Percolation on Random Recursive Trees

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ABSTRACT: We study Bernoulli bond percolation on a random recursive tree of size \( n \) with percolation parameter \( p(n) \) converging to 1 as \( n \) tends to infinity. The sizes of the percolation clusters are naturally stored in a tree structure. We prove convergence in distribution of this tree-indexed process of cluster sizes to the genealogical tree of a continuous-state branching process in discrete time. As a corollary we obtain the asymptotic sizes of the largest and next largest percolation clusters, extending thereby a recent work of Bertoin [5]. In a second part, we show that the same limit tree appears in the study of the tree components which emerge from a continuous-time destruction of a random recursive tree. We comment on the connection to our first result on Bernoulli bond percolation. © 2015 Wiley Periodicals, Inc. Random Struct. Alg., 48, 655–680, 2016

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1. INTRODUCTION

Let \( V \) be a finite and totally ordered set of vertices. An increasing tree on \( V \) is a tree rooted at the smallest element of \( V \) such that the sequence of vertices along the branch from the root to any vertex increases. A random recursive tree (RRT for short) of size \( n + 1 \) is a tree picked uniformly at random among all increasing trees on \( \{0, 1, \ldots, n\} \). Henceforth we write \( T_n \) for such a RRT. Note that the root vertex of \( T_n \) is given by 0.

We consider Bernoulli bond percolation on \( T_n \) with parameter \( p(n) \in (0, 1) \). This means we first pick \( T_n \) and then remove each edge with probability \( 1 - p(n) \), independently of the other edges. We obtain a partition of vertices into clusters, i.e. connected components, and we are concerned with the asymptotic sizes of these clusters. Let us call percolation on a RRT \( T_n \) in the regime \( p(n) \to 1 \)

- weakly supercritical, if \( \frac{1}{\ln n} \ll 1 - p(n) \ll 1 \),
Fig. 1. Left: Percolation on a recursive tree with vertices labeled 0, 1, ..., 10. The edges which were removed by the percolation are indicated by dashed lines. Right: The corresponding percolation clusters, whose sizes are encoded by $C(n)$.

- **supercritical**, if $1 - p(n) \sim \frac{t}{\ln n}$ for some $t > 0$ fixed,
- **strongly supercritical**, if $0 < 1 - p(n) \ll \frac{1}{\ln n}$.

The terminology is explained by our results: We will see that the root cluster has size $\sim np(n)$, while the next largest clusters have size of order $(1 - p(n))np(n)$. In the weakly supercritical regime, the size of the root cluster is therefore $o(n)$. In the supercritical regime, it is of order $n$ as its complement, whereas in the strongly supercritical regime, it behaves as $\sim n$.

We encode the sizes of all percolation clusters by a tree structure. We call the resulting tree-indexed process the **tree of cluster sizes**. A percolation cluster of $T_n$ is called a cluster of generation $k$, if it is disconnected from the root cluster by exactly $k$ deleted edges. In the tree of cluster sizes, vertices of level $k$ are labeled by the sizes of the clusters of generation $k$. Consequently, the root vertex represents the size of the root cluster of $T_n$. Then, if a vertex represents the size of a cluster $\tau$ of generation $k$, its children are given by the sizes of those clusters of generation $k + 1$ which are separated from $\tau$ by a single deleted edge (see Fig. 1). We use the convention of ordering the children according to their sizes.

We normalize cluster sizes of generation $k$ by a factor $(1 - p(n))^{-k}n^{-p(n)}$. Then, as $n$ tends to infinity, the rescaled tree of cluster sizes converges in distribution to a process which represents the genealogical tree of a continuous-state branching process in discrete time, with reproduction measure $\nu(da) = a^{-2}da$ on $(0, \infty)$ and started from a single particle of size 1 (Theorem 1). Moreover, we obtain precise limits for the largest non-root clusters (Corollary 1).

Asymptotic cluster sizes have been studied for numerous other random graph models. At first place, these include the Erdős–Rényi graph model (see Alon and Spencer [1, Chapter 11] for an overview with further references). Concerning trees, Pitman [16, 17] and Pavlov [15] considered uniform Cayley trees of size $n$ in the regime $1 - p(n) \sim t/\sqrt{n}$, $t > 0$ fixed, where the number of giant components is unbounded. For general large trees, Bertoin gives in [4] a criterion for the root cluster of a Bernoulli bond percolation to be the (unique) giant cluster.

Unlike random Cayley trees of size $n$, whose heights are typically of order $\sqrt{n}$, random recursive trees have heights of logarithmic order (see e.g. the book of Drmota [11]). Bertoin
proved in [5] that in the supercritical regime when $1 - p(n) \sim t/\ln n$, the size of the root cluster of a RRT on $n+1$ vertices, normalized by a factor $1/n$, converges to $e^{-t}$ in probability, while the sizes of the next largest clusters, normalized by a factor $\ln n/n$, converge to the atoms of some Poisson random measure. This result was extended by Bertoin and Bravo [8] to large scale-free random trees, which grow according to a preferential attachment algorithm and form another family of trees with logarithmic height.

Here we follow the route of [8] and analyze a system of branching processes with rare neutral mutations. In this way we gain control over the sizes of the root cluster and of the largest clusters of the first generation, in all regimes $p(n) \rightarrow 1$. An iteration of the arguments then allows us to prove convergence of higher generation cluster sizes.

The methods of [5] are based on a coupling of Iksanov and Möhle [12] between the process of isolating the root in a RRT and a certain random walk. They seem less suitable for the weakly supercritical regime, where one has to look beyond the passage time up to which the coupling is valid. This was already mentioned in the introduction of [5], where also the question is raised how the sizes of the largest clusters behave when $1 - p(n) \gg 1/\ln n$.

In the second part of this paper, we however adopt the methods of [5]. We consider a destruction process on $T_n$, where edges are equipped with i.i.d. exponential clocks and deleted at the time given by the corresponding variable. Starting with the full tree $T_n$, each removal of an edge $e$ gives birth to a new tree component rooted at the outer endpoint of $e$. The order in which the tree components are cut suggests an encoding of their sizes and birth times by a tree-indexed process, which we call the tree of components (see Fig. 2 for an example). We obtain a limit result for the tree of components (Theorem 2) which involves again the continuous-state branching process considered above.

Keeping track of the birth times allows us to consider only those tree components which are born in the destruction process up to a certain finite time. Interpreting the latter as a version of a Bernoulli bond percolation on $T_n$, tree components are naturally related to percolation clusters. This observation was made by Bertoin in [5] and then used to study

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cluster sizes in the supercritical regime. We further develop these ideas in the last section and make the link to our results on percolation from the first part of this paper.

The destruction process can be viewed as an iterative application of the cutting down or isolation of the root process, which has been analyzed in detail for RRT’s in Meir and Moon [14], Panholzer, Drmota, Iksanov, Möhle, M. and Rösler [10], Iksanov and Möhle [12], Bertoin [5] and others. The tree of components should be seen as a complement to the so-called cut-tree, which was studied for random recursive trees by Bertoin in [6]. We briefly recall its definition at the very end.

The rest of this paper is organized as follows. The goal of Section 2 is to prove our main result Theorem 1 on the sizes of percolation clusters. We first introduce the tree of cluster sizes and state the theorem. Then we establish the connection to Yule processes and obtain the asymptotic sizes of the root and first generation clusters. We then turn to higher generation clusters in the tree and finish the proof of Theorem 1. Section 3 is devoted to the analysis of the destruction process of a RRT. At first we define the tree of components and formulate our main result Theorem 2 for this tree. The splitting property of random recursive trees transfers into a branching property for the tree of components, which we illustrate together with the coupling of Iksanov and Möhle in the next part. Then we prove Theorem 2. In the last part, we sketch how our analysis of the destruction process leads to information on percolation clusters in the supercritical regime. We compare our results there with Theorem 1 and finish this paper by pointing at the connection to the cut-tree.

We finally mention that except for the very last part, Section 3 on the destruction process can be read independently of Section 2.

2. THE TREE OF CLUSTER SIZES

2.1. Our Main Results on Percolation

We use a tree structure to store the percolation clusters or, more precisely, their sizes. Recall that the universal tree is given by

$$\mathcal{U} = \bigcup_{k=0}^{\infty} \mathbb{N}^k,$$

with the convention $\mathbb{N}^0 = \emptyset$ and $\mathbb{N} = \{1, 2, \ldots\}$. In particular, an element $u \in \mathcal{U}$ is a finite sequence of strictly positive integers $(u_1, \ldots, u_k)$, and we refer to its length $|u| = k$ as the generation or level of $u$. The $j$th child of $u$ is given by $u_j = (u_1, \ldots, u_k, j), j \in \mathbb{N}$. The empty sequence $\emptyset$ is the root of the tree and has length $|\emptyset| = 0$. If no confusion occurs, we simply write $u_1 \ldots u_k$ instead of $(u_1, \ldots, u_k)$.

Now consider Bernoulli bond percolation on a RRT $T_n$ with parameter $p(n)$. This induces a family of percolation clusters, and we say that a cluster is of generation $k = 0, 1, \ldots, n$, if it is disconnected from the root $0$ by $k$ erased edges. This means that exactly $k$ edges have been removed by the percolation from the path in the original tree $T_n$ connecting $0$ to the root of the cluster. In this terminology, the only cluster of the zeroth generation is the root cluster.

We define recursively a process $C^{(n)} = (C_u^{(n)} : u \in \mathcal{U})$ indexed by the universal tree, which we call the tree of cluster sizes.

First, $C_{\emptyset}^{(n)}$ is the size of the root cluster of $T_n$. Next, we let $C_1^{(n)} \geq C_2^{(n)} \geq \cdots \geq C_{\ell(n)}^{(n)}$ denote the decreasingly ranked sequence of the sizes of the clusters of generation 1, where $\ell(n) \leq n$. 

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and in the case of ties, clusters of the same size are ordered uniformly at random. We continue
the definition iteratively as follows. Assume that for some \( u \in \mathcal{U} \) with \( 1 \leq |u| \leq n - 1 \),
\( C_u^{(n)} \) has already been defined to be the size of some cluster \( c_u^{(n)} \) of generation \(|u|\). We then
specify the children of \( C_u^{(n)} \). Among all clusters of generation \(|u| + 1\), we consider those
which are disconnected by exactly one erased edge from \( c_u^{(n)} \). Similar to above, we rank
these clusters in the decreasing order of their sizes and let \( C_u^{(n)} \) be the size of the jth largest.
An example is given in Fig. 1.

The definition is completed by putting \( C_u^{(n)} = 0 \) for all \( C_u^{(n)} \) which have not been specified
in the above way. In particular, \( C_u^{(n)} = 0 \) for all \( u \) with \(|u| > n\), and if \( C_u^{(n)} = 0 \) for some \( u \),
then all elements of the subtree of \( C_u^{(n)} \) rooted at \( u \) are set to zero.

Our limit object is given by the genealogical tree \( Z = (Z_u : u \in \mathcal{U}) \) of a continuous-state
branching process in discrete time with reproduction measure \( v(da) = a^{-2}da \), started from
a single particle. The distribution of \( Z \) is characterized by induction on the generations as follows (cf. \cite{2, Definition 1}).

- \( Z_n = 1 \) almost surely;
- for every \( k \in \{0, 1, 2, \ldots \} \), conditionally on \((Z_v : v \in \mathcal{U}, |v| \leq k)\), the sequences \((Z_u)_{u \in \mathcal{U}}\)
  for the vertices \( u \in \mathcal{U} \) at generation \(|u| = k\) are independent, and each sequence \((Z_u)_{u \in \mathcal{U}}\)
  is distributed as the family of the atoms of a Poisson random measure on \((0, \infty)\) with
  intensity \( Z_u \nu \), where the atoms are ranked in the decreasing order of their sizes.

We turn now to the statement of Theorem 1. Recall that we assume \( p(n) \to 1 \) as \( n \to \infty \).
In the strongly supercritical regime when \( 1 - p(n) \ll 1 / \ln n \), the root cluster has size \( \sim n \).
Moreover, if \((1 - p(n))np(n)\) stays bounded, the next largest clusters will be of constant size
only. In order to ensure that we observe in each generation growing cluster sizes, we shall
additionally assume that \( p(n) \) satisfies \((1 - p(n))knp(n) \to \infty \) for every \( k \in \mathbb{N} \). Without
this condition, our convergence results still hold if we restrict ourselves to generations
\( k \leq \max\{\ell \in \mathbb{N}_0 : (1 - p(n))^\ell np(n) \to \infty \} \).

**Theorem 1.** As \( n \to \infty \), in the sense of finite-dimensional distributions,
\[
\left( \frac{(1 - p(n))^{-|u|}}{p(n)} C_u^{(n)} : u \in \mathcal{U} \right) \Rightarrow (Z_u : u \in \mathcal{U}).
\]

While the theorem shows that the root cluster has size \( C_0^{(n)} \sim np(n) \) in probability, it does not
immediately answer the question how the sizes \( C_1^{(n)} \geq C_2^{(n)} \geq \ldots \) of the largest non-root
clusters behave. We will however see that for fixed \( \ell \) and large \( n \), the \( \ell \) largest non-root
clusters are with high probability given by the \( \ell \) largest clusters of the first generation.

**Corollary 1.** For each fixed \( \ell \in \mathbb{N} \), as \( n \to \infty \),
\[
\left( \frac{(1 - p(n))^{-1}}{p(n)} C_1^{(n)} , \ldots , \frac{(1 - p(n))^{-1}}{p(n)} C_\ell^{(n)} \right) \Rightarrow (Z_1, \ldots , Z_\ell),
\]
where in accordance with our definition of \( Z, Z_1 > Z_2 > \ldots \) are the atoms of a Poisson
random measure on \((0, \infty)\) with intensity \( v(da) = a^{-2}da \).

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2.2. Connection to Yule Processes with Neutral Mutations

Here we will develop the methods that enable us to prove finite-dimensional convergence of the tree of cluster sizes for generations \( \leq 1 \). We conclude this part with the proof of Corollary 1. In the next section, we lift the convergence to higher levels in the tree and thereby finish the proof of Theorem 1.

The following recursive construction of a RRT forms the basis of our approach. We consider a standard Yule process \( Z = (Z(t) : t \geq 0) \), i.e. a continuous-time pure birth process started from \( Z(0) = 1 \), with unit birth rate per unit population size. Then, if the ancestor is labeled by 0 and the next individuals are labeled in the increasing order of their birth times, the genealogical tree of the Yule process stopped at the instant

\[
\rho_n = \inf \{ t \geq 0 : Z(t) = n + 1 \}
\]

is a version of \( T_n \).

With this construction, percolation on a RRT \( T_n \) with parameter \( p \in (0, 1) \) can be interpreted in terms of neutral mutations which are superposed to the genealogical tree. In the description that follows we are guided by [2] and [8].

Except for the ancestor, we let each individual of the Yule process be a clone of its parent with probability \( p \) and a mutant with probability \( 1 - p \). Being a mutant means that the individual receives a new genetic type which was not present before. The reproduction law is neutral in the sense that it is not affected by the mutations. We record the genealogy of types by the universal tree in the following way. Every vertex represents the type of the ancestor, and for every \( u = (u_1, \ldots, u_k) \in \mathcal{U} \) and \( j \in \mathbb{N} \), the \( j \)th child of \( u \), i.e. \( u_j = (u_1, \ldots, u_k, j) \), stands for the genetic type which appeared at the instant when the \( j \)th mutant was born in the subpopulation of type \( u \).

Starting from \( Z_0^0(0) = 1 \) and \( Z_u^0(0) = 0 \) for \( u \in \mathcal{U} \setminus \emptyset \), we write \( Z_u^0(t) \) for the size of the subpopulation of type \( u \) at time \( t \geq 0 \), when neutral mutations occur at rate \( 1 - p \) per unit population size. Clearly, the sum over all subpopulations \( Z = (\sum_{u \in \mathcal{U}} Z_u^0(t) : t \geq 0) \) evolves as a standard Yule process, and we will henceforth work with \( Z \) defined in this way.

Moreover, interpreting the genealogical tree of \( Z(\rho_n) \) as a RRT \( T_n \) as above, the sizes of the clusters of generation \( k \) are given by the variables \( Z_u^0(\rho_n) \) with \( |u| = k \). Note however that in the tree of cluster sizes, the children of each element are decreasingly ordered according to their sizes, while in the population model, the sequence \( (Z_u^0(\rho_n) : j \in \mathbb{N}) \) for \( u \in \mathcal{U} \) is ordered according to the birth times of the mutants stemming from type \( u \), i.e. type \( u\i \) was born before type \( u\j \) for \( i < j \).

Let us denote the birth time of the subpopulation of type \( u \in \mathcal{U} \) by

\[
b_u^{(p)} = \inf \{ t \geq 0 : Z_u^0(t) > 0 \}.
\]

Clearly, for \( p < 1 \), each variable \( b_u^{(p)} \) is almost surely finite. Moreover, each process \( (Z_u^0(b_u^{(p)} + t) : t \geq 0) \) for \( u \in \mathcal{U} \) is distributed as a continuous-time pure birth process with birth rate \( p \) per unit population size, started from a single particle. Once an individual of a new genetic type appears, the population of that type evolves independently, which shows that the processes \( (Z_u^0(b_u^{(p)} + \cdot) : u \in \mathcal{U}) \) are independent. The sequence of subpopulations bearing a single mutation is moreover independent from the sequence of its birth times:

The processes \( (Z_i^0(b_i^{(p)} + t) : t \geq 0) \) for \( i \in \mathbb{N} \) are i.i.d. and independent of the sequence of birth times \( (b_i^{(p)} : i \in \mathbb{N}) \).

For a formal proof of this statement, see [8, Lemma 1].

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Our first aim is to obtain a joint limit law for $Z_{\rho_n}^{(p)}(\rho_n)$ and $Z_{\rho_n}^{(p)}(\rho_n)$, $i \in \mathbb{N}$, when $n \to \infty$ and $p = p(n) \to 1$. We recall that

$$W(t) = e^{-t}Z(t), \quad t \geq 0,$$

is a non-negative square-integrable martingale with terminal value $W(\infty)$ given by a standard exponential variable. The next lemma, which is similar to Lemma 2 in [8], shows that the speed of convergence is exponential.

**Lemma 1.** For every $t \geq 0$, one has

$$\mathbb{E}\left(\sup_{s \geq t} |W(s) - W(\infty)|^2\right) \leq 10e^{-t}, \quad \text{and} \quad \mathbb{E}\left(\sup_{s \geq 0} e^{2s/3}|W(s) - W(\infty)|^2\right) \leq \frac{10e^{2/3}}{(1 - e^{-1/6})^2}.$$

Similarly, for $p \in (0, 1)$ fixed, $W_{\rho}^{(p)}(t) = e^{-pt}Z_{\rho}^{(p)}(t)$, $t \geq 0$, is a martingale. Its terminal value $W_{\rho}^{(p)}(\infty)$ is again a standard exponential random variable. Moreover, for $p$ tending to 1, $W_{\rho}^{(p)}(\infty)$ converges to $W(\infty)$ in $L^2(\mathbb{P})$. This is a consequence of the following uniform convergence result, which is readily obtained from adapting the proof of [8, Lemma 3] to our case.

**Lemma 2.** For all $\varepsilon > 0$, there exists $t_\varepsilon < \infty$ such that

$$\lim_{p \to 1} \sup_{p \geq t_\varepsilon} \mathbb{E}\left(\sup_{s \geq t_\varepsilon} |W_{\rho}^{(p)}(s) - W(\infty)|^2\right) \leq \varepsilon.$$

In order to prove a joint limit law for the processes $Z_{\rho}^{(p)}(\rho_n)$, $i \in \mathbb{N}$, we need information on their birth times $b_{\rho}^{(p)}$ when $p \to 1$. This is achieved by the next lemma, which corresponds to [8, Lemma 4].

**Lemma 3.** As $p \to 1$, in the sense of finite-dimensional distributions,

$$\left( (1 - p)W(\infty) \exp\left(pb_{\rho}^{(p)}\right) : i \in \mathbb{N}\right) \Rightarrow (S_i : i \in \mathbb{N}),$$

where $S_i = e_1 + \cdots + e_i$, and $e_1, e_2, \ldots$ are i.i.d. standard exponential random variables.

As for Lemmas 1 and 2, one can follow the proof of [8] to get this last result for our model. As a consequence, we see that for all $i \in \mathbb{N}$

$$b_{\rho}^{(p)} = -(1/p) \ln(1 - p) + O(1) \quad \text{as} \quad p \to 1,$$

i.e. the set of values $b_{\rho}^{(p)} + (1/p) \ln(1 - p)$ is stochastically bounded as $p \to 1$.

For the rest of this section, we let $p = p(n)$ depend on $n$ such that $p \to 1$ as $n \to \infty$, but for ease of notation, we mostly write $p$ instead of $p(n)$.

We first compute the asymptotic size $Z_{\rho_n}^{(p)}(\rho_n)$ of the ancestral subpopulation, or, to put it differently, the asymptotic size of the root cluster of a Bernoulli bond percolation on $T_n$ with parameter $p$. 

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Lemma 4.\)
\[\lim_{n \to \infty} n^{-p} Z_{i_n}^{(p)}(\rho_n) = 1 \quad \text{in probability.}\]

**Proof.** Since \(\lim_{t \to \infty} e^{-t}Z(t) = W(\infty)\) a.s., we have \(\lim_{n \to \infty} e^{-\rho_n n} = W(\infty)\) a.s., implying
\[\lim_{n \to \infty} e^{-\rho_n n} W^{-1}(\infty) = 1 \quad \text{almost surely.} \tag{2}\]
Furthermore, we see from Lemma 2 that
\[\lim_{n \to \infty} e^{-\rho_n} Z_{i_n}^{(p)}(\rho_n) = W(\infty) \quad \text{in probability.}\]
Together with (2) the claim follows. \(\square\)

We will now implicitly assume this at least for \(k = 1\). Since we have \(\lim_{n \to \infty} (\rho_n - \ln n) = -\ln W(\infty)\) almost surely, this implies
\[\lim_{n \to \infty} (p \rho_n + \ln(1 - p)) = \infty \quad \text{almost surely.} \tag{3}\]

We now consider two independent sequences \((W_i(\infty) : i \in \mathbb{N})\) and \((e_i : i \in \mathbb{N})\) of i.i.d. standard exponential random variables. We shall assume that they are both defined on the same probability space. As before, let \(S_i = e_1 + \cdots + e_i\). Theorem 2 of [8] tailored to our needs yields finite-dimensional convergence of the \(Z_{i_n}^{(p)}(\rho_n), i \in \mathbb{N}\).

**Proposition 1.** As \(n \to \infty\), in the sense of finite-dimensional distributions,
\[
\left( \frac{(1 - p)^{-1}}{n^p} Z_{i_n}^{(p)}(\rho_n) : i \in \mathbb{N} \right) \implies \left( \frac{W_i(\infty)}{S_i} : i \in \mathbb{N} \right).
\]

**Proof.** For \(i \in \mathbb{N}\) and \(t \geq 0\), put
\[W_i^{(p)}(t) = e^{-pt} Z_{i_n}^{(p)}(b_i^{(p)} + t).
\]
Let \((t_{i_n}^{(p)})_{n \in \mathbb{N}}\) be a family of random times with \(\lim_{n \to \infty} t_{i_n}^{(p)} = \infty\) in probability. From Lemma 2 (with \(W_i^{(p)}\) and \(W_i(\infty)\) in place of \(W_{i_n}^{(p)}\) and \(W_{i_n}(\infty)\)) and the fact that the processes \(Z_{i_n}^{(p)}(b_i^{(p)} + \cdot), i \in \mathbb{N}\), are i.i.d. with the same distribution as \(Z_{i_n}^{(p)}(\cdot)\), we infer that there is the convergence in the sense of finite-dimensional laws (as \(n \to \infty\), with \(p = p(n)\) as above)
\[
\left( \exp \left(-p t_{i_n}^{(p)}\right) Z_{i_n}^{(p)}(b_i^{(p)} + t_{i_n}^{(p)}) : i \in \mathbb{N} \right) \implies (W_i(\infty) : i \in \mathbb{N}).
\]
Concerning the birth times, we have by Lemma 3 the finite-dimensional convergence
\[
\left( \frac{1}{(1 - p)W(\infty)} \exp \left(-p b_i^{(p)}\right) : i \in \mathbb{N} \right) \implies \left( \frac{1}{S_i} : i \in \mathbb{N} \right).
\]
By the remark below the definition of \(b_i^{(p)}\), the sequence \((b_i^{(p)} : i \in \mathbb{N})\) is independent of \((Z_{i_n}^{(p)}(b_i^{(p)} + \cdot) : i \in \mathbb{N})\), so that we have in fact joint weak convergence of the sequences on the left in the last two displays towards \((W_i(\infty), 1/S_i : i \in \mathbb{N})\). Now let \(t_n^{(p)} = \rho_n - b_i^{(p)}\). Then \(t_n^{(p)} \to \infty\) in probability for \(n \to \infty\) by (1) and (3). By the mapping theorem, the
element-wise product of the sequences converges to \((W_i(\infty)/S_i : i \in \mathbb{N})\) in the sense of finite-dimensional laws. Recalling (2), this proves the proposition.

In order to obtain convergence of the tree of cluster sizes for the first generation, we have to rank the sequence \((Z_{i}^{(p)}(\rho_n) : i \in \mathbb{N})\) in the decreasing order of their elements. Note that finite-dimensional convergence for the reordered sequence cannot directly be deduced from Proposition 1. We first have to show that for \(\ell\) fixed, the \(\ell\) largest subpopulations of generation 1 at time \(\rho_n\) are with high probability to be found amongst the \(k\) oldest when \(n \to \infty\) and \(k \to \infty\). In view of the last proposition and (1), we have to ensure that at time \(\rho_n\), we see only with small probability a subpopulation of size of order \((1-p)n^p\) which bears a single mutation and was born at a time much later than \(-(1/p) \ln(1-p)\).

For later use, namely for the proof of Corollary 1, it will be helpful to consider also subpopulations with more than one mutation. For that purpose, let us list the full system of subpopulations \((Z_u^{(p)} : u \in \mathcal{U})\) in the order of their birth times. We obtain a sequence \((Y_i^{(p)}(t) : t \geq 0, i \in \mathbb{N}_0)\) which represents the same process as \((Z_u^{(p)}(t) : t \geq 0, u \in \mathcal{U})\), such that \(Y_0^{(p)} = Z_0^{(p)}, Y_1^{(p)}(b_1^{(p)} + \cdot) \equiv Z_1^{(p)}(\cdot),\) and \(Y_i^{(p)}(t) = 0\) if less than \(i\) mutants were born up to time \(t\). Moreover, \((Z_i^{(p)} : i \in \mathbb{N})\) is a subsequence of \((Y_i^{(p)} : i \in \mathbb{N}_0)\) which corresponds to the subpopulations with a single mutation. We denote by

\[
N^{(p)}(t) = \left| \left\{ i \in \mathbb{N} : Y_i^{(p)}(t) > 0 \right\} \right| = \left| \left\{ u \in \mathcal{U} : b_u^{(p)} \leq t \right\} \right|
\]

the number of subpopulations born up to time \(t\), discounting the ancestral population of type \(\emptyset\). Our next statement resembles [8, Lemma 7]. However, in our setting we have to be more careful with the estimates.

**Lemma 5.** Let \(\varepsilon > 0\). Then

\[
\lim_{r \to \infty} \lim_{n \to \infty} \mathbb{P} \left( \exists i \in \mathbb{N} : Y_i^{(p)}(-(1/p) \ln(1-p) + r) = 0 \text{ and } Y_i^{(p)}(\rho_n) > \varepsilon(1-p)n^p \right) = 0.
\]

**Proof.** Denote by \((\mathcal{F}_j)_{j \geq 0}\) the natural filtration generated by the system of processes \((Y_j^{(p)} : j \in \mathbb{N}_0)\). The counting process \(N^{(p)}\) is \((\mathcal{F}_j)\)-adapted, and its jump times \(\gamma_k^{(p)} = \inf\{t \geq 0 : N^{(p)}(t) = k\}\) are \((\mathcal{F}_k)\)-stopping times. By the strong Markov property, we see that each of the processes \(Y_k^{(p)}(\gamma_k^{(p)} + \cdot)\) for \(k \in \mathbb{N}\) is a Yule process started from a single particle of size 1, with birth rate \(p\) per unit population size. Moreover, \(Y_k^{(p)}(\gamma_k^{(p)} + \cdot)\) is independent of \(\mathcal{F}_{\gamma_k^{(p)}}\). We let \(r_n = -(1/p) \ln(1-p) + r\) and \(s_n = \ln n + s\), where \(r, s > 0\). The number of processes \(Y_k^{(p)}\) born after time \(r_n\), which have at time \(s_n\) a size greater than \(\varepsilon(1-p)n^p\) is given by

\[
X_n = \sum_{k=1}^{\infty} \mathbb{1}_{r_n < \gamma_k^{(p)} \leq s_n} \mathbb{1}_{Y_k^{(p)}(s_n) > \varepsilon(1-p)n^p} = \int_{r_n}^{s_n} \mathbb{1}_{Y_k^{(p)}(s_n) > \varepsilon(1-p)n^p} \mathrm{d}N^{(p)}(t).
\]

For \(u \geq 0\) fixed, \(Y_k^{(p)}(\gamma_k^{(p)} + u)\) is geometrically distributed with parameter \(\exp(-pu)\), see e.g. Yule [18]. We obtain, using the bound \((1-x)^a \leq \exp(-ax)\) in the second inequality,

\[
\mathbb{E}(X_n) \leq \mathbb{E} \left( \int_{r_n}^{s_n} (1 - \exp(-p(s_n - t)))^{\varepsilon(1-p)n^p} \mathrm{d}N^{(p)}(t) \right).
\]
\[ \leq \mathbb{E} \left( \int_{r_n}^{s_n} \exp \left[ -\left( \frac{\epsilon}{2} \right) (1 - p) n^p \exp(-p(s_n - t)) \right] dN^{(0)}(t) \right). \]

The dynamics of the family \( \{Y_i^{(p)} : i \in \mathbb{N}\} \) and the strong Markov property entail that \( N^{(p)} \) grows at rate \( (1 - p)Z \), where \( Z = \sum_{i \in \mathbb{N}} Z_i^{(p)} = \sum_{i=0}^{\infty} Y_i^{(p)} \) is a standard Yule process. In particular, \( N^{(p)}(t) - (1 - p) \int_0^t Z(s) \, ds \) is a martingale. Since \( \mathbb{E}(Z(t)) = e^\epsilon \), we get with the substitution \( x = e^\epsilon \) in the second line

\[ \mathbb{E}(X_n) \leq (1 - p) \int_{r_n}^{s_n} e^\epsilon \exp \left[ -\left( \frac{\epsilon}{2} \right) (1 - p) n^p \exp(-p(s_n - t)) \right] dt \]

\[ = \frac{1 - p}{p} \int_{e^\epsilon r_n}^{e^\epsilon s_n} x^{(1-p)/p} \exp \left[ -x \left( \frac{\epsilon}{2} \right) (1 - p) n^p \exp(-p s_n) \right] dx. \]

We perform an integration by parts and substitute the values of \( r_n \) and \( s_n \). This gives

\[ \mathbb{E}(X_n) \leq 2 \frac{e^{\epsilon r_n} (1 - p)^{(p-1)/p}}{e^{\epsilon (1-p)r}} \exp \left[ -\left( \frac{\epsilon}{2} \right) e^{\epsilon (r-s)} \right] \]

\[ + 2 \frac{e^{\epsilon s_n} (1 - p)^{(p-1)/p}}{e^{\epsilon (1-p)s}} \int_{e^\epsilon r_n}^{e^\epsilon s_n} x^{1/(1-2p)/p} \exp \left[ -x \left( \frac{\epsilon}{2} \right) (1 - p) n^p \exp(-p s) \right] dx. \]

For large \( n \), we have \( p > 1/2 \) and \( x^{1/(1-2p)/p} \leq 1 \) on the domain of integration. For such \( n \)

\[ \mathbb{E}(X_n) \leq (4/\epsilon)(1-p)^{(p-1)/p} e^{(1-p)r} \exp \left[ -\left( \frac{\epsilon}{2} \right) e^{\epsilon (r-s)} \right] + \frac{16}{e^3 \epsilon^2} e^{2\epsilon} \exp \left[ -\left( \frac{\epsilon}{2} \right) e^{\epsilon (r-s)} \right]. \]

In particular, for fixed \( r, s, \epsilon > 0 \),

\[ \lim_{n \to \infty} \mathbb{E}(X_n) \leq 16(\epsilon^{-1} + \epsilon^{-2}) e^{2\epsilon} \exp \left[ -\left( \frac{\epsilon}{2} \right) e^{\epsilon (r-s)} \right], \]

and the right side converges to zero when \( r \to \infty \) and \( \epsilon, s \) are fixed. We have shown that

\[ \lim_{r \to \infty} \lim_{n \to \infty} \mathbb{P} \left( \exists i \in \mathbb{N} : Y_i^{(p)} (-\left( 1/p \right) \ln(1 - p) + r) = 0 \text{ and } Y_i^{(p)}(s_n) > \epsilon (1 - p) n^p \right) = 0. \]

Since \( \lim_{s \to \infty} \mathbb{P}(\rho_n > \ln n + s) = 0 \) by (3), the lemma is proved. \( \square \)

We are now in position to prove Theorem 1 restricted to generations 0 and 1. We recall that \( 0 < p = p(n) < 1 \) with \( p \to 1 \) and \( (1 - p) n^p \to \infty \) as \( n \to \infty \).

**Proposition 2.**  As \( n \to \infty \), \( C_i^{(n)} \sim n^p \) in probability, and for every fixed \( \ell \in \mathbb{N} \),

\[ \left( \frac{1 - p}{n^p} C_1^{(n)}, \ldots, \frac{1 - p}{n^p} C_\ell^{(n)} \right) \Rightarrow (Z_1, \ldots, Z_\ell). \]

**Proof.**  The convergence of the root cluster was already shown in Lemma 4. Indeed, it follows from our construction that \( Z_i^{(p)}(\rho_n) \) is distributed as the size \( C_i^{(p)}(\rho_n) \) of the root cluster of a Bernoulli bond percolation on \( T_n \) with parameter \( p(n) \). Next, we deduce from Proposition 1 and (1) together with Lemma 5 that if we write \((x_i) \uparrow\) for the decreasing rearrangement of a sequence of positive real numbers \((x_i)\) with either pairwise distinct elements or finitely many non-zero terms, we have

\[ \left( \frac{1 - p}{n^p} Z_i^{(p)}(\rho_n) : i \in \mathbb{N} \right) \uparrow \left( \frac{W_i(\infty)}{S_i} : i \in \mathbb{N} \right) \]

(4)

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in the sense of finite-dimensional distributions as \( n \) tends to infinity. Since

\[
\left( Z_{i}^{(p)}(\rho_n) : i \in \mathbb{N} \right) \overset{d}{\to} \left( C_{i}^{(n)} : i \in \mathbb{N} \right),
\]

it only remains to identify the limit on the right hand side of (4). Recalling that \((S_i : i \in \mathbb{N})\) is independent of \((W_i(\infty) : i \in \mathbb{N}), ((S_i, W_i(\infty)) : i \in \mathbb{N})\) can be viewed as the sequence of atoms of a Poisson point process on \((0, \infty) \times (0, \infty)\) with intensity \( dx \otimes e^{-r}dr. \) Since the image of this intensity measure under the map \((s, w) \mapsto a = w/s\) yields a Poisson point process on \((0, \infty)\) with intensity \( v(da) = a^{-2}da, \) the proof of the proposition is complete.

We now turn to the proof of Corollary 1 stated in Section 2.1. In view of what we have already proved, it will be sufficient to check that for each fixed \( r > 0, \) the subpopulations which were born up to time \(-{(1/p) \ln(1-p) + r} \) carry all a single mutation with high probability when \( n \to \infty. \) Similarly to the definition of \( N^{(p)}(t), \) we let

\[
M^{(p)}(t) = \left| \left\{ i \in \mathbb{N} : b_{i}^{(p)} \leq t \right\} \right|
\]

denote the number of subpopulations with a single mutation at time \( t. \) The following statement is similar to Lemma 6 in [8].

**Lemma 6.** Let \( \Delta^{(p)}(t) = N^{(p)}(t) - M^{(p)}(t) \geq 0 \) denote the number of subpopulations born up to time \( t, \) which bear more than one single mutation. Then for each \( r > 0, \)

\[
\lim_{n \to \infty} \mathbb{E} \left( \Delta^{(p)}(-{(1/p) \ln(1-p) + r}) \right) = 0.
\]

**Proof.** Let \( r_{n} = -{(1/p) \ln(1-p) + r}. \) Since \( N^{(p)}(t) - (1-p) f_{0}^{t} Z(s)ds \) is a martingale,

\[
\mathbb{E} \left( N^{(p)}(r_{n}) \right) = (1-p) \int_{0}^{r_{n}} \mathbb{E}(Z(s))ds.
\]

Similarly, we obtain

\[
\mathbb{E} \left( M^{(p)}(r_{n}) \right) = (1-p) \int_{0}^{r_{n}} \mathbb{E} \left( Y_{0}^{(p)}(s) \right) ds.
\]

Using \( \mathbb{E}(Z(s)) = e^s, \) \( \mathbb{E}(Y_{0}^{(p)}(s)) = e^{ps} \) and \( p = p(n) \to 1, \) a small computation shows \( \mathbb{E} \left( \Delta^{(p)}(r_{n}) \right) = o(1) \) for \( n \to \infty. \)

**Proof of Corollary 1.** From (1), Lemmas 5, 6 and Proposition 1, we see that the sizes of the largest non-ancestral subpopulations at time \( \rho_n \) are attained by the subpopulations with a single mutation only. Recalling the connection between subpopulations at time \( \rho_n \) and percolation clusters, the proof of the corollary is then a consequence of Proposition 2.

### 2.3. Higher Generation Convergence

The recursive structure of \( T_n \) allows us to transfer the arguments of the foregoing section to higher generation clusters. We however need some preparation.

Let \( T_n \) be a RRT on \([0, 1, \ldots, n], \) as usual. Here it will be convenient to label the edges of \( T_n \) by their outer endpoints, i.e. the edge \( e \) joining vertex \( i \) to vertex \( j, \) where \( i < j, \) is
labeled \( j \). We then say that \( e \) is the \( j \)th edge of \( T_n \). We incorporate Bernoulli bond percolation on \( T_n \), but instead of deleting edges, we simply mark them with probability \( 1 - p \) each, independently of each other. After such a marking of edges, we call a subtree of \( T_n \) intact, if it contains only unmarked edges and is maximal in the sense that no further edges without marks can be attached to it. In other words, the intact subtrees of \( T_n \) are precisely the percolation clusters of \( T_n \).

We again view \( T_n \) as the genealogical tree of a standard Yule process stopped at the instant when the \((n + 1)\)th individual is born. Henceforth we will identify vertices with individuals, i.e. we will make no difference between the vertex labeled \( j \) and the \( j \)th individual of the population system. The marked edges indicate a birth event of a mutant. This means that if the \( j \)th edge is a marked edge, then the \( j \)th individual is a mutant, and the vertices of the intact subtree rooted at \( j \) correspond to the individuals bearing the same genetic type as the \( j \)th individual. Moreover, the genetic type \( u \in \mathcal{U} \) of the \( j \)th individual can be derived from the subtree of \( T_n \) spanned by the vertices \( 0, 1, \ldots, j \) and from the marks on its edges.

Our description shows that we may generate the subpopulation sizes \( Z_u^{(\rho)}(\rho_n), u \in \mathcal{U} \), by first picking a RRT \( T_n \), then marking each edge with probability \( 1 - p \), independently of each other, and then defining \( Z_u^{(\rho)}(\rho_n) \) to be the size of the intact subtree of \( T_n \) rooted at the mutant of type \( u \).

Let us write \( \tau_u^{(n)} \) for the full genealogical (sub)tree which stems from the mutant of type \( u \). This means that \( \tau_u^{(n)} \) is the maximal subtree of \( T_n \) rooted at the mutant of type \( u \), including all marked and unmarked edges above its root. Clearly, \( \tau_u^{(n)} \) might contain several intact subtrees of \( T_n \). We let \( \tau_u^{(n)} = \emptyset \) if there is no mutant of type \( u \), and we agree that \( \tau_u^{(n)} \) is given by \( T_n \) itself. For example, the non-empty vertex sets of the genealogical subtrees of the recursive tree on the left side of Fig. 1 (dashed lines represent the marked edges) are given by \( \tau_0 = \{0, 1, \ldots, 10\}, \tau_1 = \{2\}, \tau_2 = \{3, 5, 7, 8, 9, 10\}, \tau_{21} = \{5, 9\}, \tau_{22} = \{10\} \).

Let us introduce the following terminology. For an arbitrary subset \( A \subseteq \{0, 1, \ldots, n\} \) of size \( k \), we call the bijective map from \( A \) to \( \{0, 1, \ldots, k - 1\} \), which preserves the order, the \textit{canonical relabeling} of vertices. Clearly, the canonical relabeling transforms a recursive tree on \( A \) into a recursive tree on \( \{0, 1, \ldots, k - 1\} \).

We next observe that conditionally on its size \( |\tau_u^{(n)}| = k \) and upon the canonical relabeling of its vertices, \( \tau_u^{(n)} \) is itself distributed as a RRT on \( \{0, 1, \ldots, k - 1\} \). Indeed, as we pointed out above, in order to decide whether a given vertex \( j \) of \( T_n \) is the root of the subtree encoded by \( \tau_u^{(n)} \), we have to look only at the subtree (with its marks) spanned by the vertices \( \{0, 1, \ldots, j\} \). In particular, the structure of the subtree stemming from \( j \) is irrelevant. Next, if we condition on \( |\tau_u^{(n)}| = k \) and perform the canonical relabeling of vertices, the recursive construction of \( T_n \) then implies that each increasing arrangement of the vertices \( \{0, 1, \ldots, k - 1\} \) is equally likely, that is to say \( \tau_u^{(n)} \) is a random recursive tree. Moreover, if \( u, v \in \mathcal{U} \) do not lie on the same infinite branch of \( \mathcal{U} \) emerging from the root \( 0 \), then \( \tau_u^{(n)} \) and \( \tau_v^{(n)} \) are conditionally on their sizes independent RRT’s, since their vertex sets are disjoint.

We henceforth call a subtree \( \tau_u^{(n)} \) with \( |u| = k \) a subtree of generation \( k \). Our final main step for proving Theorem 1 is a convergence result for the “tree of subtree sizes” \( \{\tau_u^{(n)} : u \in \mathcal{U}\} \). For that purpose, we decreasingly order the children of each element \( |\tau_u^{(n)}| \), but keep the parent-child relation. More precisely, each element \( |\tau_u^{(n)}| \) has finitely many non-zero children, say \( |\tau_{a_1}^{(n)}|, \ldots, |\tau_{a_\ell}^{(n)}| \), and we let \( \sigma_u : \mathbb{N} \to \mathbb{N} \) be the random bijection which sorts this sequence in the decreasing order, i.e.

\[
|\tau_{\sigma_u(a_1)}^{(n)}| \geq |\tau_{\sigma_u(a_2)}^{(n)}| \geq \cdots \geq |\tau_{\sigma_u(\ell)}^{(n)}|,
\]

with \( \sigma_u(i) = i \) for \( i > \ell \).

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Out of these maps we define the global random bijection \( \sigma = \sigma^{(n)} : U \rightarrow U \) recursively by setting \( \sigma(\emptyset) = \emptyset, \sigma(j) = \sigma_0(j), \) and then, given \( \sigma(u), \sigma(uj) = \sigma(u)\sigma_{\sigma(u)}(j), u \in U, j \in \mathbb{N}. \) Note that \( \sigma \) indeed preserves the parent-child relation, i.e. children of \( u \) are mapped into children of \( \sigma(u). \)

We recall that \( p = p(n) \rightarrow 1, \) and \( (1 - p(n))^{k^2 n^{(n)}} \rightarrow \infty \) for each \( k \in \mathbb{N}. \)

**Proposition 3.** As \( n \rightarrow \infty, \) in the sense of finite-dimensional distributions,

\[
\left( \frac{(1 - p)^{-|u|}}{n} |\tau_{\sigma(u)}^{(n)}| : u \in U \right) \Longrightarrow (Z_u : u \in U).
\]

**Proof.** The convergence of \( |\tau_{\sigma(\emptyset)}^{(n)}|/n \) is trivial. Let us first show that in the sense of finite-dimensional distributions, as \( n \rightarrow \infty, \)

\[
\left( \frac{(1 - p)^{-1}}{n} |\tau_{\sigma(i)}^{(n)}| : i \in \mathbb{N} \right) \Longrightarrow (Z_i : i \in \mathbb{N}). \tag{5}
\]

Fix \( \ell \in \mathbb{N} \) and denote by \( \tilde{\tau}_{i}^{(n)} \) the size of the root percolation cluster inside \( \tau_{i}^{(n)}, \) i.e. the size of the intact subtree with the same root node as \( \tau_{i}^{(n)}. \) Since conditionally on its size (and upon the canonical relabeling), \( \tau_{i}^{(n)} \) is a random recursive tree, Lemma 4 shows that for each \( i = 1, \ldots, \ell, \)

\[
|\tau_{i}^{(n)}| \sim \left( \tilde{\tau}_{i}^{(n)} \right)^{1/p} \text{ in probability.}
\]

Furthermore, in the notation from Section 2.2 we have the equality in distribution

\[
\left( \tilde{\tau}_{1}^{(n)}, \ldots, \tilde{\tau}_{\ell}^{(n)} \right) \overset{d}{=} \left( Z_{1}^{(p)}(\rho_{n}), \ldots, Z_{\ell}^{(p)}(\rho_{n}) \right).
\]

Proposition 1 (with \( W_{i}(\infty), S_{i} \) defined there), the last two displays and the fact that \( p \rightarrow 1 \) imply the convergence in distribution

\[
\left( \frac{(1 - p)^{-1}}{n} |\tau_{1}^{(n)}|, \ldots, \frac{(1 - p)^{-1}}{n} |\tau_{\ell}^{(n)}| \right) \Longrightarrow \left( \frac{W_{1}(\infty)}{S_{1}}, \ldots, \frac{W_{\ell}(\infty)}{S_{\ell}} \right).
\]

From Lemma 4 and (1) together with Lemma 5, we know that the \( \ell \) largest subtrees amongst \( \tau_{i}^{(n)}, i \in \mathbb{N}, \) are with high probability to be found under the first \( k, \) provided \( k \) and \( n \) are large. With our identification of the ranked sequence \( (W_{i}(\infty)/S_{i} : i \in \mathbb{N}) \) from the proof of Proposition 1, the last display therefore implies (5).

We next show that in the sense of finite-dimensional distributions,

\[
\left( \frac{(1 - p)^{-|u|}}{n} |\tau_{\sigma(u)}^{(n)}| : u \in U, |u| \leq 2 \right) \Longrightarrow (Z_u : u \in U, |u| \leq 2). \tag{6}
\]

As we already remarked, for disjoint integers \( j, k, \) the RRT’s \( \tau_{j}^{(n)} \) and \( \tau_{k}^{(n)} \) are conditionally on their sizes independent RRT’s. Since we have just proved finite-dimensional convergence of \( (|\tau_{\sigma(u)}^{(n)}| : j \in \mathbb{N}) \), it will therefore be enough to show that for \( g,j^{(n)} : [0, \infty) \rightarrow [0, 1] \)}
bounded and uniformly continuous, and \( j, \ell \in \mathbb{N} \),
\[
\mathbb{E} \left[ g \left( \frac{(1 - p)^{-1}}{n} |_{\tau_{(n)}^{(j)}} \right) f^{(1)} \left( \frac{(1 - p)^{-2}}{n} |_{\tau_{(j)}^{(1)}} \right) \ldots f^{(\ell)} \left( \frac{(1 - p)^{-2}}{n} |_{\tau_{(\ell)}^{(n)}} \right) \right] 
\rightarrow \mathbb{E} \left[ g(Z_j) f^{(1)}(Z_{\alpha_1}) \ldots f^{(\ell)}(Z_{\alpha_1}) \right],
\]
where for \( i = 1, \ldots, \ell, a_i \) is the \( i \)th largest atom of a Poisson random measure on \((0, \infty)\) with intensity \( \nu(da) = a^{-2}da \). For ease of readability, we restrict ourselves to the case \( \ell = 1 \), the cases \( \ell \geq 2 \) being similar. By the properties of \( \tau_{(n)}^{(n)} \) discussed above, we have for each \( m = 0, \ldots, n - j \),
\[
\mathbb{E} \left[ f^{(1)} \left( \frac{(1 - p)^{-2}}{n} |_{\tau_{(n)}^{(j)}} \right) \right] |_{\tau_{(j)}^{(n)}} = m + 1 = \mathbb{E} \left[ f^{(1)} \left( \frac{(1 - p)^{-2}}{n} |_{\tau_{(n)}^{(m)}} \right) \right],
\]
where \( \mathbb{E}_m \) is the mathematical expectation starting from a random recursive tree \( T_m \) with \( m + 1 \) vertices, and under \( \mathbb{E}_m \), \( \tau_{(n)}^{(m)} \) is the largest amongst all (full) genealogical subtrees of \( T_m \) stemming from a mutant with one single mutation. Note that the mutation probability is still given by \( 1 - p = 1 - p(n) \) (and not \( 1 - p(m) \)).

Now if \( m \sim (1 - p)na \) for some fixed \( a > 0 \), \( m = m(n) \) integer-valued, we obtain from the convergence of generation 1, i.e. (5), that
\[
\mathbb{E}_m \left[ f^{(1)} \left( \frac{(1 - p)^{-2}}{n} |_{\tau_{(n)}^{(m)}} \right) \right] \sim \mathbb{E} \left[ f^{(1)}(aa_1) \right],
\]
with \( a_1 \) the largest atom of a Poisson random measure with intensity \( \nu \). Since we have already proved that \( (1 - p)^{-1}n^{-1}|_{\tau_{(n)}^{(j)}} \) converges in distribution to \( Z_j \), and since the map \( (a, a_1) \mapsto g(a)f^{(1)}(aa_1) \) is uniformly continuous on bounded sets, this establishes (6). With the same arguments, we obtain finite-dimensional convergence up to generation 3, then up to 4, and so on, so that the proposition is proved.

We finish now the proof of Theorem 1.

**Proof of Theorem 1.** Write \( \tilde{C}_{u}^{(n)} \) for the size of the root percolation cluster inside \( \tau_{u}^{(n)} \). From Lemma 4 we know that as \( n \to \infty \), \( \tilde{C}_{u}^{(n)} \sim |\tau_{u}^{(n)}|^{p} \) in probability. Since \( (1 - p)^{-kp} \sim (1 - p)^{-k} \) as \( n \to \infty \) for each \( k \in \mathbb{N} \), we obtain from Proposition 3
\[
\left( \frac{(1 - p)^{-|u|}}{n^{p}} \tilde{C}_{\sigma(u)}^{(n)} : u \in \mathcal{U} \right) \implies (\mathcal{Z}_{u} : u \in \mathcal{U}) \quad \text{as} \quad n \to \infty
\]
in the sense of finite-dimensional distributions. Now observe that the process \( (\tilde{C}_{\sigma(u)}^{(n)} : u \in \mathcal{U}) \) does already encode all cluster sizes and the genealogical structure of the corresponding clusters. It is however possible that \( \tilde{C}_{\sigma(u)}^{(n)} < \tilde{C}_{\sigma(u)}^{(n)} \) for \( i < j \), since the map \( \sigma \) provides an ordering according to the sizes of the surrounding subtrees \( \tau_{u}^{(n)} \), not according to the cluster sizes.

Therefore, in order to finish the proof, we need to argue that the convergence remains true if the family \( (\tilde{C}_{\sigma(u)}^{(n)} : u \in \mathcal{U}) \) is ranked in the decreasing order, that is if the children \( (\tilde{C}_{\sigma(i)}^{(n)} : i \in \mathbb{N}) \) of each element \( \tilde{C}_{\sigma(u)}^{(n)} \) are decreasingly sorted according to their sizes, under preservation of the parent-child relation. However, Proposition 3 and the fact that \( \tilde{C}_{u}^{(n)} \sim |\tau_{u}^{(n)}|^{p} \) in probability entail that we find the \( \ell \) largest elements of \( (\tilde{C}_{\sigma(i)}^{(n)} : i \in \mathbb{N}) \)
amongst the first $k$ with probability as close to 1 as we wish, provided we choose $k$ and $n$ large enough. This completes the proof of the theorem.

The tree $C^{(n)}$ provides arguably the most natural encoding of the cluster sizes. From the point of view of a dynamical version of a Bernoulli bond percolation, where the edges are removed one after the other in a random uniform order, another possibility might however come to ones mind, which takes into account the order in which the edges are removed. We will discuss this in Section 3.4 for the supercritical regime. Our discussion is based on a result for the so-called tree of components, which we present next.

3. THE TREE OF COMPONENTS

3.1. Our Main Result on the Destruction of a RRT

We consider on $T_n$ a continuous-time destruction process with parameter $1/\ln n$. This means that we attach to each edge $e$ of $T_n$ an independent exponential clock $\tau(e)$ of parameter $1/\ln n$, and we delete edge $e$ at time $\tau(e)$. After the $n$th edge has been deleted, the tree has been completely destructed, and the process terminates.

We encode the sizes and birth times of the tree components stemming from the destruction of $T_n$ by a tree-indexed process $(B^{(n)}, b^{(n)}) = ((B_u^{(n)}, b_u^{(n)}): u \in \mathcal{U})$, the tree of components. Here, $\mathcal{U}$ denotes again the universal tree.

As it is already apparent from [5], choosing the parameter in the destruction process equals $1/\ln n$ is the most natural choice, since it leads without normalization to a simple description of the birth times in the limit $n \to \infty$.

Following the steps of the destruction process, we build the tree of components dynamically starting from the singleton $(B_0^{(n)}, b_0^{(n)}) = (n + 1, 0)$ and ending after the $n$th edge removal with the full process $(B^{(n)}, b^{(n)})$. For the ease of readability, we omit the superscript $(n)$ in the following construction.

Let $e_1, \ldots, e_n$ denote the edges of $T_n$ listed in the increasing order of their exponential clocks, i.e. such that $\tau(e_1) < \tau(e_2) < \cdots < \tau(e_n)$. Then at time $\tau(e_1)$, $e_1$ is the first edge to be removed from $T_n$, and $T_n$ splits into two subtrees, say $T_n^0$ and $T_n^+$, where $T_n^0$ contains the root 0. The size $|T_n^0|$ is viewed as the first child of $B_0$ and denoted by $B_1$, and $b_1$ is set to $\tau(e_1)$. Now first suppose that $e_2$ connects two vertices in $T_n^0$. Then, at time $\tau(e_2)$, $T_n^0$ splits into two tree components. The size of the component not containing the root of $T_n^0$ is viewed as the first child of $B_1$ and denoted by $B_2$, and $b_2$ is set to $\tau(e_2)$. On the contrary, if $e_2$ connects two vertices in $T_n^+$, then the size of the component not containing 0 is viewed as the second child of $B_0$ and denoted by $B_2$, while $b_2$ is set to $\tau(e_2)$.

It should be plain how to iterate this construction. After the $n$th edge removal, we have in this way defined $n + 1$ pairs of variables $(B_u, b_u)$ with $|u| \leq n$. We extend the definition to the full universal tree by letting $(B_u, b_u) = (0, \infty)$ for all the remaining $u \in \mathcal{U}$. Note that for a non-zero element $B_u$, we have $B_u < B_0$ and $b_u < b_0$ for $i \in \mathbb{N}$ (children are strictly smaller than their parent, and they cannot be born before their parent), and $b_u < b_j$ if $i < j$ and $b_u \neq \infty$.

We point out that $(B, b)$ represents a final state of the destruction when all edges have been deleted. In particular, as for the tree of cluster sizes, the tree of components is a process indexed by $\mathcal{U}$, not by the time. We call the first-coordinate process $B = (B_u: u \in \mathcal{U})$ simply the tree of component sizes. An example is shown in Fig. 2. Note that unlike our convention from Section 2.3 of labeling the edges by their outer endpoints, the edge labels are here...
given by the order in which the edges were removed. Similar to above, we say that a tree component is a component of generation \( k \) if its size is encoded by an element \( B_u \) with \( |u| = k \).

For our limit result, we will rank the children of each element \( (B_u^{(n)}, b_k^{(n)}) \) in the decreasing order of their first coordinate, in the same way as we ranked the subtree sizes in the foregoing section. Say \( B_u^{(n)}, \ldots, B_u^{(n)} \) are the non-zero children of \( B_u^{(n)} \). We choose a random bijection \( \sigma_u : \mathbb{N} \to \mathbb{N} \) with \( \sigma_u(i) = i \) for \( i > \ell \) such that

\[
B_{\sigma_u(1)}^{(n)} \geq B_{\sigma_u(2)}^{(n)} \geq \cdots \geq B_{\sigma_u(t)}^{(n)}.
\]

As before, \( \sigma = (\sigma^{(n)} : U \to U \) is defined recursively by setting \( \sigma(\emptyset) = \emptyset \), \( \sigma(j) = \sigma_0(j) \), and given \( \sigma(u), \sigma(uj) = \sigma(u)\sigma_{\sigma_u}(j) \), \( u \in U \), \( j \in \mathbb{N} \).

The limit object of the tree of component sizes is again given by the tree-indexed process \( (Z_u : u \in U) \) from Section 2. The birth times of the corresponding tree components are in the limit described by a sequence \( (e_u : u \in \mathcal{U}(\emptyset)) \) of i.i.d. standard exponential random variables, which are independent of \( Z \). We let \( z_\emptyset = e_\emptyset = 0 \), and, writing \( u = (u_1 \ldots u_k) \) for \( u \) of length \( k \geq 1 \),

\[
z_u = e_{u_1} + e_{u_1u_2} + \cdots + e_{u_1 \ldots u_k}.
\]

In words, \( z_u \) is the sum of all the \( e \)-values along the path in \( \mathcal{U} \) from the root \( \emptyset \) to \( u \).

We shall prove the following finite-dimensional convergence.

**Theorem 2.** As \( n \to \infty \), there is the convergence in the sense of finite-dimensional distributions,

\[
\left( \frac{\ln n)^{\lfloor a \rfloor}}{n} B_{\sigma^{(n)}(u)}, b_{\sigma^{(n)}(u)} \right) : u \in U \Rightarrow (Z_u, z_u) : u \in U.
\]

For our application to (supercritical) Bernoulli bond percolation on \( T_n \), it will be useful to consider only those tree components which are born before a certain finite time \( t(n) \to t > 0 \). In this case, the limit object is obtained from “squeezing-out” the elements \( (Z_u, z_u) \) with \( z_u \geq t \). The corresponding limit statement is Proposition 5, which is deferred to Section 3.4.

### 3.2. Some Features of RRT’s and of the Tree of Components

#### 3.2.1. The Splitting Property

As for the higher generation convergence of cluster sizes in Section 2.3, we use the fractal structure of random recursive trees to study the destruction process. Here we shall employ the fundamental splitting property. Informally, it states that if an edge is removed uniformly at random from a RRT \( T_n \), then the two subtrees which were connected by this edge are, conditionally on their sizes and upon a relabeling of vertices, independent RRT’s. Moreover, our analysis relies on the fact that the law of the sizes of these two subtrees is known explicitly.

Let us now give a precise statement. Select an edge of \( T_n \) uniformly at random and remove it. Then \( T_n \) splits into two subtrees, say \( T_n^0 \) and \( T_n^* \), where \( T_n^0 \) contains the root. Let \( \xi \) be the integer-valued variable with distribution

\[
\mathbb{P}(\xi = j) = \frac{1}{j(j + 1)}, \quad j = 1, 2, \ldots.
\]
Remember that we call the canonical relabeling of a vertex set \( A \subseteq \{0, 1, \ldots, n\} \) the relabeling of its vertices by the labels 0, 1, \ldots, |A| − 1, according to the increasing order of the original labels.

**Lemma 7.** (Meir and Moon [14]) Conditionally on the size |\( \tau_0^0 \)| = k, the subtrees \( \tau_n^0 \) and \( \tau_n^* \) are upon the canonical relabeling of their vertices independent random recursive trees on \( \{0, 1, \ldots, k-1\} \) and \( \{0, 1, \ldots, n-k\} \), respectively. Moreover, in the notation from above, |\( \tau_n^* \)| has the same law as \( \xi \) conditioned on \( \xi \leq n \), that is

\[
P(|\tau_n^*| = j) = \frac{n+1}{nj(j+1)}, \quad j = 1, \ldots, n.
\]

### 3.2.2. A Coupling of Iksanov and Möhle

Meir and Moon [14] proved Equation (8) in their study of the number \( X_n \) of random cuts that are needed to isolate the root 0 in \( T_n \). They considered the following algorithm for isolating vertex 0. Start from \( T_n \) and remove an edge chosen uniformly at random. Then iterate the procedure with the subtree which contains 0, and so on, until after \( X_n \leq n \) steps, the root is finally isolated.

In [14] Meir and Moon obtained first and second moment estimates for \( X_n \) and showed that \( \lim_{n \to \infty} \ln(n/n)X_n = 1 \) in probability. Later, Drmota, Iksanov, Möhle, and Rösler [10] proved a weak limit law, showing that \( n^{-1} \ln(n)^2X_n - \ln n - \ln \ln n \) converges in distribution to a completely asymmetric Cauchy variable. A short probabilistic proof of this result was found by Iksanov and Möhle [12], which turns out to be particularly useful for our purpose. It is based on a coupling of the algorithm for isolating the root with a random walk with step size \( \xi \). More precisely, let \( \xi_1, \xi_2, \ldots \) be a sequence of i.i.d. copies of \( \xi \), see (7), and set

\[
S_0 = 0, \quad S_n = \xi_1 + \cdots + \xi_n.
\]

Denote the last time the random walk \( S = (S_n : n \in \mathbb{N}_0) \) remains below level \( n \) by

\[
L(n) = \max\{k \geq 0 : S_k \leq n\}.
\]

**Lemma 8.** (Iksanov and Möhle [12]) One can construct on the same probability space a random recursive tree \( T_n \) together with the random algorithm for isolating the root, and a version of the random walk \( S \), such that if \( \mathcal{B}_1^{(n)}, \mathcal{B}_2^{(n)}, \ldots, \mathcal{B}_{X_n}^{(n)} \) denotes the sequence of the sizes of the subtrees which are cut off from the root component one after the other by the algorithm, then \( X_n \geq L(n) \) and

\[
\left( \mathcal{B}_1^{(n)}, \ldots, \mathcal{B}_{L(n)}^{(n)} \right) = \left( \xi_1, \ldots, \xi_{L(n)} \right).
\]

Besides the coupling, we use the following two facts about the random walk \( S \) and its last passage time \( L(n) \), which can be found in a stronger form in [12].

\[
\lim_{n \to \infty} \frac{\ln n}{n} L(n) = 1 \quad \text{and} \quad \lim_{n \to \infty} \frac{\ln n}{n} (n - S_{L(n)}) = 0 \quad \text{in probability.}
\]

Combined with extreme value theory, we will use the coupling to determine the asymptotic sizes and birth times of the tree components.

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3.2.3. Branching Property of the Tree of Components  The tree-indexed process $\mathcal{B}^{(n)}$ can be interpreted as the genealogical tree of a multi-type population model, where the type reflects the size of the tree component. In particular, the ancestor $\emptyset$ has type $n+1$. We stress that the characteristic “type” is used here in a different way than in Section 2.2. A node $u$ with $\mathcal{B}_u^{(n)} = 0$ corresponds to an empty component and is therefore absent in the population model. The splitting property leads to the following description.

Lemma 9. The population model induced by the tree of component sizes $\mathcal{B}^{(n)}$ is a multi-type Galton-Watson process starting from one particle of type $n+1$. The reproduction distribution $\lambda_i$ of an individual of type $i \geq 1$ is given by the law of the sequence of the sizes of the non-root subtrees which are produced in the algorithm for isolating the root of a RRT of size $i$.

We remark that the type of an individual is simply given by the total size of the subtree of the genealogical tree stemming from that individual. Therefore, types can be recovered from the sole structure of the genealogical tree.

When we incorporate the birth times of the tree components, Lemma 9 and basic properties of exponential variables immediately yield the following branching property.

Lemma 10. For every integer $k \geq 0$, conditionally on $(\mathcal{B}_u^{(n)}, b_u^{(n)} : |u| \leq k)$, the families of variables 

$$
\left( \left( \mathcal{B}_{u_j}^{(n)}, b_{u_j}^{(n)} \right) : j \in \mathbb{N} \right), \quad u \in \mathcal{U} \text{ of length } |u| = k,
$$

are independent, and the conditional law of each family $\left( \left( \mathcal{B}_{u_j}^{(n)}, b_{u_j}^{(n)} \right) : j \in \mathbb{N} \right)$ only depends on $(\mathcal{B}_u^{(n)}, b_u^{(n)})$. More precisely, given $(\mathcal{B}_u^{(n)}, b_u^{(n)})$ with $\mathcal{B}_u^{(n)} - 1 = m \geq 2$, there is the equality in distribution

$$
\left( \left( \mathcal{B}_{u_j}^{(n)}, b_{u_j}^{(n)} \right) : j \in \mathbb{N} \right) \overset{d}{=} \left( \left( \mathcal{B}_{u_j}^{(m)}, b_{u_j}^{(m)} + \frac{\ln n}{\ln m} B_j^{(m)} \right) : j \in \mathbb{N} \right),
$$

where $\mathcal{B}_j^{(m)}$ and $b_j^{(m)}$ stem from a destruction process on $T_m$ with parameter $1/\ln m$.

3.3. Proof of Theorem 2

Lemma 10 suggests that one first proves finite-dimensional convergence for the components of generation 1 and then uses the branching property to transfer the convergence to higher generations. For the sake of clarity, we restate the result for the first generation.

Proposition 4. For every $\ell \in \mathbb{N}$, there is the convergence in distribution as $n \to \infty$,

$$
\left( \left( \frac{\ln n}{n} \mathcal{B}_{\sigma(1)}^{(n)}, b_{\sigma(1)}^{(n)} \right), \ldots, \left( \frac{\ln n}{n} \mathcal{B}_{\sigma(\ell)}^{(n)}, b_{\sigma(\ell)}^{(n)} \right) \right) \Rightarrow ((Z_1, z_1), \ldots, (Z_{\ell}, z_{\ell})).
$$

We recall that the sequence $\mathcal{B}_i^{(n)}$ can be identified with the sizes of the tree components which are cut from the component containing the root 0 one after the other in the algorithm for isolating the root. The coupling of Iksanov and Möhle provides information on the component sizes, but it is no longer valid beyond the last passage time $L(n)$ of the random walk. Our way out is to show that for fixed $\ell \in \mathbb{N}$, the probability that only those
tree components which are born before time \( t \) do contribute to the \( \ell \) largest is as close to 1 as we wish for \( t \) and \( n \) sufficiently large. For fixed \( t > 0 \), Lemma 4 of Bertoin [5] shows that in the destruction process up to time \( t \), about \((1 - e^{-t})n/\ln n \) edges have been removed from the root component. The first statement of (10) then implies that we are in a regime where the coupling applies.

Corollary 2 of [5] already provides us with a limit result for the tree components that are cut off from the root component before time \( t(n) > 0 \). Let

\[
(B_{i,t(n)}, b_{i,t(n)}) = \begin{cases} 
(B_i^{(n)}, b_i^{(n)}) & \text{for } b_{i}^{(n)} < t(n), \\
(0, \infty) & \text{for } b_{i}^{(n)} \geq t(n)
\end{cases}
\]

and write

\[
\mathcal{C}_{\ell,t(n)} = n + 1 - \sum_{j=1}^{\infty} B_{\mu(j,t(n)}
\]

for the size of the root component of \( T_n \) at time \( t(n) \). The parameter \( n \) is dropped here as a superscript, since it already appears in \( t(n) \). Furthermore, denote by \( \mu = \mu(n, t(n)) \) a random permutation that sort the elements \((B_{i,t(n)}, b_{i,t(n)})\) in the decreasing order of their first coordinate, i.e. such that

\[
B_{\mu(1),t(n)} \geq B_{\mu(2),t(n)} \geq \ldots.
\]

**Lemma 11.** (Bertoin [5]) Let \( t(n) : n \in \mathbb{N} \) be a sequence of times converging to some \( t > 0 \). Then, for each \( \ell \in \mathbb{N} \), there is the convergence in distribution as \( n \to \infty \),

\[
\left( \left( \frac{\ln n}{n} B_{\mu(1),t(n)}, b_{\mu(1),t(n)} \right), \ldots, \left( \frac{\ln n}{n} B_{\mu(\ell),t(n)}, b_{\mu(\ell),t(n)} \right) \right) \Rightarrow \left( (Z_{1,t_1}, z_{1,t_1}), \ldots, (Z_{\ell,t_\ell}, z_{\ell,t_\ell}) \right),
\]

where \((Z_{1,t_1}, z_{1,t_1}), (Z_{2,t_2}, z_{2,t_2}), \ldots\) are the atoms of a Poisson random measure on \((0, \infty) \times (0, t)\) with intensity \( a^2 \, da \otimes e^{-s} \, ds \), ranked in the decreasing order of their first coordinate. Moreover, \( \mathcal{C}_{\ell,t(n)} \sim e^{-t} n \) in probability as \( n \to \infty \).

**Remark.** Basic properties of Poisson random measures show that the sequence of atoms \((Z_{i,t}, z_{i,t}) : i \in \mathbb{N}\) can be obtained from \((Z_{i,t}, z_{i,t}) : i \in \mathbb{N}\) by “squeezing-out” the elements \((Z_i, z_i)\) with \( z_i \geq t \). Formally, conditionally on \((z_i : i \in \mathbb{N})\), define a map \( \gamma : \mathbb{N}_0 \to \mathbb{N}_0 \) by setting \( \gamma(0) = 0 \), and then for \( i = 1, 2, \ldots \), \( \gamma(i) = \inf \{ j > \gamma(i - 1) : z_j < t \} \). Then the sequence \((Z_{\gamma(i), z_{\gamma(i)}} : i \in \mathbb{N})\) has the same distribution as \((Z_{i,t}, z_{i,t}) : i \in \mathbb{N}\). This point of view is useful for the proof of Proposition 4, which we give now.

**Proof of Proposition 4.** We will reduce the statement to Lemma 11 by showing that the \( \ell \) largest tree components of generation 1 are with high probability produced before time \( t \), provided \( t \) and \( n \) are sufficiently large. We fix \( \ell \in \mathbb{N} \), \( \varepsilon > 0 \) and let \( f : ([0, \infty) \times [0, 1])^\ell \to [0, 1] \) be a continuous function. Recall that \((z_i)_{i \in \mathbb{N}}\) is a family of i.i.d. standard exponentials, which is independent of the family \((Z_i)_{i \in \mathbb{N}}\). Choosing \( t \) so large such that \( \mathbb{P}(\max \{ z_1, \ldots, z_\ell \} > t) \leq \varepsilon \), we obtain by the remark above

\[
|\mathbb{E}[f((Z_1, z_1), \ldots, (Z_\ell, z_\ell))] - \mathbb{E}[f((Z_1, z_{1,t}), \ldots, (Z_\ell, z_{\ell,t}))]| \leq \varepsilon.
\]

We will now prove that if \( t \) is large, then for all \( n \) large enough also

\[
|\mathbb{E}\left[f\left( \frac{\ln n}{n} B_{\sigma(1)}, b_{\sigma(1)}^{(n)} \right), \ldots, \frac{\ln n}{n} B_{\sigma(\ell)}, b_{\sigma(\ell)}^{(n)} \right)] \right| \leq \varepsilon.
\]
Here, since $t$ is fixed, we write $\mathcal{B}_{\mu(t),t}^{(n)}$ instead of $\mathcal{B}_{\mu(t),t(n)}^{(n)}$ and similarly for the birth times. First, it follows from Lemma 11 that for $t_0 > 0$, there exists $\delta > 0$ such that for each $t > t_0$ and for all $n$ sufficiently large,

$$\mathbb{P}\left(\mathcal{B}_{\mu(t),t}^{(n)} \geq \delta n/\ln n \right) \geq 1 - \varepsilon/2.$$  

Next, if $\mathcal{B}_{\ast,z,t}^{(n)}$ is the size of the largest tree component amongst those which were cut off from the root component in the destruction process on $T_n$ at a time $t$, then on the event $\{\mathcal{B}_{\mu(t),t}^{(n)} \geq \delta n/\ln n\} \cap \{\mathcal{B}_{\ast,z,t}^{(n)} < \delta n/\ln n\}$, there is the equality of random vectors

$$\left(\left(\mathcal{B}_{\mu(1),t}^{(n)}, b_{\mu(1),t}^{(n)}\right), \ldots, \left(\mathcal{B}_{\mu(T_n),t}^{(n)}, b_{\mu(T_n),t}^{(n)}\right)\right) = \left(\left(\mathcal{B}_{\sigma(1)}^{(n)}, b_{\sigma(1)}^{(n)}\right), \ldots, \left(\mathcal{B}_{\sigma(T_n)}^{(n)}, b_{\sigma(T_n)}^{(n)}\right)\right).$$

Therefore, (11) follows if we show that for large $t$ and all large $n$,

$$\mathbb{P}\left(\mathcal{B}_{\ast,z,t}^{(n)} < \delta n/\ln n \right) \geq 1 - \varepsilon/2.$$  

Write $m = m(t, n)$ for the number of edges of the root component in the destruction process at time $t$. By the splitting property, conditionally on $m$, the variable $\mathcal{B}_{\ast,z,t}^{(n)}$ is distributed as the size of the largest tree component which was produced by the algorithm for isolating the root of a RRT of size $m + 1$. We now claim that $(\ln m/m)\mathcal{B}_{\ast,z,t}^{(n)}$ converges in distribution as $m \to \infty$ to the largest atom of a Poisson random measure on $(0, \infty)$ with intensity $a^{-2}da$.

Indeed, if $\xi_1, \xi_2, \ldots$ is a sequence of iid. copies of $\xi$, see (7), then for $a > 0$, the number of indices $j \leq k$ such that $\xi_j > am/\ln m$ is binomially distributed with parameters $k$ and $[am/\ln m]^{-1}$. Combining the first part of (10) with Theorem 16.16 of Kallenberg [13], we deduce that the largest variable among $\xi_1, \ldots, \xi_{L(m)}$, normalized by a factor $\ln m/m$, converges in distribution to largest atom of a Poisson random measure on $(0, \infty)$ with intensity $\nu(\cdot) = a^{-2}da$. Clearly, under the coupling of Iksanov and Möhle, $m + 1 - S_{L(m)}$ is the size of the remaining root component after $L(m)$ edge removals in the algorithm for isolating the root. Since $m + 1 - S_{L(m)} = o(m/\ln m)$ in probability by (10), an appeal to the coupling proves our claim about $\mathcal{B}_{\ast,z,t}^{(n)}$.

We finally notice that by the second part of Lemma 11, $\lim_{n \to \infty} (m/n)\mathcal{B}_{\ast,z,t}^{(n)}$ converges in distribution to the largest atom of a Poisson random measure on $(0, \infty)$ with intensity $e^{-2a}da$. Choosing $t = t(\delta)$ large enough, (12) follows. Since $\varepsilon > 0$ can be chosen arbitrarily small, an application of the triangle inequality together with Lemma 11 finishes the proof of Proposition 4.

Now we are in position to prove Theorem 2. The line of argumentation is similar to that in the proof of Proposition 3.

**Proof of Theorem 2.** The convergence of $((1/n)\mathcal{B}_{\ast}^{(n)}, b_{\ast}^{(n)})$ is trivial, and Proposition 4 shows the convergence of generation 1. Let us now show that also

$$\left(\frac{(\ln n)|w|}{n}\mathcal{B}_{\sigma(w)}^{(n)}, b_{\sigma(w)}^{(n)}: u \in \mathcal{U}, |u| \leq 2\right) \Rightarrow \left((Z_u, z_u): u \in \mathcal{U}, |u| \leq 2\right)$$

(13)
as \( n \to \infty \) in the sense of finite-dimensional laws. Let \( \ell \in \mathbb{N} \). Employing Lemma 10 and Proposition 4, it suffices to show that for \( g, f^{(i)} : [0, \infty) \times [0, \infty) \to [0, 1] \) bounded and uniformly continuous, and for \( j, \ell \in \mathbb{N} \),

\[
\mathbb{E} \left[ g \left( \frac{\ln n}{n} B^{(n)}_{\sigma(j)}, B^{(n)}_{\sigma(j)} \right) f^{(1)} \left( \frac{\ln^2 n}{n} B^{(n)}_{\sigma(j)}, B^{(n)}_{\sigma(j)} \right) \cdots f^{(\ell)} \left( \frac{\ln^2 n}{n} B^{(n)}_{\sigma(j)}, B^{(n)}_{\sigma(j)} \right) \right] \\
\to \mathbb{E} \left[ g(\mathcal{Z}_j, z_j) f^{(1)}(\mathcal{Z}_{a_1}, z_j + b_1) \cdots f^{(\ell)}(\mathcal{Z}_{a_\ell}, z_j + b_\ell) \right],
\]

where for \( i = 1, \ldots, \ell \), \((a_i, b_i)\) is the atom with the \( i \)-th largest first coordinate of a Poisson random measure on \((0, \infty) \times (0, \infty)\) with intensity \( d a \otimes e^{-r} \, dr \). We consider only the case \( \ell = 1 \). By Lemma 11, we have for each integer \( m \) with \( \mathbb{P}(B^{(n)}_{\sigma(j)} = m) > 0 \) and almost all \( s > 0 \) the equality of the conditional densities

\[
\mathbb{E} \left[ f^{(1)} \left( \frac{\ln^2 n}{n} B^{(n)}_{\sigma(j)}, B^{(n)}_{\sigma(j)} \right) \right] = \mathbb{E}_m \left[ f^{(1)} \left( \frac{\ln^2 n}{n} B^{(m)}_{\sigma(j)}, s + \frac{\ln n}{\ln m} b^{(m)} \right) \right],
\]

where \( \mathbb{E}_m \) is the mathematical expectation starting from a random recursive tree with \( m \) vertices, and under \( \mathbb{E}_m \), \((B^{(m)}_{\sigma(j)}, b^{(m)})\) is in the first coordinate the size and in the second the birth time of the largest tree component of the first generation produced by a destruction process on \( T_m \) with parameter \( 1/\ln m \). Now if \( m \sim (n/\ln n) a \) for some fixed \( a > 0 \), \( m = m(n) \) integer-valued, we obtain from Proposition 4 that

\[
\mathbb{E}_m \left[ f^{(1)} \left( \frac{\ln^2 n}{n} B^{(m)}_{\sigma(j)}, s + \frac{\ln n}{\ln m} b^{(m)} \right) \right] \sim \mathbb{E} \left[ f^{(1)}(aa_1, s + b_1) \right],
\]

where \((a_1, b_1)\) is the atom with the largest first coordinate of a Poisson random measure on \((0, \infty) \times (0, \infty)\) with intensity \( d a \otimes e^{-r} \, dr \). On the other hand, we already know that the pair \((\frac{\ln n}{n} B^{(n)}_{\sigma(j)}, b^{(n)}_{\sigma(j)})\) converges in distribution as \( n \to \infty \) towards \((\mathcal{Z}_j, z_j)\). Since the map

\[
((a, b), (a_1, b_1)) \mapsto g(a, b)f^{(1)}(aa_1, b + b_1)
\]

is uniformly continuous on bounded sets, this establishes (13). The arguments can now easily be extended to the subsequent generations, and the theorem is proved.

### 3.4. Applications of the Destruction Process and Remarks

#### 3.4.1. Connection to Bernoulli Bond Percolation

In [5], Bertoin uses the coupling of Iksanov and Möhle to study the asymptotic sizes of the largest and next largest percolation clusters of a supercritical Bernoulli bond percolation on \( T_n \) with parameter

\[
p(n) = 1 - \frac{1}{\ln n + o(1/\ln n)}, \quad t > 0 \text{ fixed.}
\]

Let us recall his strategy. If the destruction process (with parameter \( 1/\ln n \)) is stopped at time \( t(n) = -\ln n \times \ln p(n) \), then one observes a Bernoulli bond percolation on \( T_n \) with parameter \( p(n) \). Under this coupling, the tree components born in the destruction process up to time \( t(n) \) contain the non-root percolation clusters of \( T_n \). In fact, each such percolation cluster of
$T_n$ can be identified with a subtree of a tree component rooted at the same vertex, meaning that within its surrounding component, the percolation cluster forms the root cluster.

The usefulness of this point of view comes from two facts. Firstly, we know from the second part of Lemma 11 that in the regime (14), the root cluster of a RRT $T_n$ has size $\sim e^{-t}m$ as $m \to \infty$. Secondly, the asymptotic sizes of the tree components can be specified (see Proposition 5). In order to reveal the inner root percolation cluster inside a tree component, the latter has to be “unfrozen”, i.e. some additional edges have to be erased. This approach was used by Bertoin [5] to study the sizes of the root percolation clusters inside the tree components of the first generation, and our aim is to outline how these ideas can be extended to all clusters. We first lift the convergence of Lemma 11 to higher generations. Towards this end, let

$$\left( B_{n,t(n)}, b_{n,t(n)} \right) = \begin{cases} (B_{u}^{(n)}, b_{u}^{(n)}) & \text{for } b_{u}^{(n)} < t(n) \\ (0, \infty) & \text{for } b_{u}^{(n)} \geq t(n) \end{cases}.$$ 

Then we can use Lemma 11 instead of Proposition 4 to obtain a limit result for the ranked version $((B_{u}^{(n)}, b_{u}^{(n)}))_{u \in U}$. Here, by a small abuse of notation, $\sigma : U \to U$ is a random bijection that sorts the children of each element $(B_{n,t(n)}, b_{n,t(n)})$ in the decreasing order of their first coordinate, keeping the parent-child relation. The limit process $((Z_{u,t}, z_{u}))_{u \in U}$ is obtained from $((Z_{u,n}, z_{u}) : u \in U)$ by first removing those pairs $((Z_{u,n}, z_{u})$ with $z_{u} \geq t$ and then by a relabeling of the remaining elements. Alternatively, in accordance with Lemma 11, the law of the limit can also be specified as follows.

- $(Z_{u,t}, z_{u}) = (1, 0)$ almost surely;
- for every $k = 0, 1, 2, \ldots$, conditionally on $((Z_{u,t}, z_{u}) : v \in U, |v| \leq k)$, the sequences $((Z_{u,t}, z_{u})_{v \in U} : (Z_{u,t}, z_{u})_{v \in U})$ for the vertices $u \in U$ at generation $|u| = k$ are independent, and each sequence $((Z_{u,t}, z_{u}) : u \in U)$ is distributed as the family of the atoms of a Poisson random measure on $(0, \infty) \times (0, t - z_{u})$ with intensity $Z_{u,t}a^{-2}da \otimes e^{-r}dr$, ranked in the decreasing order of the first coordinate.

The analog of Theorem 2 for the tree components born up to time $t(n)$ then reads as follows.

**Proposition 5.** As $n \to \infty$, in the sense of finite-dimensional distributions,

$$\left( \left( \frac{(\ln n)^{|u|}}{n} B_{\sigma(u), t(n)}, b_{\sigma(u), t(n)} \right) : u \in U \right) \Longrightarrow \left( (Z_{u,t}, z_{u}) : u \in U \right).$$

Now the tree components have to be unfrozen to observe the percolation clusters inside. Write $\tau_{u}^{(n)}$ for the tree component whose size and birth time is stored in $B_{\sigma(u), t(n)}$ (with $\tau_{0}^{(n)} = \emptyset$ if there is no such component, and $\tau_{\emptyset}^{(n)} = T_n$). Say we want to determine the size of the root percolation cluster inside the tree component $\tau_{u}^{(n)}$. This component was cut off from a bigger subtree at time $b = b_{\sigma(u), t(n)}$. By the memoryless property of exponential variables, we are therefore lead to perform a Bernoulli bond percolation on $\tau_{u}^{(n)}$ with parameter $\exp(-t(n) - b)/\ln n$, and adapting the arguments of [5], we deduce that the root cluster $c_{u}^{(n)}$ of $\tau_{u}^{(n)}$ has size

$$|c_{u}^{(n)}| \sim e^{-(t-b)}B_{\sigma(u), t(n)}.$$ 

More generally, denote by $c_{u}^{(n)}$ for $u \in U$ the percolation cluster with the same root as $\tau_{u}^{(n)}$ (under our coupling with the destruction process). In the percolation regime $1 - p(n) \sim t/\ln n$, we have

$$\left(1 - p(n)\right)^{-k}n^{-p(n)} \sim t^{-k}e^i(\ln n)^{k}n^{-1}.$$
Using Proposition 5, the last two displays and similar arguments as in the proof of Theorem 2, we obtain the following limit result for the cluster sizes $|c_u^{(n)}|$.

**Corollary 2.** As $n \to \infty$, in the sense of finite-dimensional distributions,

$$\left(\frac{1-p(n)}{p(n)}|c_u^{(n)}| : u \in U\right) \Longrightarrow \left(r^{-|a|}\exp(z_{u,t})Z_{u,t} : u \in U\right).$$

Extending the arguments of [5, Lemma 6, 7] to higher levels in the tree, we moreover see that Corollary 2 remains true if we apply our usual ranking operation to both sides. Denote by $C^{(n)} = (C_{u}^{(n)} : u \in U)$ the ranked version of $(|c_u^{(n)}| : u \in U)$, i.e. $C_{u}^{(n)} = |c_{\hat{u}(u)}^{(n)}|$, where $\hat{\sigma} : U \to U$ is a random bijection sorting the children $(|c_{i}^{(n)}| : i \in \mathbb{N})$ of each element $|c_{u}^{(n)}|$ in the decreasing order, such that the parent-child relation is preserved. For the right hand side, let us write $G_u = r^{-|a|}\exp(z_{a,t})Z_{a,t}$ and $(G_{\hat{\sigma}(u)} : u \in U)$ for the ranked version of $(G_u : u \in U)$. Then the convergence in Corollary 2 transfers to the ranked versions, i.e.

$$\left(\frac{1-p(n)}{p(n)}C_{u}^{(n)} : u \in U\right) \Longrightarrow \left(G_{\hat{\sigma}(u)} : u \in U\right),$$

in the sense of finite-dimensional distributions in the regime (14). It is now instructive to compare this last convergence result with Theorem 1.

We first remark that as for the tree of cluster sizes $C^{(n)}$ from Section 2.1, the process $(C_{u}^{(n)} : u \in U)$ stores the size of every percolation cluster of $T_n$. But the two encodings given by $C^{(n)}$ and $C^{(n)}$ are different. Indeed, if we look at some specific percolation cluster of $T_n$ and ask for the vertex $v \in U$ to which the size of this cluster is attached in the process $(C_{u}^{(n)} : u \in U)$, we observe that its level $|v| = k$ does not merely depend on the total number of removed edges which separate the cluster from the vertex with label 0, but also on the order in which these edges were removed.

To stress the difference of the encodings, call a percolation cluster encoded by some $c_u^{(n)}$ with $|u| = k$ a cluster of rank $k$. In terms of our classification of clusters into generations from Section 2.1, a cluster of generation $k \geq 1$ with root node $v$ can be a cluster of rank $1 \leq \ell \leq k$; the rank depends on the order in which the $k$ erased edges on the path from 0 to $v$ were removed in the destruction process. Conversely, a cluster of rank $\ell$ with root node $v$ can be a cluster of generation $k$ for $\ell \leq k \leq \text{dist}(0,v)$, where $\text{dist}(\cdot, \cdot)$ denotes the graph distance on $T_n$ before the percolation was performed.

Fig. 3 illustrates the difference in the encoding by $C^{(n)}$ and $C^{(n)}$, respectively. We tacitly assume that the tree of cluster sizes $C^{(n)}$ is defined in terms of the final state of a percolation on $T_n$, which is used to define $C^{(n)}$. For example, the cluster $\{5,9\}$ is a cluster of rank 1, since the edge joining 5 to its parent 3 was the first edge from the path connecting 0 to 5 which was removed in the destruction process. On the other hand, $\{5,9\}$ is a cluster of generation 2, since it is disconnected from 0 by two deleted edges in the final outcome of percolation.

Recall the description of $((Z_{a,t}, z_{a,t}) : u \in U)$ from above. We now observe that conditionally on $(Z_{a,t}, z_{a,t})$, the family $(G_{j(u)} : j \in \mathbb{N})$ is distributed as the sequence $b_1 > b_2 > \ldots$ of the atoms of a Poisson random measure on $(0, \infty)$ with intensity

$$r^{-(|u|+1)}(t-z_{u,t})\exp(z_{u,t})Z_{a,t}a^{-2}da.$$ 

Indeed, $G_{j(u)} = r^{-(|j(u)|+1)}\exp(z_{a,t})\exp(z_{j(u),t} - z_{a,t})Z_{j(u)}$, and given $(Z_{a,t}, z_{a,t})$, the image of the measure $Z_{a,t}a^{-2}da \otimes \exp(t^2dr)$ on $(0, \infty) \times (0, t-z_{u,t})$ by the map $(a,s) \mapsto r^{-(|u|+1)}\exp(z_{u,t})\exp(s)a$ is $r^{-(|u|+1)}(t-z_{a,t})\exp(z_{a,t})Z_{a,t}a^{-2}da$ on $(0, \infty)$.
Since \((Z_\emptyset, z_\emptyset, t) = (1, 0)\), we deduce from this characterization that the sequences \((G_{\emptyset(j)} : j \in \mathbb{N})\) and \((Z_j : j \in \mathbb{N})\) have the same distribution, which implies that the finite-dimensional limits of \((C_u^{(n)} : u \in \mathcal{U}, |u| \leq 1)\) and \((C_{u}^{(n)} : u \in \mathcal{U}, |u| \leq 1)\) agree (under our normalizations).

In fact, this already follows from our previous considerations: We have seen in the proof of Corollary 1 that the largest non-root clusters are of generation 1, and every such cluster is necessarily a cluster of rank 1 (but not every cluster of rank 1 is of generation 1, see cluster \{5, 9\} in Fig. 3).

For higher levels in the trees \(C^{(n)}\) and \(C^{(n)}\), the limits do however not agree! This comes from the fact that clusters of generation \(k \geq 2\) can represent clusters of a strictly lower rank \(1 \leq \ell < k\). Roughly speaking, if such a cluster has a size of order \((1 - p(n))^{k}p^{(n)}\), it is visible in the limit under the encoding by \(C^{(n)}\), while it is not under the encoding by \(C^{(n)}\).

**Remark.** With a few modifications, the methods outlined in this section can also be applied to study cluster sizes in the strongly supercritical regime. As it is already pointed out in the introduction, it is however less clear how the coupling of Iksanov and Möhle can be used for the weakly supercritical regime. Moreover, for the results in this Section 3, we stress the importance of the splitting property, which is a very peculiar feature of random recursive trees.

### 3.4.2. Connection to the Cut-Tree

The tree of components is related to the so-called *cut-tree*, which is defined in terms of a discrete-time destruction process, where edges are removed according to some order, for example a random uniform order.

More specifically, the cut-tree is a rooted binary tree which encodes the destruction of a tree \(T\) on a finite vertex set \(V\) in the following way. The root vertex is given by the set \(V\). Then, if the first edge is removed, \(T\) splits into two subtrees with respective vertex sets \(V_1\) and \(V_2\), and these vertex sets are attached as the two children to the root \(V\). The construction is then iterated in the natural way - if, for example, the next edge is removed from the subtree with vertex set \(V_1\), the latter splits into two vertex sets \(V_{1,1}\) and \(V_{1,2}\), which are regarded as the two children of \(V_1\). In particular, the leaves of the cut-tree can be identified with the vertices of \(T\).

Unlike the tree of components, the cut-tree stores the vertex sets of the tree components and not merely their sizes. For example, in Fig. 4 the vertex sets of the tree components of...
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Fig. 4. Left: The same recursive tree as in Fig. 2, with the same order of edge removals. Right: The corresponding cut-tree.

the first generation, i.e. \( \{5, 9\}, \{3, 7, 8, 10\}, \{4\} \) and \( \{1, 2, 6\} \) (in the order of their appearance), are represented by the vertices which are attached to the branch from the root \( \{0, 1, \ldots, 10\} \) to the leaf \( \{0\} \).

The cut-tree has been analyzed for Cayley trees and random recursive trees by Bertoin in [3] and [6], and then by Bertoin and Miermont [7] and Dieuleveut [9] for Galton-Watson trees. Their results can be used to obtain limit theorems for the number of steps to isolate a certain family of nodes, and in a similar direction, we believe that the tree of components can prove helpful, too.

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