)$.
Let $\bar{w} := (\frac{2^d}{\lambda} \log n)^{1/3-\tau}$. By hypothesis 3, $\bar{w} \leq \hat{w}$ and, by Lemma 3.3.2

$$\mathbb{P}(G(V_{\geq \bar{w},C}) \text{ is connected}) \geq 1 - \frac{(2\Delta)^d}{\lambda \bar{w}^2} \xrightarrow[n\to\infty]{} 1. \tag{3.15}$$

Take now v with $w_v < \bar{w}$ and $x_v \in C$. By Lemma 3.3.1, there exists a layer path $L = \{v_0, \cdots, v_{k(\bar{w})}\}$ from v to layer $\bar{w}$ with probability $\Omega(1)$. By the definition of $\bar{w}$, the length $k(\bar{w})$ of L is $\mathcal{O}(\log \log n)$. Since the largest weight in L is $\mathcal{O}(\bar{w})$ and thus for all i

$$\text{dist}(v_i, v_{i+1}) \in \mathcal{O}\left(\frac{\bar{w}^2}{n})^{1/d}\right), \tag{3.16}$$

the total (geometric) distance made in L satisfies

$$\sum_{v_j \in L} \text{dist}(v_j, v_{j+1}) = \mathcal{O}\left((\frac{\bar{w}^2}{n})^{1/d} \log \log n\right) \tag{3.17}$$

$$= \mathcal{O}\left(\left(\frac{(\log n)^{\frac{2}{3-\tau}} (\log \log n)^d}{n}\right)^{\frac{1}{d}}\right) < \Delta \tag{3.18}$$

where the last inequality follows directly by the second hypothesis.
This means that, if we shrink uniformly in all dimensions the size of C to a region C' with side length $\Delta' = s\Delta$, with $s \leq 1$, we will have $\mu' = n(\Delta')^d = \Theta(\mu)$ and with the property that every layer path to layer $\bar{w}$ that starts in C' will remain in C.
(ii) We consider now the vertices in C' that are in the layer 0, since for them the event of having a layer path to $\bar{w}$ is independent of the number of such 0-layer vertices.
The number of vertices $|V_{0,C'}|$ in the first layer with position in C' is Poisson distributed with mean $\Theta(\mu)$ and thus

$$\mathbb{P}(\exists v \in V_{0,C'}) > 0. \tag{3.19}$$

Define now X the random variable of the portion of vertices in the first layer that have a layer path to $\bar{w}$:

$$X = \frac{|\{v : v \in V_0, \nexists \text{ layer path from } v \text{ to layer } \bar{w}\}|}{|\{v : v \in V_0\}|} \in [0, 1]. \tag{3.20}$$

By Lemma 3.3.1, the probability for a random vertex in 0-layer to possess a layer path is at least $1-p$, for some constant $p<1$, which means that $\mathbb{E}(X)\leq p$.
By the Markov inequality, $\mathbb{P}(X<c)\geq 1-\frac{p}{c}$, so choosing the constant $c\in(p,1)$ gives us that with positive non vanishing probability at least a fraction of $1-c$ vertices has a layer path to layer $\bar{w}$.
(iii) We have that for the four events

$$\begin{aligned}
&\mathcal{A}_1 := \{|V_{\geq\hat{w},C}|>0\}\\
&\mathcal{A}_2 := \{|V_{0,C'}|=\Theta(\mu)\}\\
&\mathcal{A}_3 := \{|\{v\in V_{0,C'}:\exists \text{ layer path from } v \text{ to layer } \bar{w}\}|=\Theta(\mu)\}\\
&\mathcal{A}_4 := \{G(V_{\geq\bar{w}}) \text{ is connected}\}
\end{aligned}$$

it holds that $\mathbb{P}(\mathcal{A}_1)=\mathbb{P}(\mathcal{A}_2)=\mathbb{P}(\mathcal{A}_3)=\Omega(1)$ and $\mathcal{A}_1 \perp\!\!\!\perp \mathcal{A}_2 \perp\!\!\!\perp \mathcal{A}_3$, so that the event $\mathcal{A}:=$ 'The cell C contains a $\hat{w}$-weight vertex and a linear part of its vertices has a path to layer $\bar{w}$' has probability $\Omega(1)$. By Lemma 3.3.2 $\mathbb{P}(\mathcal{A}_4)$ happens asymptotically almost surely, so

$$\mathbb{P}(\mathcal{A}\cap\mathcal{A}_4)=\mathbb{P}(\mathcal{A})+\mathbb{P}(\mathcal{A}_4)-\mathbb{P}(\mathcal{A}\cup\mathcal{A}_4)=\Omega(1),$$

i.e., since a $\hat{w}$-weighted vertex $v_{\hat{w}}$ is connected to any other $\bar{w}$-weight vertex inside the cell C, the connected component of $v_{\hat{w}}$ inside C contains a linear fraction of the vertices in the cell with non vanishing probability. □

Step 3.
Choose $\hat{w}=\sqrt{\frac{n}{\lambda}}$ the core weight and the cell size Δ so that

$$\mu=\mathbb{E}(V_C)=n\Delta^d=\hat{w}^{\tau-1}.$$

The total number of cell is then

$$r=\Theta\left(\frac{1}{\Delta^d}\right)=\Theta\left(n^{\frac{3-\tau}{2}}\right)$$

and we are in the hypothesis of previous Lemma, so the graph induced in each cell contains a core vertex whose connected component has size $\Theta(\mu)$ with non vanishing probability. We are then in the situation of a independent coin flip for each cell, where the probability of success to satisfy Lemma 3.3.3 is strictly positive.
Let $X_1,\dots,X_r$ the independent random variables associated to cells $C_1,\dots,C_r$ and representing these coin flips, with $\mathbb{P}(X_i=1)=1-\mathbb{P}(X_i=0)=p_i\geq p>0$ for all i is the probability that the size of the connected component of

cell C_i is indeed $\Theta(\mu)$. Define $X = \sum_i X_i$ and note that $\mathbb{E}(X) = \Theta(r)$. By Chernoff bound 6.3, it follows that, for every $0 < \delta < 1$,

$$\mathbb{P}(X \leq (1-\delta)\mathbb{E}(X)) \leq e^{-\frac{\mathbb{E}(X)\delta^2}{2}} \tag{3.21}$$

i.e.

$$\mathbb{P}(X \leq (1-\delta)\Theta(r)) \leq e^{-\frac{\Theta(r)\delta^2}{2}}. \tag{3.22}$$

For $\delta \to 1$, this finally leads to

$$\mathbb{P}(X \in \mathcal{O}(r)) \leq e^{-\Theta(r)} \xrightarrow[n\to\infty]{} 0, \tag{3.23}$$

that is, by the definition of r, with high probability $X \in \Omega(n^{\frac{3-\tau}{2}})$.
So what has been proved is that w.h.p. $\Omega(n^{\frac{3-\tau}{2}})$ cell will possess a core vertex having its connected component of size $\Omega(n^{\frac{\tau-1}{2}})$. Since all this components are connected together via the edge between their core vertices, they form w.h.p. a global connected component of size

$$|\mathcal{C}_{\max}| = \Omega(n^{\frac{3-\tau}{2}})\Omega(n^{\frac{\tau-1}{2}}) = \Omega(n). \tag{3.24}$$

□

Chapter 4

Bootstrap percolation

Percolation serves as a framework for simulating random damage inflicted upon a network. This process acts globally on the graph, where typically a random set of edges and/or nodes is removed from the graph. It stands out as one of the most straightforward models capable of illustrating a phase transition phenomenon: as the network experiences increasingly severe damage, it fractures into numerous small connected components. Conversely, when the damage is minimal, a single large component persists. It can be studied both on deterministic and random graphs.
Bootstrap percolation on the other hand is, in a sense, a process acting locally, where its evolution is determined by the neighbourhood structure of nodes in the graph. It's a powerful theoretical framework that has gained significant attention in the study of graph theory and complex networks. It provides a simple yet effective mechanism to model various dynamic processes, such as the spread of information, influence, or disease within a network. This concept was first introduced by Chalupa, Leath, and Reich in 1979 in the context of magnetic disordered systems, where in their study the underlying structure was a particularly simple type of graph, namely a lattice, and since then, it has been extensively studied due to its applicability and intriguing properties.
In this chapter, we will introduce the concept of bootstrap percolation applied to graphs. We will provide a comprehensive definition of this process and offer an overview of the significant findings related to its application in random graph models. Specifically, we will compare the threshold results obtained for various models presented in this thesis, elucidating the similarities and differences between them.

4.1 Motivation and definition of the model

A bootstrap percolation process with activation threshold an integer $r \geq 2$ on a graph $G = G(V, E)$ is a deterministic process evolving in rounds. Every vertex can have two status: active or inactive, and the process is initialized by the definition of a (random) subset $V^0 \subset V$ in which every vertex is activated, whereas every other vertex remains inactive. Subsequently, in each subsequent round, if an inactive vertex has at least r of its neighbours activated, then it also becomes active and remains so forever:

$$V^{t+1} = V^t \cup \{v \in V : |\Gamma(v) \cap V^t| \geq r\}$$

The process stops when no more vertex become active between two subsequent rounds, and the main goal is to find the dependence from both the parameters of the random graph model and the percolation process of the initial set V^0 and the final set of active node V^∞.
The relation between the initial and final infected sets A^0 and A^∞ is the central problem to be typically studied, as well as the number of rounds τ needed for the process to stabilize

$$\tau := \inf\{t \geq 1 : V^t = V^{t-1}\}$$

or to expand in the (almost) totality of the graph, which in case of random graphs is considered to be a linear part of it, as the number of the total nodes tends to infinity (as done when analyzing the rise of the giant component).
Denoting with $a = a(n) = |A^0|$ and observing that the event 'for the process starting from A^0 it holds that $|A^\infty| > c$' is an increasing event of $\mathcal{G}_n$, these leads to look for a threshold function for a.

Clearly the evolution of the process in any model depends sensitively on its parameters: if we consider for example the Erdős-Renyi model with $p = o(n^{-2}$, the resulting graph has w.h.p. no edges and then, whatever the activation parameter r is, in the limit it will always hold that $A^0 = A^\infty$. In [10] the authors discuss thresholds for percolation in $\mathbb{G}(n, p)$ reformulating the process considering the effect of one infected vertex at each time and an auxiliar 'marking' process to keep track of vertices that will eventually become infected. Their study is focused both on thresholds for p given the size a and viceversa, i.e. given specific windows for the function $p(n)$ and so a prescribed structure of the graph, analyze constraints for a. One of the main results is that, for $r \geq 2$ and

$$\frac{1}{n} \ll p(n) \ll \frac{1}{n^{1/r}}$$

the model exhibits a sharp phase transition with respect to a threshold $a_c = a_c(r, n, p(n))$, where the final size infection with high probability is either $n - o(n)$ or it is $o(n)$; in particular, when $|A^0| = o(n)$, w.h.p. there is no evolution of the process, and instead one needs positive density ($|A^0| = \Omega(n)$) of the initial infection in order to spread effectively. This analysis in the subcritical case, meaning under the threshold a_c, is then deepened to prove that the final size is near in the limit to a normal distribution.

4.2 Known results for IRG

We switch framework to highlight some result on bootstrap percolation performed on a inhomogeneous random graph with power-law degrees, in particular the Chung-Lu model. This brief summary will also serve as an example to highlight similarities and differences with the geometric model introduced in section 3, the latter being based on the former.
The behaviour here is in glaring contrast with the ER model briefly discussed above: now even with a sublinear number of initially activated vertices the process can explode and propagate to a linear part of the graph. Under the usual hypothesis of the exponent in (2.12) $\tau \in (2, 3)$ and weights to be bounded below by a positive constant and above by the function n^{ζ}, with $\zeta \leq \frac{1}{1-\tau}$, the key point in the proof, similarly to the proof of the existence of the giant component seen in the previous chapter and that will be again essential in the next section, is the presence of high weight vertices, forming a fairly dense graph and guaranteeing the spread of the infection. We remark that for $\tau > 3$ this is not true anymore and one find a similar situation as of ER
To achieve this fact, authors in [8] define, for a function $f : \mathbb{N} \to \mathbb{R}^+$, the f-kernel of the graph as

$$V_f := \{v \in V : w_v \geq f(n)\}$$

and consider the subgraph induced by this set of vertices. The goal is to find an $f = \omega(1)$ that grows fast enough in order to activate a large part of the graph once V_f is infected, and at the same time grows slow enough in order to have $G(V_f)$ dense enough in the graph.
In the subcritical case (where such an f is not achievable), there will be no evolution at all: with high probability, $V^{\infty} = V^0$. This is done showing that under the threshold the expected number of vertices with at least r neighbour in V^0 is in $o(1)$ and applying first moment argument.
In the supercritical case, there exists such a function $f(n) = f(n; \tau, r, a(n))$,

which must be in $\wp(n^{\zeta})$ (otherwise $V_f = \varnothing$) and is, most important, shown to be such that

$$a(n) \ll |V_f|.$$

One can construct a coupling between the induced subgraph $G(V_f)$, where the probability of its edges is by definition always larger than $p_f := \frac{f^2}{\sum w}$, and the Erdős-Renyi random graph

$$\mathbb{G}(|V_f|, p_f).$$

Thus, one may apply results obtained in [10] for the percolation in the ER model to get that w.h.p. almost all the high weight vertices become infected; observe that this comes from a sublinear initial infection.
The second step is done by splitting the vertex set into layer depending on weights in a decreasing way starting from layer V_f, and proving by induction that the infection spread from one layer to the adjacent one w.h.p. up to a constant layer $V_{\geq C}$: specifically, it is shown that

Proposition 4.2.1. *There exist $\delta = \delta(\tau)$ such that, for every $\epsilon \leq \delta$ there exist a constant $C = C(\epsilon, \tau, r,) > 0$ with the property that, if at least a $(1-\epsilon)|V_f|$ part of the vertices in V_f becomes infected, then w.h.p. at least $(1-\epsilon)|V_{\geq C}|$ vertices of $V_{\geq C}$ will become infected.*

The conclusion follows since clearly $|V_{\geq C}| = \Theta(n)$.
These results are then enriched in [11] by the same authors to show a law of large number for the size of V^{∞} (in more general settings) in the linear case of initial infection size, i.e. when every vertex in the graph is initially infected independently with a fixed constant probability p; they also refine the supercritical-sublinear case (that in which $a(n) = \wp(n) \cap \omega(a_c(n)))$ to show that the size of the final set of infected nodes does not depend on $a(n)$.

Bootstrap percolation has been studied intensively in a wide range of graphs based on its application, from fairly simple structures, as lattices in statistical physics, to more complex ones, such as random graphs incorporating geometry, the topic of the next section.

4.3 Bootstrap percolation on GIRG

In the following we will study the spread of a disease in a population through bootstrap percolation on a geometric graph [1]; the underlying geometry, in addition to determining the graph structure as discussed in the previous chapter, enables us to define the epicenter of the infection in a localized manner:

percolation in previous model started with the activation of a random set of nodes, that could be far apart (in an edge-distance sense) in the graph, while here we will restrict the initial activation to a predefined region in the torus, leading to a more realistic representation of the phenomenon .
We will be interested in finding thresholds for the behaviour of the process, like explosion (infection of an infinite number of nodes in finite time in the case of a infinite graph, or a $\Theta(n)$ number of nodes in case of graph of size n) and the speed of the diffusion in the case of global spread.
With an abuse of notation, for $V' \subset V$ and $A \subset \mathbb{T}^d$, we denote with

$$V' \cap A = \{v \in V' : x_v \in A\}$$

and, in line with the previous chapter, $V_{\geq w,A} = \{v \in V : w_v \geq w, x_v \in A\}$.
The model is the GIRG introduced before, with the slight difference that nodes and positions of the graphs are generated by a homogeneous Poisson point process on the torus with intensity $n \in \mathbb{N}$.
Formally, for any Lebesgue-measurable subset A of $\mathbb{T}^d$, we assume that

$$|V \cap A| \sim \text{Poi}(n\text{Vol}(A)) \tag{4.1}$$

and that $|V \cap A| \perp\!\!\!\perp |V \cap B|$ for any disjoint measurable subsets A, B.
Observe that in this case the total number of vertices is also random, being itself Poisson distributed with mean n. One consequence is that, given a random vertex $v = (x_v, x_w)$, conditioning on $x_v \in A$, then x_v is uniformly distributed in A. In this framework, conditioning on the Poisson point process, an edge between two distinct vertices (x_u, w_u) and (x_v, w_v) will appear with probability (3.1). Having fixed the underlying structure, we define objects and fix notations that will be used in the description of the process on GIRG:

Definition 4.3.1. Fix a constant threshold $k \geq 2$, the initial infection rate $\rho \leq 1$ and a starting region $B_0 \subset \mathbb{T}^d$, assumed to be a ball centered in 0.
Define V^0 the set of infected at time 0 selecting all vertices in $V \cap B_0$ independently with probability ρ, and for each $t \in \mathbb{N}$, each vertices with at least k infected neighbours will be infected:

$$V^{t+1} := V^t \cup \{v \in V : |\Gamma(v) \cap V^t| \geq k\},$$

where we allow $t \in \mathbb{R}$ meaning in that case $\lceil t \rceil$.

Call $V^\infty = \bigcup_{t\in\mathbb{N}} V^t$ and denote the infection time of a vertex v with

$$L_v := \inf\{t \geq 0 : v \in V_t\}$$

and $L_v = \infty$ if the infimum doesn't exist. Finally, call $\nu = \nu(n) = n|\mathrm{Vol}(B_0)|$ the expected number of vertices initially infected.

The following theorem determines a threshold for the outcome of the percolation process, showing a phase transition from a subcritical regime where the spread of the disease ends immediately to the supercritical regime where, roughly speaking, all vertices will be infected, passing through a critical window in which both these outcomes are possible. It also establish a time of explosion for the process in the subcritical regime, i.e. the step at which a linear part of the nodes become infected whp:

Theorem 4.3.2. *In the above settings, with constants parameters $\alpha, \tau, w_{\min}, d$ and k, for the bootstrap percolation on a GIRG$_n$ with initial infection rate $\rho = \rho(n)$ and initial infection region $B_0(n)$ with volume $\nu(n) = \omega(1)$, call*

$$\rho_c(n) = \nu^{-\frac{1}{\tau-1}}. \tag{4.2}$$

Then it holds that

(i) If $\rho = o(\rho_c)$ then whp $|V^\infty| = V_0$

(ii) If $\rho = \Theta(\rho_c)$ then both $|V^\infty| = \Theta(n)$ and $|V^\infty| = V^0$ have non vanishing probabilities

(iii) If $\rho = \omega(\rho_c)$ then whp $|V^\infty| = \Theta(n)$

In particular, defining

$$i_\infty := \frac{\log\log_\nu n + \log\log n}{|\log(\tau-2)|},$$

it holds that

$$|V^{(1+\delta)i_\infty}| = \Omega(n) \tag{4.3}$$

whp in the case (iii) and with probability $\Omega(1)$ in the critical regime.

Proof (sketch). In the subcritical regime (i), the percolation process ends immediately, since whp it holds that $|V^1| = |V^0|$.
Indeed, since by construction and Lemma 6.1.7, the random variable $|\Gamma(v) \cap V^0|$ (the number of neighbours of v that are activated at the beginning of the process) is Poisson distributed with mean $\rho\mu_v$, we have that

$$\mathbb{P}(|\Gamma(v) \cap V_0| \geq k) = \mathcal{O}(1)\min\{1, (\rho\mu_v)^k\}.$$

Now we can bound the number of vertices that become active at first round $|V^{=1}| := |V^1 \setminus V^0|$ with the number of vertices that has at least k neighbours in V_0. Split them in those that lies inside the ball $2B_0$ and call this subset $V_{in}^{=1}$, and those outside it, $V_{out}^{=1}$.
Applying lemma 3.2.3 and using the hypothesis $\rho = o(\nu^{-1/(\tau-1)})$, we can bound $\mathbb{E}(|V_{in}^{=1}|) = o(1)$; for $\mathbb{E}(|V_{out}^{=1}|)$ we only need that $\rho = \mathcal{O}(\rho_c)$ to deduce

$$\mathbb{E}(|V_{out}^{=1}|) = \nu^{-(\tau-2)(1-1/m)}$$

which, since $m > 1$, is also $o(1)$. Thus $\mathbb{E}(|V^{=1}|) = o(1)$ and so by Markov inequality, no vertices will be activated in round 1 whp.

In the critical regime (ii), the bound on $\mathbb{E}(|V_{out}^{=1}|)$ still holds since only $\rho = \mathcal{O}(\rho_c)$ was sufficient. To bound $\mathbb{E}(|V_{in}^{=1}|)$, let $\xi > 0$ constant to be determined and we further divide vertices in low-weighted $V_{\leq w_0\xi}$ and heavy-weighted $V_{\geq w_0\xi}$, where $w_0 =: \nu^{1/(\tau-1)}$.
Again by 6.1.7, $|V_{\geq w_0\xi} \cap 2B_0|$ is Poisson distributed with mean $\mathcal{O}(\nu(\xi w_0)^{1-\tau}) = \mathcal{O}(1)$, so the event $A = \{|V_{\geq w_0\xi} \cap 2B_0| = 0\}$ occurs with $\Omega(1)$ probability, thus it is enough to prove that

$$\mathbb{P}(V_{\leq w_0\xi}^{=1} \cap 2B_0 = V^0 | A)$$

occurs with probability $\Omega(1)$.
Now by Lemma 6.1.7 and Lemma 3.2.2

$$\mathbb{P}(|\Gamma(v) \cap V_0| \geq k \mid A) = \mathcal{O}((\rho w_v)^k), \tag{4.4}$$

which implies $\mathbb{E}\left[\left|V_{\leq \xi w_0}^{=1} \cap 2B_0\right| \mid A\right] = \mathcal{O}(\xi^{k+1-\tau}) \leq \frac{1}{2}$ for small enough ξ, which in the end implies that $\left|V_{\leq \xi w_0}^{=1} \cap 2B_0\right| = 0$ with probability at least $1/2$ (since it has values in $\mathbb{N}_0$). Thus with positive probability the process ends at the first round, as in the subcritical case.

To see that the process 'survives' with positive probability (at least until round 1), consider the random variable $|V_{\geq w} \cap B_0|$, which is Poisson with mean $\Theta(\nu w_0^{1-\tau}) = \Theta(1)$, thus with probability $\Omega(1)$ there exist k vertices $v_1, \ldots, v_k$ with $w_i \geq w_0$ and $x_i \in B_0$. Consider the balls B_i centered in v_i of volume $\frac{\nu^{1/(\tau-1)}}{n}$, and call

$$C_i = B_i \cap B_0.$$

Since $|V^0 \cap C_i| \sim \mathrm{Poi}(\rho n \mathrm{Vol}(C_i))$, for every i the event

$$\mathcal{C}_i = \{|V^0 \cap C_i| \geq k\}$$

has probability $\Omega(1)$. Since the events $\mathcal{C}_i$ are either independent or positively related, i.e.

$$\mathbb{P}(\mathcal{C}_i | \mathcal{C}_{i_1}, \ldots, \mathcal{C}_{i_s}) \geq \mathbb{P}(\mathcal{C}_i), \quad \forall i, i_1, \ldots i_s \leq k$$

and so $\mathbb{P}(\mathcal{C}_i, \forall i) \geq \prod_{i=1}^{k} \mathbb{P}(\mathcal{C}_i) = \Omega(1)$.
Condition now on weights and positions of v_i and on $\mathcal{C}_i$, and fix $u_j^{(i)}$, for $j = 1 \dots k$ the existing vertices in $V^0 \cap \mathcal{C}_i$, for every i. Then conditioned on weights and position of all the u_j^i, we have that

$$\mathbb{P}(v_i \sim u_j^{(i)}) = \Omega\left(\min\left\{1, \left(\frac{w_0}{\nu^{1/(\tau-1)}}\right)^{\alpha}\right\}\right) = \Omega(1)$$

and so the probability that all the edges $\{u_j^{(i)} \sim v_i\}_{i,j}$ appear has still probability $\Omega(1)$, due to independence of the edges given weights and positions. This means that $V^1 \cap B_0$ contains at least k heavy-weighted vertices with probability $\Omega(1)$.

Now, if there are at least k activated vertices in the first round (so with probability $\Omega(1)$ in the critical regime) or if $\rho = \Theta(\rho_c)$ (supercritical regime), the infection starts spreading; in the following we summarize its evolution, whose outcome and speed is stated in 4.3.
Define $\zeta = \frac{1}{\tau-2} > 1$ and let $0 < \epsilon < \zeta - 1$. For $\eta = \varnothing(\epsilon)$ and

$$\nu_i = \nu^{(\zeta-\epsilon)^i}.$$

let $w_{i,\epsilon} = w_{i,l}(\epsilon) = \nu_i^{\frac{(\zeta-\epsilon)^{-l}}{\tau-1+\eta}}$ and for all $i > 0$ the increasing sequence of nested balls $B_i = B_i(\epsilon)$ centered in 0 and with volume $\frac{\nu_i}{n}$. The key idea is that the infection spreads in two ways:

- from heavy vertices in one region to heavy vertices in the next region, whose volume grows exponentially fast: at time i, a a big portion of $V_{\geq w_i, B_i}$ becomes infected w.h.p and is responsible, in the following rounds, of the infection of $V_{\geq w_{i+1}, B_{i+1}}$. It can be shown that w.h.p. and for all i every sufficiently heavy vertex of B_i will be infected within the next three rounds, i.e. the events

$$\mathcal{H}_i := \{\forall u \in B_i \cap V_{\geq w_i}, u \in V^{i+3}\} \tag{4.5}$$

  occur with high probability. This ensures that the infection spreads and eventually reaches the boundaries of $\mathbb{T}^d$, at least for enough heavy vertices.

- from 'low' weight vertices to nearby low weight vertices: once ensured the 'heavy spread' at step $i+3$ in the whole ball i, it can be shown that all vertices in B_i with weight larger thatn $w_{i,l}$ will become infected in the next l rounds with 'large enough' probability $\Omega(1)$.

The key point in the second step, which is the reason why in the end a linear part of the nodes will be infected, is the usage of a function that regulates the relation between weights and distance in any ball in the correct way. Select i and l such that $i+l \leq (1+\epsilon)B_i = \mathbb{T}^d$ and $w_{i,l} = \mathcal{O}(1)$, one can then choose $h \in \omega(1)$ with $\log\log h \in o(\log\log n)$ such that

$$\mathbb{P}(v \in V^j | w_v \geq w_h) = 1 - h^{-\Omega(1)} \tag{4.6}$$

with $w_h = h^{\frac{1}{\beta-1+\eta}}$ and $j = (1+\epsilon/2)i_\infty$.
Decompose now the tours into balls $Q_1, \dots Q_s$ of volume $\Theta(\frac{h}{n})$, with $s = \Theta(\frac{n}{h})$, and divide them into 'good' if at round j half of vertices in $Q \cap V_{\geq w_h}$ are infected, 'bad' otherwise; let X_σ the Bernoulli random variable associated to Q_σ. with $X_\sigma = 1$ if Q_σ is good. By (4.6), the expected fraction of vertices still inactive at round j in $Q \cap V_{\geq w_h}$ is $h^{-\Omega(1)} = o(1)$, so by Markov inequality the probability that a ball is bad is $o(1)$. Then in expectation a $o(1)$ fraction of the balls is bad, so again by Markov

$$\mathbb{P}(\sum_{\sigma \leq s} \mathbb{1}_{\{X_\sigma = 0\}} \geq \frac{s}{2}) \leq 2\frac{\mathbb{E}(\sum_{\sigma \leq s} \mathbb{1}_{\{X_\sigma=0\}})}{s} = o(1),$$

i.e. with high probability at least half of the balls is good. Now for a good ball Q, consider the percolation process restricted to it (in which only the interaction of vertices inside Q is taken into account, in particular for the infection probability), and define finally $Y_Q = |Q \cap V_{\geq C} \cap V^{j+l_1}|$, for suitable constant C and $l_1 = o(\log\log h)$ (so that for large n we have $j + l_1 \leq (1+\epsilon)i_\infty$). With the same reasoning it can be shown that

$$\mathbb{P}\left(Y_Q \geq \frac{\mathbb{E}(|V_{\geq C} \cap Q|}{2}\right) = \Omega(1)$$

Since restricted processes to different Q_{σ_s} are independent, so in particular $Y_{Q_{\sigma_s}}$ are independent, we can apply Chernoff bound to get that an $\Omega(1)$ fraction of the ball satisfies w.h.p.

$$Y_Q \geq \frac{\mathbb{E}(|V_{\geq C} \cap Q|}{2} = \Omega(h)$$

and then w.h.p $|V^{j+l_1}| = s \cdot \Omega(1) \cdot \Omega(h) = \Omega(sh) = \Omega(n)$, leading us to the lower bound of the global infection time □

Chapter 5

Numerical simulation

In this chapter we are going to test numerically the results of 4 by concretely performing bootstrap percolation on a geometric inhomogeneous random graph.

5.1 Methods and assumption

We will run the simulations with spread parameter $k = 2$, i.e. the least possible choice, in order to 'minimize' the speed of convergence (expecting the latter to be decreasing with k) and be able to observe different behaviors for different scales of the graph size. The power-law exponent of the weights is set to $\tau = 2.9$, the torus is 2-dimensional and for graphical reason, its size is scaling as the vertex size n, i.e.

$$\mathrm{Vol}(\mathbb{T}^2) = n$$

so that it has side length $\sqrt{n}$. From this, it follows that the hypothesis $\nu(n) = \omega(1)$, i.e. the expected number of vertices in the initial region of infection B_0 going to infinity for n going to infinity, is translated as

$$\mathbb{E}(V_{B_0}) = n\frac{\mathrm{Vol}(B_0)}{\mathrm{Vol}(\mathbb{T}^2)} = \mathrm{Vol}(B_0).$$

We thus control this quantity through the 'infection radius' of the ball B_0, setting it to be

$$r_0 = \left(\frac{\sqrt{n}}{\pi}\right)^{\frac{1}{2}},$$

so that $\nu = r_0^2\pi = \sqrt{n}$.
With this calibrations, the threshold function will be approximately $\nu^{-1/\tau-1} \approx$

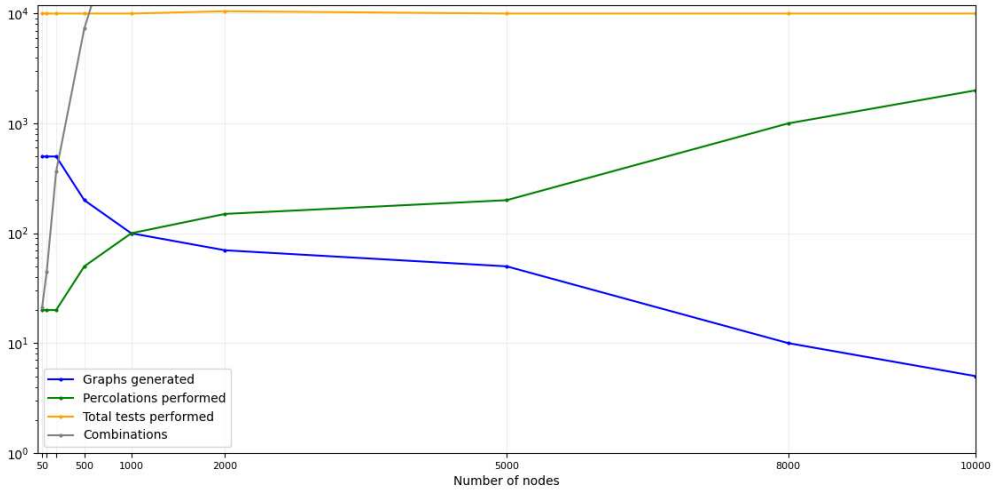

Figure 5.1: The number of graphs generated decreases with the graph size (in blue), while the number of percolation run on each of them increases (in green), in order to keep the number of simulations almost constant (10000) for each size considered (yellow). Observe that the number of bootstrap percolations performed starts and remains below the gray curve, representing the number (at the threshold, in expectation) of possible ways to start the infection (equal to the binomial coefficient of the expected number of nodes in B_0 and the expected number of initial nodes infected in B_0).

$n^{-0.26}$. We consider graph sizes from 50 to 10000 nodes and for each of these we perform the simulations by iteration on two parameters, namely the number of of graph generated l and the number of bootstrap percolations m run on each of them; we will decrease l with the graph size and increase m with the graph size for two reasons: first computational (generating a big size graph takes way more time than performing percolation on it), and second, because percolating the same graph l times when starting from a small (compared on l) number of expected vertices inside the initial region of activation will end up in repeating the exact same process approximately

$$l/\binom{\lceil \nu \rceil}{\lceil \rho\nu \rceil}$$

times, while instead the percolation can start from an enormous combination of different sets of nodes (even of the same size) when the vertex set is big, changing completely the outcome of the process.

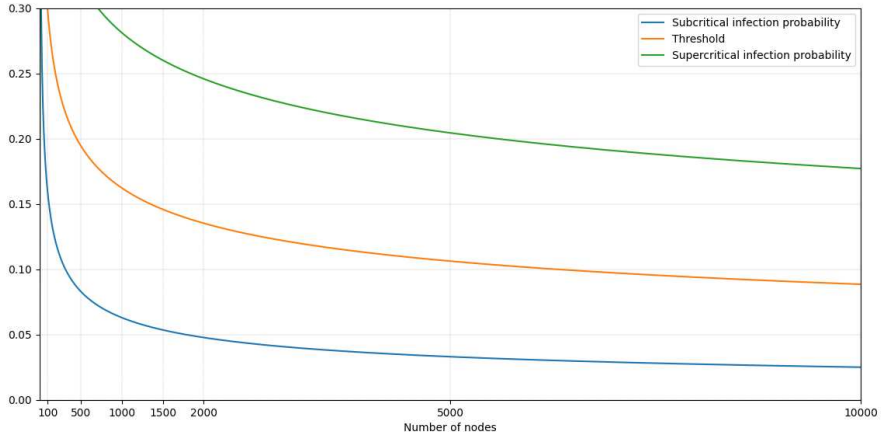

Figure 5.2: Plot of the threshold function $p_c(n)$ and the initial infection rate $\rho(n)$.

5.2 Subcritical regime

In the subcritical case, to effectively measure the number of percolation that ends in a 'negligible' portion of the graph infected, we consider a variable that count the number of simulation in which the process ends before round $f(n) = \lfloor \log(n) \rfloor$ (this quantity may be affected in a small decrease in the graphs with size between powers of 10; the choice of $f(n)$ can be refined, and a deeper analysis can be done considering together the number of infected nodes and the average number of steps - both scaled by other functions of the number of nodes).
We set the infection probability $\rho = n^{-0.4} \ll \rho_c$. As we can see in the figure,

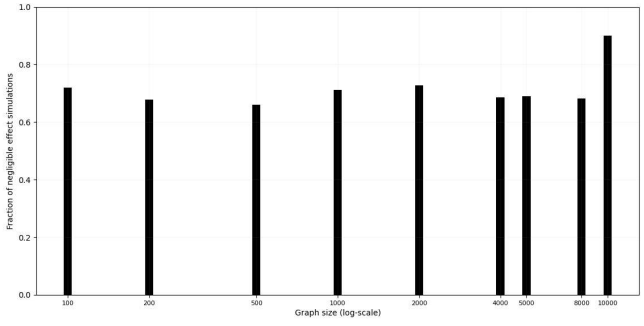

Figure 5.3: Fraction of the number of percolations that stop almost immediately (before round $\lfloor \log(n) \rfloor$)

the number of simulations that die almost immediately increase with the

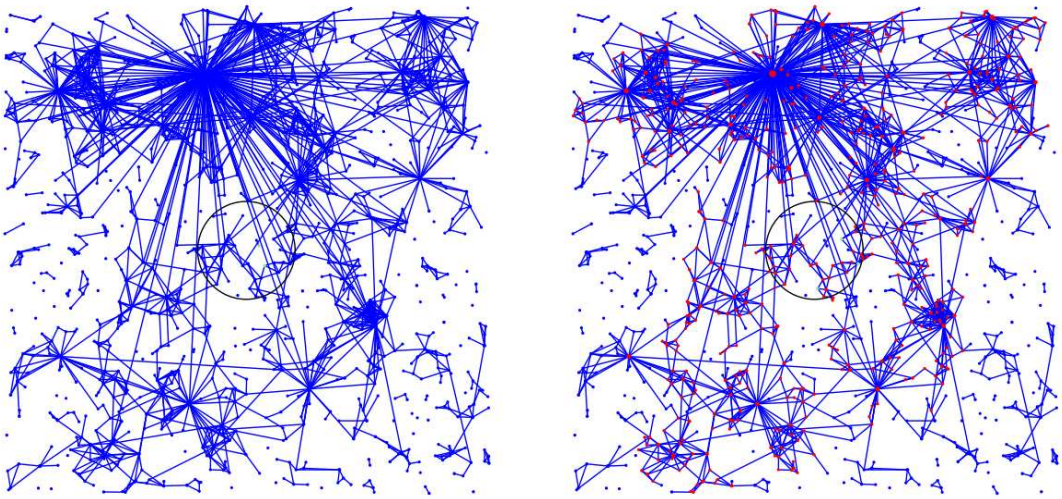

Figure 5.4: Bootstrap percolation performed on the same graph with 1000 in the subcritical regime, the black circle represents the initial region of infection: on the left, the 2 initial nodes activated (in green) trigger no more vertex; on the right, 2 of the initial 3 nodes activated trigger a new round, starting a waterfall of infection that turn into the activation of the high-weight vertex (the highly connected node positioned on the top of the torus), leading to the infection of a big portion of the graph

graph size, except for the oscillation between different power of 10 due to the function considered as discriminant on the number of rounds; in particular focusing on sizes $100, 1000, 10000$, the ratio is strictly increasing.

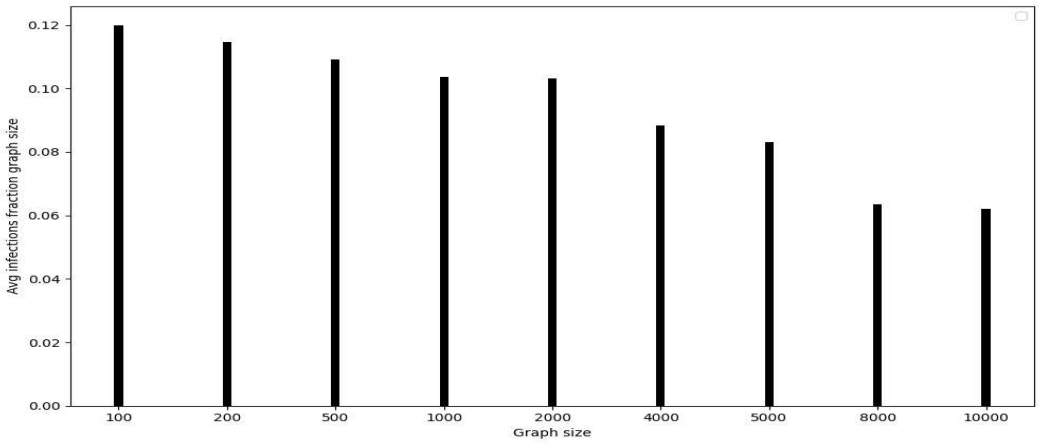

Figure 5.5: Average number of infected nodes after round 0, scaled by the number of nodes of the corresponding graph in which the simulation is performed. The fraction of the graph infected at the end of the process is strictly decreasing with the graph size.

Percolating the same graph can lead to opposite outcomes based on the realization of the starting infection, both in the number of its nodes and their relative position and weigth: in the figure above, a graphs of size 10^3, with the same number of node activated at round 0, the first stopping immediately, the second reaching a huge fraction of the nodes in the graph.
The average number of infected nodes indeed increases with n for the sizes we considered as well as the average number of rounds performed by the infections; nevertheless, the size of infected nodes fraction the number of total nodes decrease, as shown in the picture.

5.3 Supercritical Regime

In the supercritical regime, we consider the initial activation probability ρ to be equal to the threshold function multiplied by a function in $\omega(1) \cap \mathcal{O}(\frac{1}{\rho_c})$; precisely, we define

$$\rho(n) = \rho_c(n) \cdot (\log_{10}(n))^{\frac{1}{2}}$$

so that $\rho = \omega(\rho_c)$ and also $\rho(n) = \mathcal{O}(1)$, in particular $\rho \in [0, 1]$ and is decreasing with the number of nodes (and with the number of expected vertices in the region of initial infection). To show evidence of the result of the theorem in the supercritical case, we again measure the fraction of infected nodes at the end of the percolation process $\frac{|V^\infty(n)|}{n}$: in the figure, we can observe that this quantity increase with the graph size, and seems to stabilize around a certain constant C. We then consider the number of

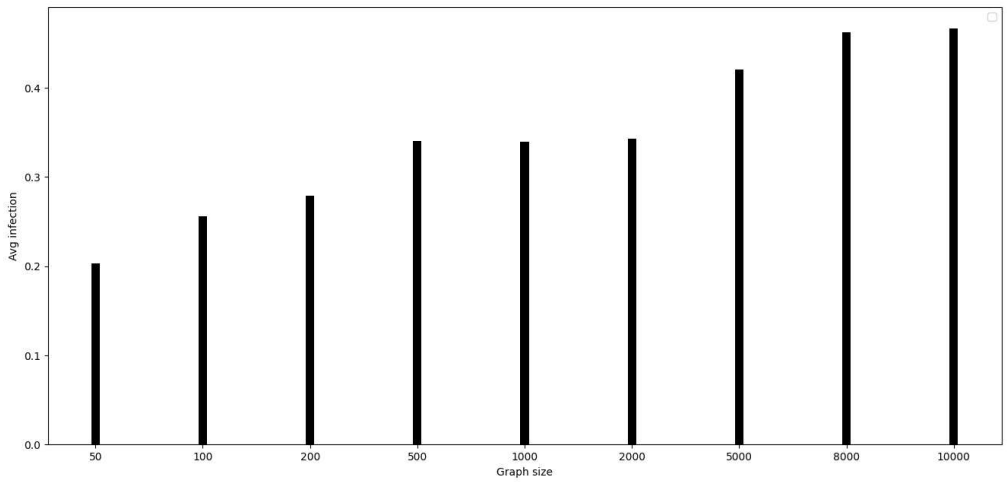

Figure 5.6: Average number of infected nodes after round 0, scaled by the number of nodes of the corresponding graph in which the simulation is performed. The fraction of the graph infected at the end of the process increases in the sizes range considered.

simulations that infect a fixed positive fraction $C \in [0, 1]$ of the vertex set within round $i_\infty(n)$; we choose $C \approx 0.2$, the infimum of the fraction obtained in the simulation above (see figure). By the theorem, we expect this quantity to increase toward 1 with the graph size, and indeed it is verified as shown in the figure below.

The frequency of the rounds performed during the process tends to have

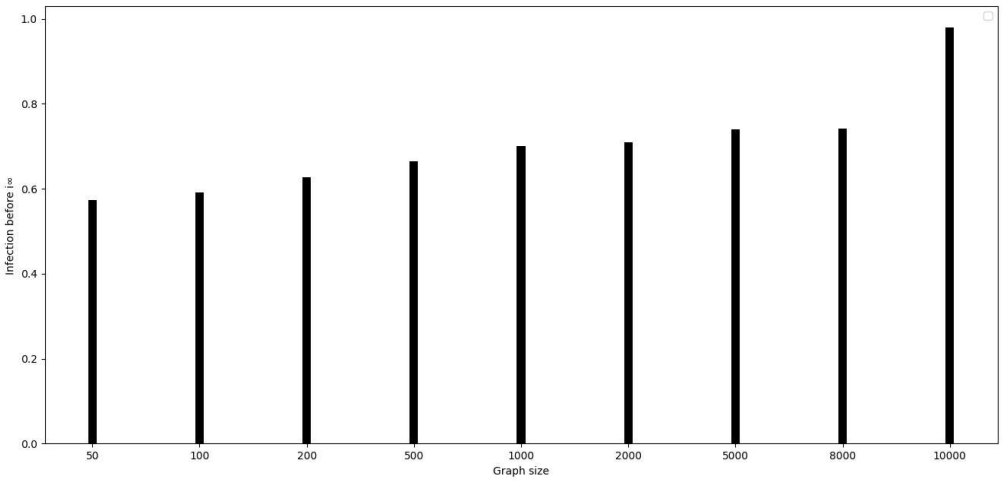

Figure 5.7: Fraction of simulation run that reach a positive portion ($C \approx \frac{1}{5}$) of the graph size before the round i_∞.

two distinct dense region, one around 0, represented by process that die immediately, and one near the average; the first peak become more and more rare and shifted on the right (the probability of no percolation going to 0 for n increasing), while the second grows. In particular, a 'desert' area

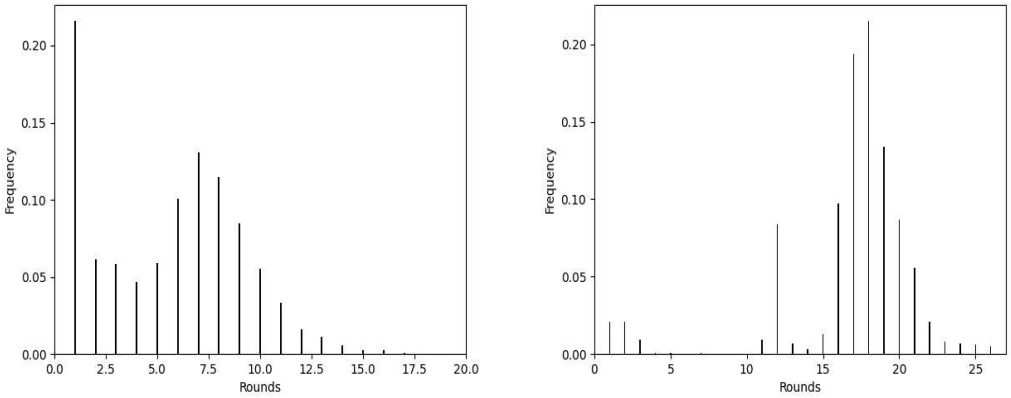

Figure 5.8: Frequencies for 100 (left) and 1000 nodes (right)

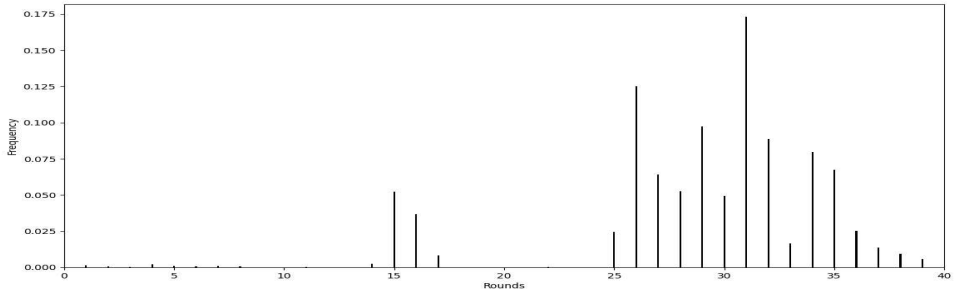

Figure 5.9: Frequencies of the number of rounds performed by bootstrap percolation on a random graph of 100 nodes (upper left), 1000 nodes (upper right) and 10000 nodes (down). The mass in the supercritical regime is shifted from the left peak to the right one as n grows, creating an interval of rounds for which almost no process end up with.

between the two appears already for $n = 10000$, reflecting what is predicted by the theorem and enclose the meaning of the sharp threshold behavior: either the process does not start or (almost) complete percolation happens.

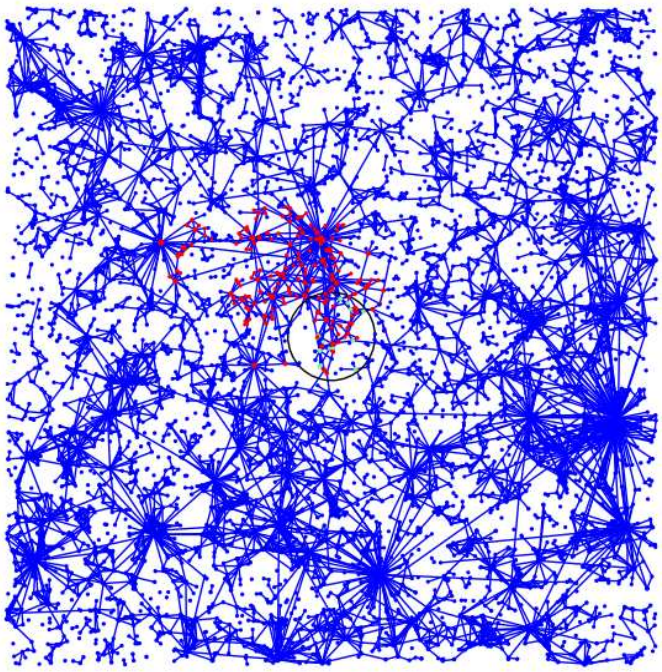

Figure 5.10: In this graph with 5000 nodes, repeating the percolation ends up frequently with the infection of the same nodes as those activated (in red) in the figure, due to a particular distribution of node positions and edges in and near the initial ball, performing a small positive number of rounds. As n grows, this situation becomes less and less likely.

5.4 Conclusions

One interesting part, which we won't treat here, is to estimate numerically the dependence of the convergence in probability from the spread coefficient k: since the result is independent of k, indeed the threshold in (4.2) being a function of the graph realization (through n, positions and the power-law exponent of the weight) and the parameter driving the initial infection (the ball's volume, specifically the expected number of vertices inside it), the global infection or the zero infection will happen above and below this threshold respectively with probability tending to 1 for graph size large enough, no matter how large is k. What instead varies is how fast (for n growing) is tending to 1.

Chapter 6

Appendix

6.1 Inequalities

Let X a random variable with finite mean μ and variance σ.

- Markov inequality: if X is non-negative random variable, then

$$\mathbb{P}(X \geq a) \leq \frac{\mathbb{E}(X)}{a}$$

- Chebyshev inquality:

$$\mathbb{P}(|X - \mu| > a) \leq \frac{\sigma^2}{a^2}$$

- Chernoff bound: let $S_n = \sum_{i \leq n} X_i$, with X_i i.i.d. $\sim X$. From the Central Limit Theorem we know that

$$\frac{S_n - n\mu}{\sigma\sqrt{n}} \xrightarrow{d} N(0,1)$$

  i.e. $S_n \approx n\mu + \mathcal{O}(\sqrt{n})$. Applying the exponential form of Markov inequality to

$$\mathbb{P}(S_n > an) = \mathbb{P}(S_n > \mu n + (a - \mu)n)$$

  leads to

$$\begin{aligned} \text{If } a > \mu &\implies \mathbb{P}(S_n \geq an) \leq e^{-nI(a)} \\ \text{If } a < \mu &\implies \mathbb{P}(S_n \leq an) \leq e^{-nI(a)} \end{aligned}$$

where $I : \mathbb{R} \to \bar{\mathbb{R}}$ is the Legendre transform of the logarithm of the moment generating function of X, i.e.

$$I(a) = \inf_t \{ta - \log(\mathbb{E}(e^{tX}))\}$$

For $S_n \sim \text{Binomial}(n, p)$ and $S_n \sim \text{Poisson}(n\lambda)$, we have respectively

$$I_{Bin(p)}(a) = a \log \frac{p}{a} + (1-a) \log \frac{1-p}{1-a} \tag{6.1}$$

$$I_{Poi(\lambda)}(a) = \lambda - a - a \log \frac{\lambda}{a} \tag{6.2}$$

In the case of distinct independent Bernoulli random variables X_i taking values in $\{0, 1\}$ with $\mathbb{P}(X_i = 1) = p_i > 0 \forall i$, denote with $m = \mathbb{E}(\sum X_i)$, we get the following lower bound for the concentration inequality of S_n around its mean: for every $0 < \delta < 1$

$$\mathbb{P}(S_n \leq (1-\delta)m) \leq e^{-\frac{m\delta^2}{2}} \tag{6.3}$$

Theorem 6.1.1. *Let S_n a random walk starting from 0 and with i.i.d. integer increments $X_k \geq -1$. For $k > 0$ let $T_k = \inf\{n : S_n = -k\}$. Then*

$$\forall N \in \mathbb{N} \quad \mathbb{P}(T_{-k} = N) = \frac{k}{N} \mathbb{P}(S_N = -k) \tag{6.4}$$

Lemma 6.1.2. *Let X, Y random variables such that $X \sim Bin(n, p)$ and $Y|X \sim Bin(X, q)$. Then $Y \sim Bin(n, pq)$.*

Lemma 6.1.3. *Let $X_n \sim Bin(n, p = p(n))$, with $\lim_{n\to\infty} n \cdot p = \lambda$. Then as $n \to \infty$, $X_n \xrightarrow{d} Poi(\lambda)$*

Definition 6.1.4. Let μ, ν probability measures on some space $(\Omega, \mathcal{F})$. A coupling of μ and ν is a measure γ defined on the product space $(\Omega \times \Omega, \mathcal{F} \times \mathcal{F})$ such that

$$\gamma(A \times \Omega) = \mu(A), \gamma(\Omega \times A) = \nu(A), \quad \forall A \in \mathcal{F}$$

Using coupling we can easily prove that

Lemma 6.1.5. *For $A \subset \mathcal{G}_n$ increasing event and $p_1 \leq p_2$, it holds that $\mathbb{P}_{n,p_1}(A) \leq \mathbb{P}_{n,p_2}(A)$*

Proof. Consider i.i.d. uniform random variables $(U_e^n)_{e \in \mathcal{E}_n}$ for each edge and, for any $p \in [0, 1]$, the random graphs

$$\mathbb{G}(\underline{U}^n, p) := \{e \in \mathcal{E}_n : U_e \leq p\}$$

Since for all p it holds that

$$\mathbb{P}(\mathbb{G}(\underline{U}^n, p) = G) = p^{|E(G)|} \cdot (1-p)^{\binom{n}{2}-|E(G)|} = \mathbb{P}(\mathbb{G}(n,p) = G)$$

we defined a coupling of the probability measures $(\mathbb{P}_{n,p})_{p\in[0,1]}$. Now if $p_1 \leq p_2$, we have that

$$\begin{aligned}\mathbb{G}(n,p_1) = \mathbb{G}(\underline{U}^n, p_1) &= \{e \in \mathcal{E}_n : U_e \leq p_1\} \\ \subseteq \{e \in \mathcal{E}_n : U_e \leq p_2\} &= \mathbb{G}(\underline{U}^n, p_2) = \mathbb{G}(n,p_2)\end{aligned}$$

□

Lemma 6.1.6. *If X is a power-law exponent random variable with exponent τ, then $Y = \mathrm{Poi}(X)$ follows a power-law with same exponent.*

Lemma 6.1.7. *Let $\lambda \in \mathbb{R}_{\geq 0}$ and let $X \sim \mathrm{Poi}(\lambda)$. Given $0 \leq q \leq 1$, let Y be a random variable which conditioned on $\{X = x\}$, for any $x \in \mathbb{N}_0$, is the sum of x independent Bernoulli random variables with mean q. Then Y is Poisson distributed with mean $q\lambda$.*

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