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Cutting edges at random in large recursive trees

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Abstract

We comment on old and new results related to the destruction of a random recursive tree (RRT), in which its edges are cut one after the other in a uniform random order. In particular, we study the number of steps needed to isolate or disconnect certain distinguished vertices when the size of the tree tends to infinity. New probabilistic explanations are given in terms of the so-called cut-tree and the tree of component sizes, which both encode different aspects of the destruction process. Finally, we establish the connection to Bernoulli bond percolation on large RRT's and present recent results on the cluster sizes in the supercritical regime.

Key words: Random recursive tree, destruction of graphs, isolation of nodes, disconnection, supercritical percolation, cluster sizes, fluctuations.

1 Introduction

Imagine that we destroy a connected graph by removing or cutting its edges one after the other, in a uniform random order. The study of such a procedure was initiated by Meir and Moon in [32]. They were interested in the number of steps needed to isolate a distinguished vertex in a (random) Cayley tree, when the edges are removed uniformly at random from the current component containing this vertex. Later on, Meir and Moon [33] extended their analysis to random recursive trees. The latter form an important family of increasing labeled trees (see

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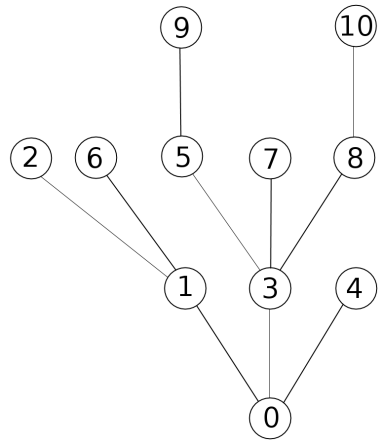

Figure 1
A recursive tree on the vertex set $\{0, 1, \ldots, 10\}$.

Section 2 for the definition), and it is the goal of this paper to shed light on issues related to the destruction of such trees.

Mahmoud and Smythe [31] surveyed a multitude of results and applications for random recursive trees. Their recursive structure make them particularly amenable to mathematical analysis, from both a combinatorial and probabilistic point of view. We focus on the probabilistic side. Our main tools include the fundamental splitting property, a coupling due to Iksanov and Möhle [23] and the so-called *cut-tree* (see [10]), which records the key information about the destruction process. The cut-tree allows us to re-prove the results of Kuba and Panholzer [29] on the multiple isolation of nodes. Moreover, we gain information on the number of steps needed to disconnect a finite family nodes.

Finally, we relate the destruction of a random recursive tree to Bernoulli bond percolation on the same tree. We explain some results concerning the sizes of percolation clusters in the supercritical regime, where the root cluster forms the unique giant cluster.

2 Main tools

In this section, we present some basic tools in the study of random recursive trees which will be useful to our purposes.

2.1 The recursive construction, Yule process and Pólya urn

Consider a finite and totally ordered set of vertices, say V. A tree on V is naturally rooted at the smallest element of V, and is called increasing if and only if the sequence of vertices

along a segment from the root to an arbitrary vertex increases. Most of the time we shall take $V = \{0, 1, \ldots, n\}$, which induces of course no loss of generality. More precisely, it is convenient to introduce the following notion. For an arbitrary totally ordered set V with cardinality $|V| = n + 1$, we call the bijective map from V to $\{0, 1, \ldots, n\}$ which preserves the order, the canonical relabeling of vertices. Plainly the canonical relabeling transforms an increasing tree on V into an increasing tree on $\{0, 1, \ldots, n\}$. Such relabelings enable us to focus on the structure of the rooted tree without retaining specifically the elements of V.

A *random recursive tree* (in short, RRT) on $\{0, 1, \ldots, n\}$ is a tree picked uniformly at random amongst all the increasing trees on $\{0, 1, \ldots, n\}$; it shall be denoted henceforth by T_n. In particular, T_n has n edges and size (i.e. number of vertices) $|T_n| = n + 1$. The terminology stems from the easy observation that a version of T_n can be constructed by the following simple recursive random algorithm in which vertices are incorporated one after the other. The vertex 1 is naturally connected by an edge to the root 0, then 2 is connected either to 0 or to 1 with equal probability 1/2, and more generally, the parent of the vertex i is chosen uniformly at random amongst $0, 1, \ldots, i-1$ and independently of the other vertices. This recursive construction is a close relative to the famous Chinese Restaurant construction of uniform random permutations (see, for instance, Section 3.1 in Pitman [35]), and in particular the number of increasing trees of size $n + 1$ equals $n!$.

Another useful observation is that this recursive construction can be interpreted in terms of the genealogy of a Yule process. Recall that a Yule process describes the evolution in continuous time of a pure birth process in which each individual gives birth to a child at unit rate and independently of the other individuals. We label individuals in the increasing order of their birth times, the ancestor receiving by convention the label 0. If we let the process evolve until the population reaches size $n + 1$, then its genealogical tree, that is the tree where individuals are viewed as vertices and edges connect children to their parent, is clearly a RRT. Here is an application to percolation on T_n which will be useful later on.

Lemma 1 *Perform a Bernoulli bond percolation on T_n with parameter $0 < p < 1$ (i.e. each edge of T_n is deleted with probability $1 - p$, independently of the other edges), and let $C_n^0(p)$ denote the size of the cluster containing the root. Then*

$$\lim_{n\to\infty} n^{-p} C_n^0(p) = C^0(p) \qquad \textit{in distribution,}$$

where $C^0(p) > 0$ a.s. is some random variable.

Proof: We view T_n as the genealogical tree of a standard Yule process $(\mathcal{Y}_s)_{s\geq 0}$ up to time $\rho_n = \inf\{s \geq 0 : \mathcal{Y}_s = n + 1\}$. It is well-known that the process $\mathrm{e}^{-s}\mathcal{Y}_s$ is a martingale which converges a.s. to some random variable W with the exponential distribution, and it follows

that

$$\lim_{n\to\infty} n^{-1}\mathrm{e}^{\rho_n} = 1/W \qquad \text{a.s.}$$

In this setting, performing a Bernoulli bond percolation can be interpreted as superposing neutral mutations to the genealogical tree, namely each child is a clone of its parent with probability p and a mutant with a new genetic type with probability $1-p$, independently of the other children. Neutrality means that the rate of birth does not depend on the genetic type. Then the process $(\mathcal{Y}_s(p))_{s\geq 0}$ of the number of individuals with the same genetic type as the ancestor is again a Yule process, but now with birth rate p. As a consequence

$$\lim_{s\to\infty} \mathrm{e}^{-ps}\mathcal{Y}_s(p) = W(p) \qquad \text{a.s.},$$

where $W(p)$ denotes another exponentially distributed random variable. We then observe that

$$C_n^0(p) = \mathcal{Y}_{\rho_n}(p) \sim W(p)\mathrm{e}^{p\rho_n} \sim W(p)W^{-p}n^p,$$

which completes the proof. □

Plainly, the recursive construction can also be interpreted in terms of urns, and we conclude this section by exemplifying this connection. Specifically, the size of the root cluster $C_n^0(p)$ in the above lemma can be identified as the number of red balls in the following Pólya-Hoppe urn. Start with one red ball which represents the root of the tree. A draw is effected as follows: (i) Choose a ball at random from the urn, observe its color, and put the ball back to the urn. (ii) If its color was red, add a red ball to the urn with probability p, and add a black ball to the urn with probability $1-p$. If its color was black, add another black ball to the urn. Then, after n draws, the number of red balls is given by $C_n^0(p)$, and in this way, Lemma 1 yields a limit theorem for the proportion of red balls.

The choice $p=1$ in this urn scheme corresponds to the usual Pólya urn. Here, if one starts with one red ball and k black balls, then the number of red balls after $n-k$ draws is distributed as the size of the subtree T_n^k of a RRT T_n that stems from the vertex k. It is well-known from the theory of Pólya urns that this number follows the beta-binomial distribution with parameters $(n-k,1,k)$. Moreover,

$$\lim_{n\to\infty} n^{-1}|T_n^k| = \beta(1,k) \qquad \text{in distribution,} \tag{1}$$

where $\beta(1,k)$ is a beta$(1,k)$-distributed random variable. We will use this fact several times below.

2.2 The splitting property

The *splitting property* (also called randomness preserving property) reveals the fractal nature of RTT's: roughly speaking, if one removes an edge from a RRT, then the two subtrees resulting from the split are in turn, conditionally on their sizes, independent RRT's. This is of course of crucial importance when investigating the destruction of a RRT, as we can then apply iteratively the splitting property when removing the edges uniformly at random and one after the other.

We select an edge of T_n uniformly at random and remove it. Then T_n splits into two subtrees, say τ_n^0 and τ_n^*, where τ_n^0 contains the root 0. We denote by T_n^0 and T_n^* the pair of increasing trees which then result from the canonical relabelings of the vertices of τ_n^0 and τ_n^*, respectively. Introduce also an integer-valued variable ξ with distribution

$$\mathbb{P}(\xi = j) = \frac{1}{j(j+1)}, \qquad j = 1, 2, \ldots \tag{2}$$

Proposition 1 (Meir and Moon [33]) *In the notation above, $|\tau_n^*| = |T_n^*|$ has the same law as ξ conditioned on $\xi \leq n$, that is*

$$\mathbb{P}(|T_n^*| = j) = \frac{n+1}{nj(j+1)}, \qquad j = 1, 2, \ldots, n.$$

Further, conditionally on $|T_n^*| = j$, T_n^0 and T_n^* are two independent RRT's with respective sizes $n - j + 1$ and j.

Proof: There are $nn!$ configurations $(\mathbf{t}, e)$ given by an increasing tree $\mathbf{t}$ on $\{0, 1, \ldots, n\}$ and a distinguished edge e. We remove the edge e and then relabel vertices canonically in each of the resulting subtrees. Let us enumerate the configurations that yield a given pair $(\mathbf{t}^0, \mathbf{t}^*)$ of increasing trees on $\{0, 1, \ldots, n-j\}$ and $\{0, 1, \ldots, j-1\}$, respectively.

Let $k \in \{0, 1, \ldots, n-1\}$ denote the extremity of the edge e which is the closest to the root 0 in $\mathbf{t}$, and V^* the set of vertices which are disconnected from k when e is removed. Since $\mathbf{t}$ is increasing, all the vertices in V^* must be larger than k, and since we want $|V^*| = j$, there are $\binom{n-k}{j}$ ways of choosing V^* (note that this is possible if and only if $k \leq n-j$). There are a unique increasing tree structure on V^* and a unique increasing tree structure on $\{0, 1, \ldots, n\} \backslash V^*$ that yield respectively $\mathbf{t}^*$ and $\mathbf{t}^0$ after the canonical relabelings.

Conversely, given $\mathbf{t}^0$, $\mathbf{t}^*$, $k \in \{0, 1, \ldots, n-j\}$ and $V^* \subset \{k+1, \ldots, n\}$ with $|V^*| = j$, there is clearly a unique configuration $(\mathbf{t}, e)$ which yields the quadruple $(k, V^*, \mathbf{t}^0, \mathbf{t}^*)$. Namely, relabeling vertices in $\mathbf{t}^0$ and $\mathbf{t}^*$ produces two increasing tree structures τ^0 and τ^* on $\{0, 1, \ldots, n\} \backslash V^*$ and V^*, respectively. We let e denote the edge $(k, \min V^*)$ and then $\mathbf{t}$ is the increasing tree obtained by connecting τ^0 and τ^* using e.

It follows from the analysis above that

$$\mathbb{P}(T_n^0 = \mathbf{t}^0, T_n^* = \mathbf{t}^*) = \frac{1}{nn!} \sum_{k=0}^{n-j} \binom{n-k}{j}.$$

Now recall that

$$\sum_{k=0}^{n-j} \binom{n-k}{j} = \sum_{\ell=j}^{n} \binom{\ell}{j} = \binom{n+1}{j+1}$$

to conclude that

$$\mathbb{P}(T_n^0 = \mathbf{t}^0, T_n^* = \mathbf{t}^*) = \frac{n+1}{n(n-j)!(j+1)!} = \frac{n+1}{nj(j+1)} \times \frac{1}{(n-j)!(j-1)!}.$$

Since there are $(n-j)!$ increasing trees with size $n-j+1$ and $(j-1)!$ increasing trees with size j, this yields the claim. □

Remark. It can be easily checked that the splitting property holds more generally when one removes a fixed edge, that is the edge connecting a given vertex $k \in \{1, \ldots, n\}$ to its parent. Of course, the distribution of the sizes of the resulting subtrees then changes; see the connection to Pólya urns mentioned in the beginning.

2.3 The coupling of Iksanov and Möhle

The splitting property was used by Meir and Moon [33] to investigate the following random algorithm for isolating the root 0 of a RRT. Starting from T_n, remove a first edge chosen uniformly at random and discard the subtree which does not contain the root 0. Iterate the procedure with the subtree containing 0 until the root is finally isolated, and denote by X_n the number of steps of this random algorithm. In other words, X_n is the number of random cuts that are needed to isolate 0 in T_n.

Iksanov and Möhle [23] derived from Proposition 1 a useful coupling involving an increasing random walk with step distribution given by (2). Specifically, let $\xi_1, \xi_2, \ldots$ denote a sequence of i.i.d. copies of ξ and set $S_0 = 0$,

$$S_n = \xi_1 + \cdots + \xi_n. \tag{3}$$

Further, introduce the last time that the random walk S remains below the level n,

$$L(n) = \max\{k \geq 0 : S_k \leq n\}. \tag{4}$$

Corollary 1 (Iksanov and Möhle [23]) *One can construct on the same probability space a*

random recursive tree T_n together with the random algorithm of isolation of the root, and a version of the random walk S, such that if

$$T^0_{n,0} = T_n \supset T^0_{n,1} \supset \cdots \supset T^0_{n,X_n} = \{0\} \tag{5}$$

denotes the nested sequence of the subtrees containing the root induced by the algorithm, then $X_n \geq L(n)$ and

$$(|T^0_{n,0} \backslash T^0_{n,1}|, \ldots, |T^0_{n,L(n)-1} \backslash T^0_{n,L(n)}|) = (\xi_1, \ldots, \xi_{L(n)}). \tag{6}$$

Proof: Let us agree for convenience that $T^0_{n,j} = \{0\}$ for every $j > X_n$, and first work conditionally on $(|T^0_{n,i}|)_{i\geq 1}$. Introduce a sequence $((\varepsilon_i, \eta_i))_{i\geq 1}$ of independent pairs of random variables such that for each i, ε_i has the Bernoulli law with parameter $1/|T^0_{n,i-1}| = \mathbb{P}(\xi \geq |T^0_{n,i-1}|)$ and η_i is an independent variable distributed as ξ conditioned on $\xi \geq |T^0_{n,i-1}|$. Then define for every $i \geq 1$

$$\xi_i = \begin{cases} |T^0_{n,i-1}| - |T^0_{n,i}| & \text{if} \quad \varepsilon_i = 0 \\ \eta_i & \text{if} \quad \varepsilon_i = 1 \end{cases}$$

and the partial sums $S_i = \xi_1 + \cdots + \xi_i$. Observe that $\varepsilon_i = 1$ if and only if $\xi_i \geq |T^0_{n,i-1}|$, and hence, by construction, there is the identity

$$\min\{i \geq 1 : \varepsilon_i = 1\} = \min\{i \geq 1 : S_i \geq n+1\}.$$

Therefore, (6) follows if we show that $\xi_1, \xi_2 \ldots$ are (unconditionally) i.i.d. copies of ξ. This is essentially a consequence of the splitting property. Specifically, for $j \leq n$, we have

$$\mathbb{P}(\xi_1 = j) = \mathbb{P}(\varepsilon_1 = 0)\mathbb{P}(n+1-|T^0_{n,1}| = j) = \frac{n}{n+1}\mathbb{P}(|T^*_n| = j) = \frac{1}{j(j+1)},$$

where we used the notation and the result in Proposition 1, whereas for $j > n$ we have

$$\mathbb{P}(\xi_1 = j) = \mathbb{P}(\varepsilon_1 = 1)\mathbb{P}(\xi = j \mid \xi \geq n+1) = \frac{1}{j(j+1)}.$$

Next, consider the conditional law of ξ_2 given ξ_1 and $|T^0_{n,1}|$. Of course, $|T^0_{n,1}| \geq n+1-\xi_1$, and this inequality is in fact an equality whenever $\xi_1 \leq n$. We know from the splitting property that conditionally on its size, say $|T^0_{n,1}| = m+1$ with $m \leq n-1$, $T^0_{n,1}$ is a RRT. Therefore

Proposition 1 yields again for $j \leq m$

$$\begin{aligned}
& \mathbb{P}\left(\xi_2 = j \mid \xi_1 \text{ and } |T^0_{n,1}| = m+1\right) \\
= \; & \mathbb{P}\left(\varepsilon_2 = 0 \mid \xi_1 \text{ and } |T^0_{n,1}| = m+1\right) \mathbb{P}(m+1-|T^0_{n,2}| = j \mid \xi_1 \text{ and } |T^0_{n,1}| = m+1) \\
= \; & \frac{m}{m+1}\mathbb{P}(|T^*_m| = j) \\
= \; & \frac{1}{j(j+1)}.
\end{aligned}$$

Similarly for $j > m$

$$\begin{aligned}
& \mathbb{P}(\xi_2 = j \mid \xi_1 \text{ and } |T^0_{n,1}| = m+1) \\
= \; & \mathbb{P}(\varepsilon_2 = 1 \mid \xi_1 \text{ and } |T^0_{n,1}| = m+1)\mathbb{P}(\xi = j \mid \xi \geq m+1) \\
= \; & \frac{1}{j(j+1)}.
\end{aligned}$$

This shows that ξ_2 has the same distribution as ξ and is independent of ξ_1 and $|T^0_{n,1}|$. Iterating this argument, we get that the ξ_i form a sequence of i.i.d. copies of ξ, which completes the proof. □

3 The number of random cuts needed to isolate the root

Recall the algorithm of isolation of the root which was introduced in the preceding section, and that X_n denotes its number of steps for T_n, i.e. X_n is the number of random cuts that are needed to isolate the root 0 in T_n. Meir and Moon [33] used Proposition 1 to investigate the first two moments of X_n and showed that

$$\lim_{n\to\infty} \frac{\ln n}{n} X_n = 1 \qquad \text{in probability.} \tag{7}$$

The problem of specifying the fluctuations of X_n was left open until the work by Drmota *et al.*, who obtained the following remarkable result.

Theorem 1 (Drmota, Iksanov, Möhle and Rösler [17]) *As $n \to \infty$,*

$$\frac{\ln^2 n}{n} X_n - \ln n - \ln\ln n$$

converges in distribution to a completely asymmetric Cauchy variable X with characteristic function

$$\mathbb{E}(\exp(itX)) = \exp\left(it\ln|t| - \frac{\pi}{2}|t|\right), \qquad t \in \mathbb{R}. \tag{8}$$

In short, the starting point of the proof in [17] is the identity in distribution

$$X_n \overset{(d)}{=} 1 + X_{n-D_n}, \tag{9}$$

where D_n is a random variable with the law of ξ given $\xi \leq n$, and D_n is assumed to be independent of $X_1, \ldots, X_n$. More precisely, (9) derives immediately from the splitting property (Proposition 1). Drmota *et al.* deduce from (9) a PDE for the generating function of the variables X_n, and then singularity analysis provides the key tool for investigating the asymptotic behavior of this generating function and elucidating the asymptotic behavior of X_n.

Iksanov and Möhle [23] developed an elegant probabilistic argument which explains the unusual rescaling and the Cauchy limit law in Theorem 1. We shall now sketch this argument.
Sketch proof of Theorem 1: One starts observing that the distribution in (2) belongs to the domain of attraction of a completely asymmetric Cauchy variable X whose law is determined by (8), namely

$$\lim_{n\to\infty} \left(n^{-1}S_n - \ln n\right) = -X \qquad \text{in distribution.} \tag{10}$$

Then one deduces from (10) that the asymptotic behavior of the last-passage time (4) is given by

$$\lim_{n\to\infty} \left(\frac{\ln^2 n}{n} L(n) - \ln n - \ln\ln n\right) = X \qquad \text{in distribution,} \tag{11}$$

see Proposition 2 in [23]. This limit theorem resembles of course Theorem 1, and the relation between the two is explained by the coupling of the algorithm of isolation of the root and the random walk S stated in Corollary 1, as we shall now see.

Let the algorithm for isolating the root run for $L(n)$ steps. Then the size of the remaining subtree that contains the root is $n + 1 - S_{L(n)}$, and as a consequence, there are the bounds

$$L(n) \leq X_n \leq L(n) + n - S_{L(n)},$$

since at most $\ell - 1$ edge removals are needed to isolate the root in any tree of size ℓ. On the other hand, specializing a renewal theorem of Erickson [18] for the increasing random walk S, one gets that

$$\lim_{n\to\infty} \ln(n - S_{L(n)})/\ln n = U \qquad \text{in distribution,}$$

where U is a uniform $[0, 1]$ random variable. In particular

$$\lim_{n\to\infty} \frac{\ln^2 n}{n}(n - S_{L(n)}) = 0 \qquad \text{in probability.}$$

Thus Theorem 1 follows from (11). □

It should be noted that there exists a vertex version of the isolation algorithm, where one chooses a vertex at random and destroys it together with its descending subtree. The algorithm continues until the root is chosen. Using an appropriate coupling with X_n, one readily shows that the number of random vertex removals $X_n^{(v)}$ needed to destroy a RRT T_n satisfies $(X_n - X_n^{(v)}) = o(n/\ln^2 n)$ in probability. Henceforth, we concentrate on cutting edges.

Remark. Weak limit theorems for the number of cuts to isolate the root vertex have also been obtained for other tree models, like conditioned Galton-Watson trees including e.g. uniform Cayley trees and random binary trees (Panholzer [34] and, in greater generality, Janson [25]), deterministic complete binary trees (Janson [24]) and random split trees (Holmgren [21, 22]). More generally, Addario-Berry *et al.* [1] and Bertoin [6] found the asymptotic limit distribution for the number of cuts required to isolate a fixed number $\ell \geq 1$ of vertices picked uniformly at random in a uniform Cayley tree. This result was further extended by Bertoin and Miermont [12] to conditioned Galton-Watson trees. We point to the remark after Corollary 3 for more on this. Turning back to RRT's, recent generalizations of Theorem 1 were found first by Kuba and Panholzer [28, 29] and then by Bertoin [10], some of which will be discussed in the reminder of this paper.

In [29], Kuba and Panholzer considered the situation when one wishes to isolate the *first* ℓ vertices of a RRT T_n, $0, 1, \ldots, \ell - 1$, where $\ell \geq 1$ is fixed. In this direction, one modifies the algorithm of isolation of the sole root in an obvious way. A first edge picked uniformly at random in T_n is removed. If one of the two resulting subtrees contains none of the vertices $0, 1, \ldots, \ell - 1$, then it is discarded forever. Else, the two subtrees are kept. In both cases, one iterates until each and every vertex $0, 1, \ldots, \ell - 1$ has been isolated, and we write $X_{n,\ell}$ for the number of steps of this algorithm.

The approach of Kuba and Panholzer follows analytic methods similar to the original proof of Theorem 1 by Drmota *et al.* [17]. We point out here that the asymptotic behavior of $X_{n,\ell}$ can also be deduced from Theorem 1 by a probabilistic argument based on the following elementary observation, which enables us to couple the variables $X_{n,\ell}$ for different values of ℓ. Specifically, we run the usual algorithm of isolation of the root, except that now, at each time when a subtree becomes disconnected from the root, we keep it aside whenever it contains at least one of the vertices $1, \ldots, \ell - 1$, and discard it forever otherwise. Once the root 0 of T_n has been isolated, we resume with the subtree containing 1 which was set aside, meaning that we run a further algorithm on that subtree until its root 1 has been isolated, keeping aside the further subtrees disconnected from 1 which contain at least one of the vertices $2, \ldots, \ell - 1$. We then continue with the subtree containing the vertex 2, and so on until each and every vertex $0, 1, \ldots, \ell - 1$ has been isolated. If we write $X'_{n,\ell}$ for the number of steps of this algorithm, then it should be plain that $X'_{n,\ell}$ has the same law as $X_{n,\ell}$, and further $X_n = X'_{n,1} \leq \cdots \leq X'_{n,\ell}$.

We shall now investigate the asymptotic behavior of the increments $\Delta_{n,i} = X'_{n,i+1} - X'_{n,i}$ for $i \geq 1$ fixed. In this direction, suppose that we now remove the edges of T_n one after the other in a uniform random order until the edge connecting the vertex i to its parent is removed. Let τ_n^i denote the subtree containing i that arises at this step.

Lemma 2 *For each fixed $i \geq 1$,*

$$\lim_{n\to\infty} \frac{\ln |\tau_n^i|}{\ln n} = U \qquad \textit{in distribution,}$$

where U is a uniform $[0,1]$ random variable.

For the moment, let us take Lemma 2 for granted and deduce the following.

Corollary 2 *We have*

$$\lim_{n\to\infty} \frac{\ln \Delta_{n,i}}{\ln n} = U \qquad \textit{in distribution,}$$

where U is a uniform $[0,1]$ random variable.

Proof: Just observe that $\Delta_{n,i}$ has the same law as the number of cuts needed to isolate the root i of τ_n^i, and recall from an iteration of the splitting property that conditionally on its size, τ_n^i is a RRT. Our statement now follows readily from (7) and Lemma 2. □

Writing $X'_{n,\ell} = X_n + \Delta_{n,1} + \cdots + \Delta_{n,\ell-1}$, we now see from Theorem 1 and Corollary 2 that for each fixed $\ell \geq 1$, there is the weak convergence

$$\lim_{n\to\infty} \left(\frac{\ln^2 n}{n} X'_{n,\ell} - \ln n - \ln\ln n \right) = X \qquad \text{in distribution,} \tag{12}$$

which is Theorem 1 in [29]. We now proceed to the proof of Lemma 2.

Proof: Let T_n^i denote the subtree of T_n that stems from the vertex i, and equip each edge e of T_n with a uniform $[0,1]$ random variable U_e, independently of the other edges. Imagine that the edge e is removed at time U_e, and for every time $0 \leq s \leq 1$, write $T_n^i(s)$ for the subtree of T_n^i which contains i at time s. Hence, if we write $U = U_e$ for e the edge connecting i to its parent, then $\tau_n^i = T_n^i(U)$. Further, since U is independent of the other uniform variables, conditionally on U and T_n^i, τ_n^i can be viewed as the cluster that contains the root vertex i after a Bernoulli bond percolation on T_n^i with parameter $1-U$. Thus, conditionally on $|T_n^i| = m+1$ and $U = 1-p$, $|\tau_n^i|$ has the same law as $C_m^0(p)$ in the notation of Lemma 1.

From (1) we know that $n^{-1}|T_n^i|$ converges in distribution as $n \to \infty$ to a beta variable with parameters $(1,i)$, say β, which is of course independent of U. On the other hand, conditionally

on its size, and after the usual canonical relabeling of its vertices, T_n^i is also a RRT (see the remark at the end of Section 2). It then follows from Lemma 1 that

$$\lim_{n\to\infty} \frac{\ln|\tau_n^i|}{\ln n} = 1 - U \qquad \text{in probability,}$$

which establishes our claim. □

4 The destruction process and its tree representations

Imagine now that we remove the edges of T_n one after the other and in a uniform random order, no matter whether they belong to the root component or not. We call this the *destruction process* of T_n. After n steps, no edges are present anymore and all the vertices have been isolated. In particular, the random variable which counts only the number of edge removals from the root component can be identified with X_n from the previous section.

The purpose of this section is to introduce and study the asymptotic behavior of two trees which can be naturally associated to this destruction process, namely the tree of component sizes and the cut-tree. Furthermore, we give some applications of the cut-tree to the isolation and disconnection of nodes and comment on ordered destruction of a RRT.

4.1 The tree of component sizes

In this part, we are interested in the sizes of the tree components produced by the destruction process. Our analysis will also prove helpful for studying percolation clusters of a RRT in Section 5.

The component sizes are naturally stored in a tree structure. As our index set, we use the universal tree

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

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 its length $|u| = k$ represents the "generation" of u. The jth child of u is given by $uj = (u_1, \ldots, u_k, j)$, $j \in \mathbb{N}$. The empty sequence $\emptyset$ is the root of the tree and has length $|\emptyset| = 0$. If no confusion occurs, we drop the separating commas and write $(u_1 \cdots u_k)$ or simply $u_1 \cdots u_k$ instead of $(u_1, \ldots, u_k)$. Also, $\emptyset u$ represents the element u.

We define a tree-indexed process $\mathcal{B}^{(n)} = (\mathcal{B}_u^{(n)} : u \in \mathcal{U})$, which encodes the sizes of the tree components stemming from the destruction of T_n. We will directly identify a vertex u with its

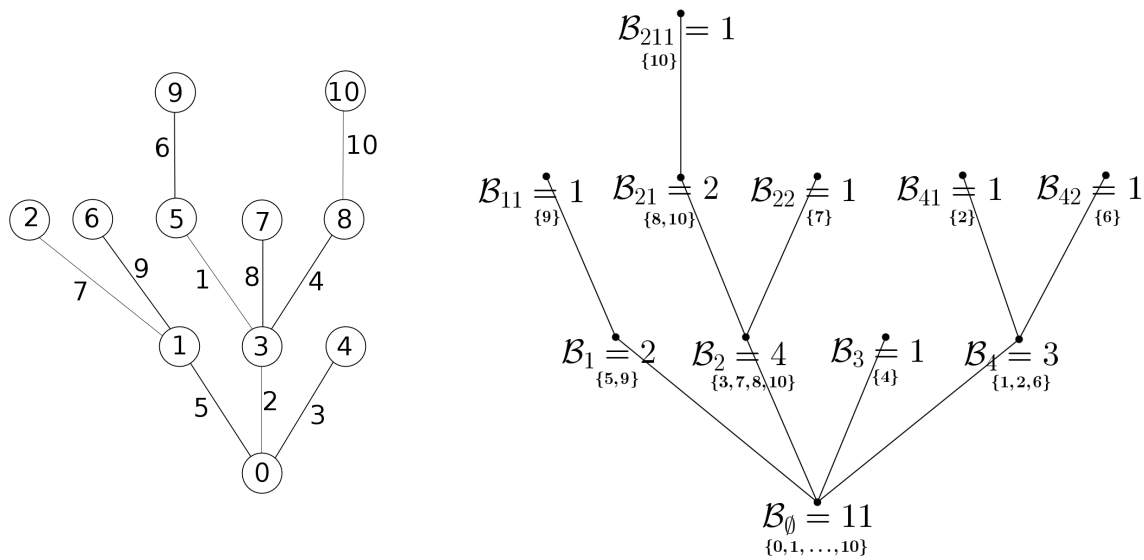

Figure 2

Left: A recursive tree with vertices labeled $0, 1, \ldots, 10$. *The labels on the edges indicate the order in which they are removed by the destruction process.*
Right: The corresponding tree of component sizes, with the vertex sets of the tree components. The elements $\mathcal{B}_u^{(n)}$ *of size* 0 *are omitted.*

label $\mathcal{B}_u^{(n)}$. Following the steps of the destruction process, we build this process dynamically starting from the singleton $\mathcal{B}_\emptyset^{(n)} = n+1$ and ending after n steps with the full process $\mathcal{B}^{(n)}$. More precisely, when the first edge of T_n is removed in the destruction process, T_n splits into two subtrees, say τ_n^0 and τ_n^*, where τ_n^0 contains the root 0. We stress that τ_n^0 is naturally rooted at 0 and τ_n^* at its smallest vertex. The size $|\tau_n^*|$ is viewed as the first child of $\mathcal{B}_\emptyset^{(n)}$ and denoted by $\mathcal{B}_1^{(n)}$. Now first suppose that the next edge which is removed connects two vertices in τ_n^*. Then, τ_n^* splits into two tree components. The size of the component not containing the root of τ_n^* is viewed as the first child of $\mathcal{B}_1^{(n)}$ and denoted by $\mathcal{B}_{11}^{(n)}$. On the other hand, if the second edge which is removed connects two vertices in τ_n^0, then the size of the component not containing 0 is viewed as the second child of $\mathcal{B}_\emptyset^{(n)}$ and denoted by $\mathcal{B}_2^{(n)}$. It should now be plain how to iterate this construction. After n steps, we have in this way defined $n+1$ variables $\mathcal{B}_u^{(n)}$ with $|u| \le n$, and we extend the definition to the full universal tree by letting $\mathcal{B}_u^{(n)} = 0$ for all the remaining $u \in \mathcal{U}$. We refer to Figure 2 for an example. The tree components whose sizes are encoded by the elements $\mathcal{B}_u^{(n)}$ with $|u| = k$ are called the components of generation k.

To sum up, every time an edge is removed in the destruction process, a tree component τ_n splits into two subtrees, and we adjoin the size of the subtree which does not contain the root of τ_n as a new child to the vertex representing τ_n. Note that the root $\mathcal{B}_\emptyset^{(n)}$ has X_n many nontrivial children, and they represent the sizes of the tree components which were cut from the root one after the other in the algorithm for isolating the root.

We now interpret $\mathcal{B}^{(n)}$ as the genealogical tree of a multi-type population model, where the type reflects the size of the tree component (and thus takes integer values). In particular the ancestor $\emptyset$ has type $n+1$; furthermore, a node u with $\mathcal{B}_u^{(n)} = 0$ corresponds to an empty component and is therefore absent in the population model. We also stress that the type of an individual is always given by the sum of the types of its children plus 1. As a consequence, types can be recovered from the sole structure of the genealogical tree. More precisely, the type of an individual is simply given by the total size of the subtree of the genealogical tree stemming from that individual.

The splitting property of a RRT immediately transfers into a branching property for this population model.

Lemma 3 *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 λ_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.*

Even though the coupling of Iksanov and Möhle is not sufficient to fully describe the reproduction law, it nonetheless provides essential information on λ_i in terms of a sequence of i.i.d. copies of ξ. As we will see next, extreme value theory for the i.i.d. sequence then enables us to specify asymptotics of the population model when the type $n+1$ of the ancestor goes to infinity.

To give a precise statement, we rank the children of each individual in the decreasing order of their types. Formally, given the individual indexed by $u \in \mathcal{U}$ has exactly ℓ children of type ≥ 1, we let σ_u be the random permutation of $\{1, \ldots, \ell\}$ which sorts the sequence of types $\mathcal{B}_{u1}^{(n)}, \ldots, \mathcal{B}_{u\ell}^{(n)}$ in the decreasing order, i.e.

$$\mathcal{B}_{u\sigma_u(1)}^{(n)} \geq \mathcal{B}_{u\sigma_u(2)}^{(n)} \geq \ldots \geq \mathcal{B}_{u\sigma_u(\ell)}^{(n)},$$

where in the case of ties, children of the same type are ranked uniformly at random. We extend σ_u to a bijection $\sigma_u : \mathbb{N} \to \mathbb{N}$ by putting $\sigma_u(i) = i$ for $i > \ell$.

We then define the global random bijection $\sigma = \sigma^{(n)} : \mathcal{U} \to \mathcal{U}$ recursively by setting $\sigma(\emptyset) = \emptyset$, $\sigma(j) = \sigma_\emptyset(j)$, and then, given $\sigma(u)$, $\sigma(uj) = \sigma(u)\sigma_{\sigma(u)}(j)$, $u \in \mathcal{U}$, $j \in \mathbb{N}$. Note that σ preserves the parent-child relationship, i.e. children of u are mapped into children of $\sigma(u)$. We simply write $(\mathcal{B}_u^{(n)\downarrow} : u \in \mathcal{U}) = (\mathcal{B}_{\sigma(u)}^{(n)} : u \in \mathcal{U})$ for the process which is ranked in this way.

Now, if the sizes of the components of generation k are normalized by a factor $\ln^k n/n$, we obtain finite-dimensional convergence of $\mathcal{B}^{(n)\downarrow}$ towards the genealogical tree of a continuous-state branching process with reproduction measure $\nu(da) = a^{-2}\mathrm{d}a$ on $(0, \infty)$. More precisely,

the limit object is a tree-indexed process $\mathcal{Z} = (\mathcal{Z}_u : u \in \mathcal{U})$ with initial state $\mathcal{Z}_\emptyset = 1$, whose distribution is characterized by induction on the generations as follows.

(*a*) $\mathcal{Z}_\emptyset = 1$ almost surely;

(*b*) for every $k = 0, 1, 2, \ldots$, conditionally on $(\mathcal{Z}_v : v \in \mathcal{U}, |v| \leq k)$, the sequences $(\mathcal{Z}_{uj})_{j\in\mathbb{N}}$ for the vertices $u \in \mathcal{U}$ at generation $|u| = k$ are independent, and each sequence $(\mathcal{Z}_{uj})_{j\in\mathbb{N}}$ is distributed as the family of the atoms of a Poisson random measure on $(0, \infty)$ with intensity $\mathcal{Z}_u\nu$, where the atoms are ranked in the decreasing order of their sizes.

Proposition 2 *As $n \to \infty$, there is the convergence in the sense of finite-dimensional distributions,*

$$\mathcal{Z}^{(n)} = \left(\frac{(\ln n)^{|u|}}{n} \mathcal{B}_u^{(n)\downarrow} : u \in \mathcal{U} \right) \Longrightarrow \mathcal{Z}.$$

We only sketch the proof and refer to the forthcoming paper [5] for details. Basically, if $\xi_1, \xi_2, \ldots$ is a sequence of of i.i.d. copies of ξ, then for $a > 0$, the number of indices $j \leq k$ such that $\xi_j \geq an/\ln n$ is binomially distributed with parameters k and $\lceil an/\ln n \rceil^{-1}$. From (11) and Theorem 16.16 in [26] we deduce that for a fixed integer j, the j largest among $\xi_1, \ldots, \xi_{L(n)}$, normalized by a factor $\ln n/n$, converge in distribution to the j largest atoms of a Poisson random measure on $(0, \infty)$ with intensity $\nu(da) = a^{-2}\mathrm{d}a$. Since $n - S_{L(n)} = o(n/\ln^2 n)$ in probability, finite-dimensional convergence of $\mathcal{Z}^{(n)}$ restricted to generations ≤ 1 then follows from (6). Lemma 3 enables us to transport the arguments to the next generations.

4.2 The cut-tree

Consider for a while a deterministic setting where T is an arbitrary tree on some finite set of vertices V. Imagine that its edges are removed one after the other in some given order, so at the end of the process, all the vertices of T have been disconnected from each other. We shall encode the destruction of T by a rooted binary tree, which we call the cut-tree and denote by $\mathrm{Cut}(T)$. The cut-tree has internal nodes given by the non-singleton connected components which arise during the destruction, and leaves which correspond to the singletons and which can thus be identified with the vertices in V. More precisely, the root of $\mathrm{Cut}(T)$ is given by V, and when the first edge of T is removed, disconnecting V into, say, V_1 and V_2, then V_1 and V_2 are viewed as the two children of V and thus connected to V by a pair of edges. Suppose that the next edge which is removed connects two vertices in V_1, so removing this second edge disconnects V_1 into, say $V_{1,1}$ and $V_{1,2}$. Then $V_{1,1}$ and $V_{1,2}$ are viewed in turn as the two children of V_1. We iterate in an obvious way, see Figure 3 for an example.

For the sake of simplicity, this notation does not record the order in which the edges are removed, although the latter is of course crucial in the definition of the cut-tree. In this part, we are concerned with uniform

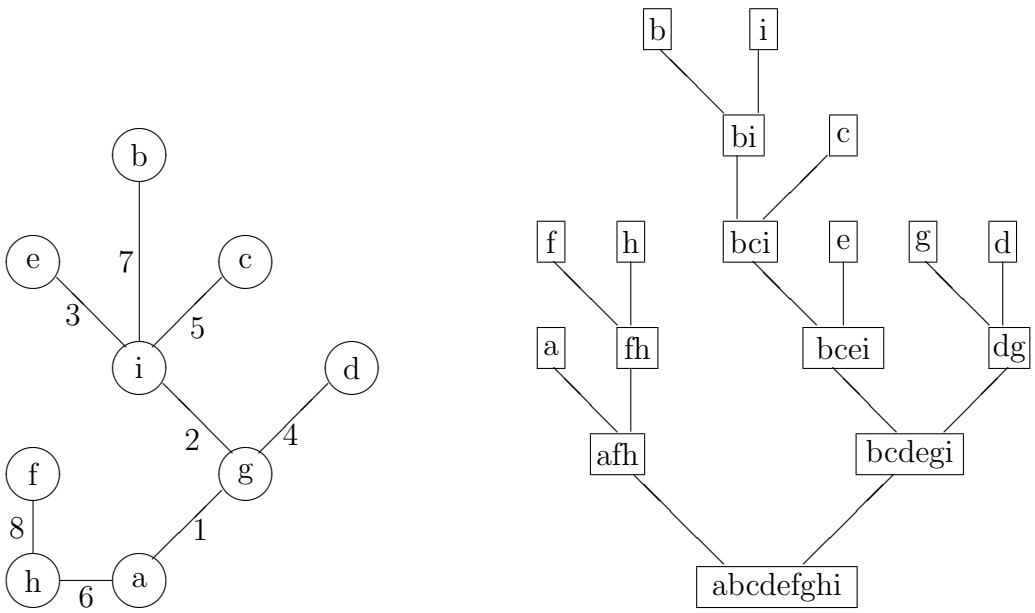

Figure 3

Left: Tree T with vertices labeled a,...,i; edges are enumerated in the order of the cuts. Right: Cut-tree $\mathrm{Cut}(T)$ *on the set of blocks recording the destruction of T.*

It should be clear that the number of cuts required to isolate a given vertex v in the destruction of T (as previously, we only count the cuts occurring in the component which contains v) corresponds precisely to the height of the leaf $\{v\}$ in $\mathrm{Cut}(T)$. More generally, the number of cuts required to isolate k distinct vertices $v_1, \ldots, v_k$ coincides with the total length of the cut-tree reduced to its root and the k leaves $\{v_1\}, \ldots, \{v_k\}$ minus $(k-1)$, where the length is measured as usual by the graph distance on $\mathrm{Cut}(T)$. In short, the cut-tree encapsulates all the information about the numbers of cuts needed to isolate any subset of vertices.

We now return to our usual setting, that is T_n is a RRT of size $n+1$, whose edges are removed in a uniform random order, and we write $\mathrm{Cut}(T_n)$ for the corresponding cut-tree. We point out that the genealogical tree of component sizes which was considered in the previous section can easily be recovered from $\mathrm{Cut}(T_n)$. Specifically, the root $\{0, 1, \ldots, n\}$ of $\mathrm{Cut}(T_n)$ has to be viewed as the ancestor of the population model, its type is of course $n+1$. Then the blocks of $\mathrm{Cut}(T_n)$ which are connected by an edge to the segment from the root $\{0, 1, \ldots, n\}$ to the leaf $\{0\}$ are the children of the ancestor in the population model, the type of a child being given by the size of the corresponding block. The next generations of the population model are

random edge removal, while in the last part of this section, we look at ordered destruction of a RRT, where edges are removed in the order of their endpoints most distant from the root.

then described similarly by an obvious iteration.

The segment of $\mathrm{Cut}(T_n)$ from its root $\{0, 1, \ldots, n\}$ to the leaf $\{0\}$ is described by the nested sequence (5), and the coupling of Iksanov and Möhle stated in Corollary 1 expresses the sequence of the block-sizes along the portion of this segment starting from the root and with length $L(n)$, in terms of the random walk S. We shall refer to this portion as the trunk of $\mathrm{Cut}(T_n)$ and denote it by $\mathrm{Trunk}(T_n)$. The connected components of the complement of the trunk, $\mathrm{Cut}(T_n)\backslash\mathrm{Trunk}(T_n)$ are referred to as the branches of $\mathrm{Cut}(T_n)$.

Roughly speaking, it has been shown in [10] that upon rescaling the graph distance of $\mathrm{Cut}(T_n)$ by a factor $n^{-1}\ln n$, the latter converges to the unit interval. The precise mathematical statement involves the notion of convergence of pointed measured metric spaces in the sense of the Gromov-Hausdorff-Prokhorov distance.

Theorem 2 *Endow* $\mathrm{Cut}(T_n)$ *with the uniform probability measure on its leaves, and normalize the graph distance by a factor* $n^{-1}\ln n$*. As* $n \to \infty$*, the latter converges in probability in the sense of the pointed Gromov-Hausdorff-Prokhorov distance to the unit interval* $[0, 1]$ *equipped with the usual distance and the Lebesgue measure, and pointed at* 0*.*

Providing the background on the Gromov-Hausdorff-Prokhorov distance needed to explain rigorously the meaning of Theorem 2 would probably drive us too far away from the purpose of this survey, so we shall content ourselves here to give an informal explanation. After the rescaling, each edge of $\mathrm{Cut}(T_n)$ has length $n^{-1}\ln n$, and it follows from (11) that the length $n^{-1}\ln n \times L(n)$ of $\mathrm{Trunk}(T_n)$ converges in probability to 1 as $n \to \infty$. Because the trunk is merely a segment, if we equip it with the uniform probability measure on its nodes, then we obtain a space close to the unit interval endowed with the Lebesgue measure. The heart of the argument of the proof in [10] is to observe that in turn, $\mathrm{Trunk}(T_n)$ is close to $\mathrm{Cut}(T_n)$ when n is large, both in the sense of Hausdorff and in the sense of Prokhorov. First, as $\mathrm{Trunk}(T_n)$ is a subset of $\mathrm{Cut}(T_n)$, the Hausdorff distance between $\mathrm{Trunk}(T_n)$ and $\mathrm{Cut}(T_n)$ corresponds to the maximal depth of the branches of $\mathrm{Cut}(T_n)$, and one thus have to verify that all the branches are small (recall that the graph distance has been rescaled by a factor $n^{-1}\ln n$). Then, one needs to check that the uniform probability measures, respectively on the set of leaves of $\mathrm{Cut}(T_n)$ and on the nodes of $\mathrm{Trunk}(T_n)$, are also close to each other in the sense of the Prokhorov distance between probability measures on a metric space. This is essentially a consequence of the law of large numbers for the random walk defined in (3), namely

$$\lim_{n\to\infty} \frac{S_n}{n \ln n} = 1 \qquad \text{in probability;}$$

see (10).

4.3 Applications

Theorem 2 enables us to specify the asymptotic behavior of the number of cuts needed to isolate randomly chosen vertices of T_n. For a given integer $\ell \geq 1$ and for each $n \geq 1$, let $U_1^{(n)}, \ldots, U_\ell^{(n)}$ denote a sequence of i.i.d. uniform variables in $\{0, 1, \ldots, n\}$. We write $Y_{n,\ell}$ for the number of random cuts which are needed to isolate $U_1^{(n)}, \ldots, U_\ell^{(n)}$. The following corollary, which is taken from [10], is a multi-dimensional extension of Theorem 3 of Kuba and Panholzer [29].

Corollary 3 *As $n \to \infty$, the random vector*

$$\left(\frac{\ln n}{n} Y_{n,1}, \ldots, \frac{\ln n}{n} Y_{n,\ell}\right)$$

converges in distribution to

$$(U_1, \max\{U_1, U_2\}, \ldots, \max\{U_1, \ldots, U_\ell\}),$$

where $U_1, \ldots, U_\ell$ are i.i.d. uniform $[0, 1]$ random variables. In particular, $\frac{\ln n}{n} Y_{n,\ell}$ converges in distribution to a beta$(\ell, 1)$ variable.

Proof: Recall that $U_1^{(n)}, \ldots, U_\ell^{(n)}$ are ℓ independent uniform vertices of T_n. Equivalently, the singletons $\{U_1^{(n)}\}, \ldots, \{U_\ell^{(n)}\}$ form a sequence of ℓ i.i.d. leaves of $\mathrm{Cut}(T_n)$ distributed according to the uniform law. Let also $U_1, \ldots, U_l$ be a sequence of ℓ i.i.d. uniform variables on $[0, 1]$. Denote by $\mathcal{R}_{n,\ell}$ the reduction of $\mathrm{Cut}(T_n)$ to the ℓ leaves $\{U_1^{(n)}\}, \ldots, \{U_\ell^{(n)}\}$ and its root $\{0, 1, \ldots, n\}$, i.e. $\mathcal{R}_{n,\ell}$ is the smallest subtree of $\mathrm{Cut}(T_n)$ which connects these nodes. Similarly, write $\mathcal{R}_\ell$ for the reduction of I to $U_1, \ldots, U_\ell$ and the origin 0. Both reduced trees are viewed as combinatorial trees structures with edge lengths, and Theorem 2 entails that $n^{-1} \ln n \mathcal{R}_{n,\ell}$ converges in distribution to $\mathcal{R}_\ell$ as $n \to \infty$. In particular, focusing on the lengths of those reduced trees, there is the weak convergence

$$\lim_{n\to\infty} \left(\frac{\ln n}{n} |\mathcal{R}_{n,1}|, \ldots, \frac{\ln n}{n} |\mathcal{R}_{n,\ell}|\right) = (|\mathcal{R}_1|, \ldots, |\mathcal{R}_\ell|) \qquad \text{in distribution.} \tag{13}$$

This yields our claim, as plainly $|\mathcal{R}_i| = \max\{U_1, \ldots, U_i\}$ for every $i = 1, \ldots, \ell$. □

Remark. The nearly trivial proof of this corollary exemplifies the power of Theorem 2, and one might ask for convergence of the cut-tree for other tree models. In fact, employing the work of Haas and Miermont [20], it has been shown in [6] that if $T_n^{(c)}$ is a uniform Cayley tree of size n, then $n^{-1/2}\mathrm{Cut}(T_n^{(c)})$ converges weakly in the sense of Gromov-Hausdorff-Prokhorov to the Brownian Continuum Random Tree (CRT), see Aldous [2]. Since the total length of the CRT reduced to the root and ℓ i.i.d leaves picked according to its mass-measure follows the

Chi(2ℓ)-distribution, one readily obtains the statement corresponding to Corollary 3 for uniform Cayley trees ([6] and also, by different means, [1]). Bertoin and Miermont [12] extended the convergence of the cut-tree towards the CRT to the full family of critical Galton-Watson trees with finite variance and conditioned to have size n, in the sense of Gromov-Prokhorov. As a corollary, one obtains a multi-dimensional extension of Janson's limit theorem [25]. Very recently, Dieuleveut [15] proved the analog of [12] for the case of Galton-Watson trees with offspring distribution belonging to the domain of attraction of a stable law of index $\alpha \in (1, 2)$.

With Corollary 3 at hand, we can also study the number $Z_{n,\ell}$ of random cuts which are needed to isolate the ℓ *last* vertices of T_n, i.e. $n - \ell + 1, \ldots, n$, where $\ell \geq 1$ is again a given integer. As Kuba and Panholzer [29] proved in their Theorem 2, $Z_{n,\ell}$ has the same asymptotic behavior in law as $Y_{n,\ell}$. The following multi-dimensional version was given in [10], relying on Theorem 2 of [29]. Here we give a self-contained proof of the same statement.

Corollary 4 *As $n \to \infty$, the random vector*

$$\left(\frac{\ln n}{n} Z_{n,1}, \ldots, \frac{\ln n}{n} Z_{n,\ell}\right)$$

converges in distribution to

$$(U_1, \max\{U_1, U_2\}, \ldots, \max\{U_1, \ldots, U_\ell\}),$$

where $U_1, \ldots, U_\ell$ are i.i.d. uniform $[0, 1]$ random variables.

Proof: For ease of notation, we consider only the case $\ell = 1$, the general case being similar. The random variable $Z_n = Z_{n,1}$ counts the number of random cuts needed to isolate the vertex n, which is a leaf of T_n. If we write v for the parent of n in T_n, then v is uniformly distributed on $\{0, 1, \ldots, n-1\}$, and it follows that the number Y'_n of cuts needed to isolate v has the same limit behavior in law as $Y_{n-1,1}$. In view of Corollary 3, it suffices therefore to verify that

$$\lim_{n\to\infty} \frac{\ln n}{n} (Y'_n - Z_n) = 0 \qquad \text{in probability.}$$

We now consider the algorithm for isolating the vertex v. Clearly, the number of steps of this algorithm until the edge e joining v to n is removed is distributed as Z_n. In particular, we obtain a natural coupling between Y'_n and Z_n with $Z_n \leq Y'_n$. Denote by $[0; n]$ the segment of T_n from the root 0 to the leaf n, and write k for the outer endpoint of the first edge from $[0; n]$ which is to be removed by the isolation algorithm. Since $|[0; n]| \sim \ln n$ in probability (see e.g. Theorem 6.17 of [16]), and since the isolation algorithm chooses its edges uniformly at random, the probability that k is equal to n tends to zero. Moreover, with high probability $|[k; n]|$ will

still be larger than $(\ln n)^{1/2}$, say. By conditioning on k and repeating the above argument with $[k;n]$ in place of $[0;n]$, we see that we can concentrate on the event that before n is isolated, at least two edges different from e are removed from the segment $[0;n]$. On this event, after the second time an edge from $[0;n]$ is removed, the vertices v and n lie in a tree component which can be interpreted as a tree component of the second generation in the destruction process. As a consequence of Proposition 2, the size of this tree component multiplied by factor $\ln n/n$ converges to zero in probability. Since the size of the component gives an upper bound on the difference $Y'_n - Z_n$, the claim follows. $\square$

As another application of the cut-tree, Theorem 2 allows us to determine the number of cuts $A_{n,\ell}$ which are required to *disconnect* (and not necessarily isolate) $\ell \geq 2$ vertices in T_n chosen uniformly at random. For ease of description, let us assume that the sequence of vertices $U_1^{(n)}, \ldots, U_\ell^{(n)}$ is chosen uniformly at random in $\{0, 1, \ldots, n\}$ without replacement. Note that in the limit $n \to \infty$, it makes no difference whether we sample with or without replacement.

We run the algorithm for isolating the vertices $U_1^{(n)}, \ldots, U_\ell^{(n)}$, with the modification that we discard emerging tree components which contain at most one of these ℓ vertices. We stop the algorithm when $U_1^{(n)}, \ldots, U_\ell^{(n)}$ are totally disconnected from each other, i.e. lie in ℓ different tree components. Write $A_{n,2}$ for the (random) number of steps of this algorithm until for the first time, the vertices $U_1^{(n)}, \ldots, U_\ell^{(n)}$ do no longer belong to the same tree component, further $A_{n,3}$ for the number of steps until for the first time, the ℓ vertices are spread out over three distinct tree components, and so on, up to $A_{n,\ell}$, the number of steps until the ℓ vertices are totally disconnected. We obtain the following result.

Corollary 5 *As $n \to \infty$, the random vector*

$$\left(\frac{\ln n}{n} A_{n,2}, \ldots, \frac{\ln n}{n} A_{n,\ell}\right)$$

converges in distribution to

$$\left(U_{(1,\ell)}, \ldots, U_{(\ell-1,\ell)}\right),$$

where $U_{(1,\ell)} \leq U_{(2,\ell)} \leq \cdots \leq U_{(\ell-1,\ell)}$ denote the first $\ell - 1$ order statistics of an i.i.d. sequence $U_1, \ldots, U_\ell$ of uniform $[0,1]$ random variables.

In particular, $\frac{\ln n}{n} A_{n,2}$ converges in distribution to a beta$(1,\ell)$ random variable, and $\frac{\ln n}{n} A_{n,\ell}$ converges in distribution to a beta$(\ell-1, 2)$ law.

Proof: Since the branches of $\mathrm{Cut}(T_n)$ are asymptotically small compared to the trunk (see e.g. Proposition 1 in [10]), with probability tending to 1 as $n \to \infty$ the ℓ vertices $U_1^{(n)}, \ldots, U_\ell^{(n)}$ are cut from the root component one after the other, i.e. in no stage of the disconnection algorithm, a non-root tree component will contain more than one of the $U_1^{(n)}, \ldots, U_\ell^{(n)}$. On this

event, writing again $\mathcal{R}_{n,\ell}$ for the reduction of $\mathrm{Cut}(T_n)$ to the ℓ leaves $\{U_1^{(n)}\}, \ldots, \{U_\ell^{(n)}\}$ and its root $\{0, 1, \ldots, n\}$, the variable $A_{n,i+1} - 1$ is given by the length of the path in $\mathcal{R}_{n,\ell}$ from the root to the ith branch point. Now, if $U_1, \ldots, U_\ell$ and $\mathcal{R}_\ell$ are defined as in the proof of Corollary 3, the distance in $\mathcal{R}_\ell$ from the root 0 to the ith smallest among $U_1, \ldots, U_\ell$ is distributed as $U_{(i,\ell)}$. Together with (13), this proves the claim.

Remark. With a proof similar to that of Corollary 4, one sees that the statement of Corollary 5 does also hold if $A_{n,2}, \ldots, A_{n,\ell}$ are replaced by the analogous quantities for disconnecting the ℓ last vertices $n-\ell+1, \ldots, n$. On the other hand, if one is interested in disconnecting the first ℓ vertices $0, \ldots, \ell-1$, and if $B_{n,2}, \ldots, B_{n,\ell}$ denote in this case the quantities corresponding to $A_{n,2}, \ldots, A_{n,\ell}$, one first observes the trivial bound

$$B_{n,2} \leq \cdots \leq B_{n,\ell} \leq X_{n,\ell},$$

where $X_{n,\ell}$ is the number of steps needed to isolate $0, 1, \ldots, \ell-1$. Now, $B_{n,2}$ can be identified with the number of steps in the algorithm for isolating the root until for the first time, an edge connecting one of the vertices $1, \ldots, \ell-1$ to its parent is removed. By similar means as in the proof of Lemma 2, one readily checks that at this time, the root component has a size of order n^β, with β having a beta$(\ell-1, 1)$-distribution. In particular, we see that $(X_n - B_{n,2}) = o(n/\ln^2 n)$ in probability, where X_n is the number of steps to isolate the root 0. But by (12), also $(X_n - X_{n,\ell}) = o(n/\ln^2 n)$ in probability. Therefore, the variables $B_{n,i}$ have the same limit behavior in law as X_n, that is as $n \to \infty$, $\frac{\ln^2 n}{n} B_{n,i} - \ln n - \ln\ln n$, $i = 2, \ldots, \ell$, converge all to the same completely asymmetric Cauchy variable X defined by (8).

4.4 Ordered destruction

Here, we consider briefly another natural destruction procedure of a RRT, where instead of removing edges in a uniform random order, we remove them deterministically in their *natural* order. That is the ith edge of T_n which is removed is now the one connecting the vertex i to its parent, for $i = 1, \ldots, n$.

We first point at the fact that the number of ordered edge removals which are now needed to isolate the root (recall that we only take into account edge removals inside the current subtree containing the root) can be expressed as $d_n(0) = \beta_1 + \cdots + \beta_n$, where $\beta_i = 1$ if the parent of vertex i in T_n is the root 0, and 0 otherwise. That is to say that $d_n(0)$ is the degree of the root. Further the recursive construction entails the β_i are independent variables, such that each β_i has the Bernoulli distribution with parameter $1/i$. As is well-known, it then follows e.g. from

Lyapunov's central limit theorem that

$$\lim_{n\to\infty} \frac{d_n(0) - \ln n}{\sqrt{\ln n}} = \mathcal{N}(0,1) \qquad \text{in distribution.}$$

We refer to Kuba and Panholzer [27] for many more results about the degree distributions in random recursive trees.

We then turn our attention to the cut-tree described in Section 4.2, which encodes the ordered destruction of T_n. We write $\mathrm{Cut}^{\mathrm{ord}}(T_n)$ for the latter and observe that the recursive construction of T_n implies that in turn, $\mathrm{Cut}^{\mathrm{ord}}(T_n)$ can also be defined by a simple recursive algorithm. Specifically, $\mathrm{Cut}^{\mathrm{ord}}(T_1)$ is the elementary complete binary tree with two leaves, $\{0\}$ and $\{1\}$, and root $\{0,1\}$. Once T_n and hence $\mathrm{Cut}^{\mathrm{ord}}(T_n)$ have been constructed, T_{n+1} is obtained by incorporating the vertex $n+1$ and creating a new edge between $n+1$ and its parent U_{n+1}, which is chosen uniformly at random in $\{0,1,\ldots,n\}$. Note that this new edge is the last one which will be removed in the ordered destruction of T_{n+1}. In terms of cut-trees, this means that the leaf $\{U_{n+1}\}$ of $\mathrm{Cut}^{\mathrm{ord}}(T_n)$ should be replaced by an internal node $\{U_{n+1}, n+1\}$ to which two leaves are attached, namely $\{U_{n+1}\}$ and $\{n+1\}$. Further, any block (internal node) B of $\mathrm{Cut}^{\mathrm{ord}}(T_n)$ with $U_{n+1} \in B$ should be replaced by $B \cup \{n+1\}$. The resulting complete binary tree is then distributed as $\mathrm{Cut}^{\mathrm{ord}}(T_{n+1})$.

If we discard labels, this recursive construction of $\mathrm{Cut}^{\mathrm{ord}}(T_n)$ corresponds precisely to the dynamics of the Markov chain on complete binary trees described e.g. in Mahmoud [30] for Binary Search Trees (in short, BST). We record this observation in the following proposition.

Proposition 3 *The combinatorial tree structure of* $\mathrm{Cut}^{\mathrm{ord}}(T_n)$ *is that of a BST with* $n+1$ *leaves.*

BST have been intensively studied in the literature, see Drmota [16] and references therein, and the combination with Proposition 3 yields a number of precise results about the number of ordered cuts which are needed to isolate vertices in T_n. For instance, the so-called *saturation level* $\bar{H}_n$ in a BST is the minimal level of a leaf, and can then be viewed as the smallest number of ordered cuts after which some vertex of T_n has been isolated. Similarly, the height H_n is the maximal level of a leaf, and thus corresponds to the maximal number of ordered cuts needed to isolate a vertex in T_n. The asymptotic behaviors of the height and of the saturation level of a large BST are described in Theorem 6.47 of Drmota [16], in particular one has

$$\lim_{n\to\infty} \frac{\bar{H}_n}{\ln n} = \alpha_- \quad \text{and} \quad \lim_{n\to\infty} \frac{H_n}{\ln n} = \alpha_+$$

where $0 < \alpha_- < \alpha_+$ are the solutions to the equation $\alpha \ln(2\mathrm{e}/\alpha) = 1$. In the same vein, the asymptotic results of Chauvin *et al.* on the profile of large BST can be translated into sharp

estimates for the number of vertices of T_n which are isolated after exactly k ordered cuts (see in particular Theorem 3.1 in [14]).

Finally, let us look at component sizes when edges are removed in their natural order. Compared to uniform random edge removal, the picture is fairly different. Indeed, when removing an edge from T_n picked uniformly at random, the size of the subtree not containing 0 is distributed according to the law of ξ conditioned on $\xi \leq n$. If, in contrast, the first edge to be removed is the edge joining 1 to its parent 0, then we know from (1) that both originating subtrees are of order n. Since the splitting property still holds when we remove a fixed edge, the component sizes again inherit a branching structure. In fact, it is an immediate consequence of the definition that the structure of the tree of component sizes corresponding to the ordered destruction on T_n agrees with the structure of T_n and therefore yields the same RRT of size $n+1$.

5 Supercritical percolation on RRT's

5.1 Asymptotic sizes of percolation clusters

In Section 3 it has become apparent that Bernoulli bond percolation on T_n is a tool to study the sizes of tree components which appear in isolation algorithms. Here, we take in a certain sense the opposite point of view and obtain results on the sizes of percolation clusters using what we know about the sizes of tree components. Throughout this section, we use the term cluster to designate connected components induced by percolation, while we use the terminology tree components for connected components arising from isolation algorithms.

More specifically, the algorithm for isolating the root can be interpreted as a dynamical percolation process in which components that do not contain the root are instantaneously frozen. Imagine a continuous-time version of the algorithm, where each edge of T_n is equipped with an independent exponential clock of some parameter α. When a clock rings, the corresponding edge is removed if and only if it currently belongs to the root component. At time $t > 0$, the root component can naturally be viewed as the root cluster of a Bernoulli bond percolation on T_n with parameter $p = \exp(-\alpha t)$. Moreover, under this coupling each percolation cluster is contained in some tree component which was generated by the isolation process up to time t. In order to discover the percolation clusters inside a non-root tree component T', the latter has to be unfrozen, i.e. additional edges from T' have to be removed. In particular, the percolation cluster containing the root of T' can again be identified as the root component of an isolation process on T', stopped at an appropriate time.

These observations lead in [8] to the study of the asymptotic sizes of the largest and next

largest percolation clusters of T_n, when the percolation parameter $p(n)$ satisfies

$$p(n) = 1 - \frac{t}{\ln n} + o(1/\ln n) \qquad \text{for } t > 0 \text{ fixed.} \tag{14}$$

This regime corresponds precisely to the supercritical regime, in the sense that the root cluster is the unique giant cluster, and its complement in T_n has a size of order n, too. Indeed, the height h_n of a vertex u picked uniformly at random in a RRT of size $n+1$ satisfies $h_n \sim \ln n$. Since the probability that u is connected to the root is given by the first moment of $(n+1)^{-1}C_{0,n}$, where $C_{0,n}$ denotes the size of the root cluster, one obtains

$$\mathbb{E}((n+1)^{-1}C_{0,n}) = \mathbb{E}\left(p(n)^{h_n}\right) \sim \mathrm{e}^{-t}.$$

A similar argument shows $\mathbb{E}((n^{-1}C_{0,n})^2) \sim \mathrm{e}^{-2t}$, which proves $\lim_{n\to\infty} n^{-1}C_{0,n} = \mathrm{e}^{-t}$ in $L^2(\mathbb{P})$.

Let us now consider the next largest clusters in the regime (14). We write $C_{1,n}, C_{2,n}, \ldots$ for the sizes of the non-root percolation clusters of T_n, ranked in the decreasing order. We quote from [8] the following limit result.

Proposition 4 *For every fixed integer $j \geq 1$,*

$$\left(\frac{\ln n}{n}C_{1,n}, \ldots, \frac{\ln n}{n}C_{j,n}\right)$$

converges in distribution as $n \to \infty$ towards

$$(x_1, \ldots, x_j),$$

where $x_1 > x_2 > \ldots$ denotes the sequence of the atoms of a Poisson random measure on $(0,\infty)$ with intensity $t\mathrm{e}^{-t}x^{-2}\mathrm{d}x$.

The intensity is better understood as the image of the intensity measure $a^{-2}\mathrm{d}a \otimes \mathrm{e}^{-s}\mathrm{d}s$ on $(0,\infty) \times (0,t)$ by the map $(a,s) \mapsto x = \mathrm{e}^{-(t-s)}a$. In fact, from our introductory remarks and Proposition 2 it should be clear that the first coordinate of an atom (a,s) stands for the asymptotic (and normalized) size of the tree component containing the percolation cluster, while the second encodes the time when the component was separated from the root.

Instead of providing more details here, let us illustrate an alternative route to prove the proposition, which was taken in [11] to generalize the results to *scale-free random trees*. These random graphs form a family of increasing trees indexed by a parameter $\beta \in (-1,\infty)$ that grow according to a preferential attachment algorithm, see [3]. In the boundary case $\beta \to \infty$, one obtains a RRT, while in the case $\beta = 0$, the ith vertex is added to one of the first $i-1$

vertices with probability proportional to its current degree. In [11], the connection of scale-free random trees to the genealogy of Yule processes was employed, and it should not come as a surprise that this approach can be adapted to random recursive trees. In fact, the case of RRT's is considerably simpler, since one has not to keep track of the degree of vertices when edges are deleted. Let us sketch the main changes. Denote by $T(s)$ the genealogical tree of a standard Yule process $(\mathcal{Y}_r)_{r\geq 0}$ at time s. Similar to Section 3 of [11], we superpose Bernoulli bond percolation with parameter $p = p(n)$ to this construction. Namely, if a new vertex is attached to the genealogical tree, we delete the edge connecting this vertex to its parent with probability $1 - p$. We write $T^{(p)}(s)$ for the resulting combinatorial structure at time s, and $T_0^{(p)}(s), T_1^{(p)}(s), \ldots$ for the sequence of the subtrees at time s, enumerated in the increasing order of their birth times, where we use the convention that $T_j^{(p)}(s) = \emptyset$ if less than j edges have been deleted up to time s. In particular, $T_0^{(p)}(s)$ is the subtree containing the root 0, and $\sum_{i\geq 0} |T_i^{(p)}(s)| = \mathcal{Y}_s$. Furthermore, if $b_i^{(p)}$ denotes the birth time of the ith subtree, then the process $(T_i^{(p)}(b_i^{(p)} + s) : s \geq 0)$ is a Yule process with birth rate p per unit population size, started from a single particle of size 1. By analyzing the birth times as in [11], one readily obtains the analogous statements of Section 2 and 3 there. This leads to another proof of Proposition 4.

Remark. As it is shown in the forthcoming paper [5], the approach via Yule processes can be extended further to all percolation regimes $p(n) \to 1$. Moreover, if the entire family of cluster sizes is encoded by a tree structure similar to the tree of component sizes, one can specify the finite-dimensional limit of this "tree of cluster sizes". Details will be given in [5].

5.2 Fluctuations of the root cluster

We finally take a closer look at the size of the root cluster $C_{0,n}$ for supercritical percolation with parameter

$$p(n) = 1 - \frac{t}{\ln n}.$$

As we have already discussed, $C_{0,n}$ satisfies a law of large numbers, but as we will point out here, $C_{0,n}$ exhibits non-Gaussian fluctuations. This should be seen in sharp contrast to other graph models, were asymptotic normality of the giant cluster has been established, e.g. for the complete graph on n vertices and percolation parameter c/n, $c > 1$ fixed (Stephanov [38], Pittel [36], Barraez *et al.* [4]).

For RRT's, the fluctuations can be obtained from a recent result of Schweinsberg [37]. Among other things, he studied how the number of blocks in the Bolthausen-Sznitman coalescent changes over time. The Bolthausen-Sznitman coalescent was introduced in [13] in the context of spin glasses, and Goldschmidt and Martin [19] discovered the following connection to the

random cutting of RRT's: Equip each edge of a RRT of size n on the vertex set $\{1,\dots,n\}$ with an independent standard exponential clock. If a clock rings, delete the corresponding edge, say e, and the whole subtree rooted at the endpoint of e most distant from the root 1. Furthermore, replace the label of the vertex of e which is closer to the root 1, say i, by the label set consisting of i and all the vertex labels of the removed subtree. Then the sets of labels form a partition of $\{1,\dots,n\}$, which evolves according to the dynamics of the Bolthausen-Sznitman coalescent started from n blocks $\{1\},\dots,\{n\}$ (see Proposition 2.2 of [19] for details).

Note that in this framework, the variable X_n counting the number of steps in the algorithm for isolating the root can be interpreted as the number of collision events which take place until there is just one block left.

Theorem 1.7 in [37], rephrased in terms of $C_{0,n}$, now reads as follows.

Theorem 3 (Schweinsberg [37]) *There is the weak convergence*

$$\left(n^{-1}C_{0,n}-\mathrm{e}^{-t}\right)\ln n - t\mathrm{e}^{-t}\ln\ln n \Longrightarrow t\mathrm{e}^{-t}(X-\ln t),$$

where X is a completely asymmetric Cauchy variable whose law is determined by (8).

This statement was re-proved in [9], with a different approach which does not rely on the Bolthausen-Sznitman coalescent. Instead, three different growth phases of a RRT T_n are considered, and the effect of percolation is studied in each of these phases. This approach makes again use of the coupling of Iksanov and Möhle and the connection to Yule processes, providing an intuitive explanation for the correction terms in the statement.

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