A RANDOM GRAPH MODEL DRIVEN
BY TIME-DEPENDENT BRANCHING DYNAMICS

Tamás F. Móri and Sándor Rokob

(Budapest, Hungary)

Dedicated to the memory of Professor Antal Iványi

Abstract. Consider an increasing group of individuals who are organized by pairwise collaborations. A successful collaboration attracts newcomers, who start collaborating with one or both participants. However, the new connections can weaken and exhaust the attracting pair's collaboration, which eventually ceases. We investigate the corresponding random graph process in the framework of general time-dependent branching processes.

1. Introduction

Consider an increasing group of individuals who are organized by pairwise collaborations. A successful collaboration attracts newcomers, who start collaborating with one or both participants. However, the new connections can weaken and exhaust the attracting pair's collaboration, which eventually ceases. Representing collaborations with edges, we get an evolving graph process.

Just for a moment, suppose that the edges cannot run low. In the case where the newcomers always collaborate with both participants, the model is reduced to the so-called random cherry tree. Cherry trees were introduced by

Bukszár and Prékopa [4] for constructing Bonferroni type upper bounds of third order for the probability of the union of random events. On the other hand, the opposite extremal parametrization, where the new node is connected to exactly one of the chosen collaborating edge's endpoint, leads to the intensively studied Barabási–Albert random tree. Many properties of this model, such as the asymptotic degree distribution, the maximal degree, the height, or the profile of the tree, and so on, have already been investigated.

Although the techniques used in the proofs of the preceding results strongly depend on martingale theory, there is another, very natural way to answer questions of these kind (which, however, is also closely connected with martingales). Considering the new edges (collaborations) as the attractor edge's children, we can model our graph process in the context of general time-dependent branching processes. Such processes are widely applied in the theory of random graphs and networks, especially when the ancestor-descendant relationship is prescribed between the nodes of the randomly evolving graph.

An early usage of this embedding is due to Devroye [5], who has shown, with the help of the Galton–Watson process, that the height of a random binary search tree on n vertices, divided by $\log n$, converges to a constant in probability and in mean. Later, this result was generalized to random recursive and m-ary search trees by Pittel in [21] by using the fact that the consecutive states of the evolving graph can be considered as the sequence of the general branching process' "snapshots". As pointed out by Biggins and Gray in [2], these random trees (and others like the random binary pyramid [15]) are all just particular cases of a general randomly evolving tree, the height of which can be computed similarly, by using general branching processes. Further applications of general (and some special) branching processes in the analysis of the properties of tree-type data structures can be found in [6].

Due to the popularity of the Barabási-Albert random graph model, this branching process approach is often used in the analysis of random trees that evolve with preferential attachment-like dynamics, that is, vertices are chosen with probabilities proportional to some function of their degrees. The model introduced by Athreya, Ghosh and Sethuraman [1] uses a weight function which is linear in the chosen node's degree, and the new vertex connects with a random number of edges. Embedding in a Markov branching process allows of the extensions of the law of large numbers and the asymptotics of the growth rate of the maximal degree. The class of linear weight functions can be extended as in [13] and [14], still ensuring that the limiting degree sequence is not trivial in the sense that there won't be a single dominant vertex. Oliveira and Spencer showed [20] that if the weight function is chosen to be the power of the degree, then its exponent cannot exceed 1. A general form of sublinear preferential attachment models is considered by Rudas and Tóth in [23]. The authors, basing again on general branching processes, give local results

concerning the neighborhood of a uniformly sampled vertex, and also global ones on the probability that a randomly choosen node is a descendant of a fixed vertex. It is worth mentioning the work of Jog and Loh [11], where the terminal centrality of a similar random graph is analyzed with the branching process approach. Recently, various other randomly evolving tree models, like fringe trees and fragmentation trees, have also been investigated with the help of general branching processes in the survey [9] of Holmgren and Janson, see also [7] and [22].

Our approach is different from the former ones in the sense that edges, not vertices, are subject to branching. Since in our model the embedding of the graph in the branching process takes place through the edges, the resulting structure loses its tree-like nature. Hence, it does not fit into the above framework of random graph models.

The paper is organized as follows. In Section 2 we briefly summarize what we will use from the theory of general time-dependent branching processes. In Section 3 a continuous time random graph model is introduced, which can be treated with the tools of Section 2. The asymptotic analysis of the model is carried out in Sections 4, 5, and 6. Section 4 contains results on the life history of an edge. We compute the survival function and the expectation of the life span of an edge, and the distribution of the number of edges considered its direct descendants. Section 5 deals with the evolution of the graph process: the probability of extinction, the growth rate of the numbers of edges and vertices, and the number of birth or death events. In Section 6, we focus on the history of a vertex: how its degree varies with time. Section 7 introduces a slowed down discrete time version of the graph process, where at every step either a new vertex with a new edge or edges are added to the graph, or an edge is deleted. The results obtained for the continuous time model can easily be transferred to this case. Finally, Section 8 emphasises two particular cases which give back well known graph processes but with the extra feature of aging edges.

2.   Basic properties of Crump–Mode–Jagers processes

In this section, we give an informal introduction to general time dependent branching processes, or Crump–Mode–Jagers (CMJ) processes. The interested reader may find more formal descriptions in the monographs [10] or [8].

In a CMJ branching process there are individuals who reproduce and die. This is characterized by a random point process $\xi(t)$, called the reproduction process, and a nonnegative random variable λ, which is the life span. They

are not supposed to be independent. Most often there is no reproduction after death, i.e., $\xi(t) = \xi(\lambda)$ for $t > \lambda$ (but this is not necessarily required). Let $\mu(t) = E\xi(t)$ denote the mean offspring number of an individual up to time t.

The reproduction process $\xi(t)$ can be equivalently given by the successive birth times $\tau_1, \tau_2, \ldots$, and the corresponding litter sizes $\varepsilon_1, \varepsilon_2, \ldots$. Thus the total number of children born in the first n birth events is $S_n = \varepsilon_1 + \cdots + \varepsilon_n$.

The life history of every individual e is described by the pair $(\xi_e(\cdot), \lambda_e)$; they are iid copies of $(\xi(\cdot), \lambda)$ introduced above. If individual e was born at time σ_e, then at time t the number of its children (dead or alive) is $\xi_e(t - \sigma_e)$ ($\xi_e(t)$ is defined as zero for negative t), and it deceases at time $\sigma_e + \lambda_e$.

Now let $\xi(\cdot)$ and λ be completed with another random process $\phi(\cdot)$, which is connected with the history of an individual, and supposed to change exclusively during the lifetime: $\phi(t) = 0$ for $t \leq 0$ and $\phi(t) = \phi(\lambda)$ for $t \geq \lambda$. This ϕ is called a random characteristic. We are interested in the stochastic process

$$Z^\phi(t) = \sum_e \phi_e(t - \sigma_e),$$

called *the time-dependent branching process counted by random characteristics*. By suitably choosing ϕ we can access the evolution of interesting properties of our process. For instance, $\phi(t) = I(0 \leq t < \lambda)$ produces $Z^\phi(t) = Z(t)$, the number of individuals alive at time t.

The following results can be found in [10] and [19].

The individuals being present at time zero form the 0-th generation (ancestors). Most often the process starts with a single ancestor. Children of the k-th generation form the $(k + 1)$-st generation. Since an individual can give birth at different times, the generations overlap: several generations coexist. Only concentrating on generations we find an embedded Galton–Watson branching process, which makes it easier to analyze the problem of extinction. Clearly, a CMJ process dies out eventually if and only if there exists an empty generation. The total size of progeny of an individual is $\xi(\infty)$. Like the classical Galton–Watson processes, CMJ processes are classified according to the expected number of children. A process is called *subcritical, critical, or supercritical*, if $E\xi(\infty) = \mu(\infty)$ is less than, equal to, or greater than 1, respectively. Suppose the process starts with a single ancestor. Let $g_\xi(y) = E(y^{\xi(\infty)})$, $|y| \leq 1$, the probability generating function of the total number of children, then the probability of extinction is equal to the smallest nonnegative solution of equation $g_\xi(y) = y$. In the case where the number of ancestors is a random variable with generating function g_0, the probability of extinction is equal to $g_0(y)$, where y is the extinction probability for a process with a single ancestor. Extinction is almost sure in subcritical and critical processes, while its probability is less than one for supercritical processes.

In the sequel we are interested in supercritical processes. We do not intend to formulate the basic results in their most general forms, because we want to apply them to a model with nice properties. Therefore we suppose that $1 < E\xi(\infty) < \infty$, and the Lebesgue–Stieltjes measure generated by μ is not lattice, i.e., it is not concentrated on a set of the form $\{ku + v : k \in \mathbb{Z}\}$ with $u > 0$, $v \in \mathbb{R}$.

Such processes grow exponentially fast on the event of non-extinction. The rate of growth is described by the so called *Malthusian parameter* α. It is the only positive solution of the equation

$$\int_0^\infty e^{-\alpha t} \mu(dt) = 1.$$

Combining Proposition 2.2, Theorems 3.1 and 5.4 of [19] we get the following limit theorem.

Proposition 2.1. *Suppose the random characteristic ϕ satisfies the following conditions:*

(i) *$\phi(t) \geq 0$,*

(ii) *the trajectories of ϕ belong to the Skorohod D-space, that is, they do not have discontinuities of the second kind,*

(iii) *$E[\sup_t \phi(t)] < \infty$,*

(iv) *$E\phi(t)$ is Lebesgue-a.e. continuous.*

Furthermore, with the definition

$$M = \int_0^\infty e^{-\alpha t} \xi(dt),$$

suppose that $E[M \log^+ M] < \infty$ holds. Then

$$\lim_{t \to \infty} Z^\phi(t) = Y_\infty m_\infty^\phi \quad \text{a.s. and in } L^1,$$

where

$$m_\infty^\phi = \frac{\int_0^\infty e^{-\alpha t} E\phi(t)\, dt}{\int_0^\infty t\, e^{-\alpha t} \mu(dt)},$$

Y_∞ is a nonnegative random variable, which is positive on the event of non-extinction, it has expectation 1, and it does not depend on the choice of ϕ.

Particularly, for the number $Z(t)$ of individuals alive at time t we have

(2.1)
$$\lim_{t \to \infty} e^{-\alpha t} Z(t) = Y_\infty \frac{\int_0^\infty e^{-\alpha t}[1 - L(t)]\, dt}{\int_0^\infty t\, e^{-\alpha t} \mu(dt)},$$

where $L(t) = P(\lambda \leq t)$, the distribution function of the life length.

3.   The model

We start with a single edge. Whenever a new edge is born, it starts producing offspring according to a homogeneous Poisson process with unit intensity. At every birth event a new vertex is added to the graph, and it is joined to the endpoints of the reproducing edge with one or two edges, namely, with probability $p \in [0, 1]$ the new vertex gets connected to both ends, while with probability $q = 1 - p$ it is connected to one of the endpoints, selected at random. The number of reproduction events up to time t is called *the biological age* of the edge. The life span of an edge is finite: it dies with a hazard rate which is an increasing linear function of the biological age. At death the edge is deleted. The life histories of different edges are supposed to be independent. In this way, from the viewpoint of edges, our process is a Markov branching process, which is a particular case of general CMJ processes.

Let us introduce some notations. Consider a generic edge. By $\pi(t)$, $t \geq 0$, we denote the Poisson process that governs reproduction. Then the reproduction process is the point process given by

$$\xi(t) = \sum_{\tau_i \leq t \wedge \lambda} \varepsilon_i = S_{\pi(t \wedge \lambda)}.$$

where $\wedge$ stands for minimum. Thus, $\xi(t)$ is just the compound Poisson process $S_{\pi(\cdot)}$ stopped at $\lambda \wedge t$. By Wald's identity we have

$$\mu(t) = E\xi(t) = E(\varepsilon_1)E(\lambda \wedge t) = (1 + p) \int_0^t [1 - L(s)]\,ds.$$

The hazard rate of the life span for an edge of physical age t and biological age $\xi(t)$ is $b + c\,\xi(t)$, where b and c are positive constants.

Our CMJ process starts with a single ancestor at time 0. The history of every edge e is characterized by the triple

$$\big(\lambda_e,\, \pi_e(\cdot),\, \xi_e(\cdot)\big)$$

which are iid copies of $\big(\lambda,\, \pi(\cdot),\, \xi(\cdot)\big)$ introduced above.

4.   Life history of an edge

In this section, we first compute $1 - L(t)$, the survival function of an edge's lifetime, then the joint distribution of the number of birth events and the total number of children of an edge.

Theorem 4.1.

$$1 - L(t) = \exp\left(-(1+b)t + \frac{1}{2c}\left(1 - e^{-ct}\right)\left(2 - p(1 - e^{-ct})\right)\right).$$

Proof. Let us first compute the conditional survival function of λ given the number of birth events up to time t, the times of reproductions and the litter sizes. After the birth time τ_i, if the total number of children is j, the death rate is $b + cj$. Hence the probability that the edge does not die before the next birth event is $\exp\left(-(b+cj)(\tau_{i+1} - \tau_i)\right)$. Therefore,

$$P(\lambda > t \mid \pi(t) = k,\, \tau_1, \ldots, \tau_k,\, \varepsilon_1, \ldots, \varepsilon_k) =$$
$$= e^{-b\tau_1} \cdot e^{-(b+cS_1)(\tau_2 - \tau_1)} \cdot e^{-(b+cS_2)(\tau_3 - \tau_2)} \cdots e^{-(b+cS_k)(t-\tau_k)} =$$
$$= \exp\left(c \sum_{i=1}^{k} \varepsilon_i \tau_i - (b + cS_k)t\right).$$

Given $\pi(t) = k$, the conditional joint distribution of the birth times $\tau_1, \ldots, \tau_k$ coincides with that of $(tU_1^{(k)}, \ldots, tU_k^{(k)})$, where $(U_1^{(k)}, \ldots, U_k^{(k)})$ is an ordered sample of size k from the uniform distribution $U(0,1)$ (and independent of the litter sizes $\varepsilon_1, \ldots, \varepsilon_k$). Hence,

$$P(\lambda > t \mid \pi(t) = k) = E\left(\exp\left(-bt + ct \sum_{i=1}^{k} \varepsilon_i(U_i^{(k)} - 1)\right)\right).$$

Since $\varepsilon_1, \ldots, \varepsilon_k$ are interchangeable, we get

$$P(\lambda > t \mid \pi(t) = k) = E\left(\exp\left(-bt + ct \sum_{i=1}^{k} \varepsilon_i(U_i - 1)\right)\right),$$

where $U_1, \ldots, U_k$ are iid random variables with $U(0,1)$ distribution, and they are independent of the ε. Thus, by independence,

$$P(\lambda > t \mid \pi(t) = k) = e^{-bt}\left[E\left(\frac{1 - e^{-ct\varepsilon_1}}{ct\varepsilon_1}\right)\right]^k =$$
$$= e^{-bt}\left[p\,\frac{1 - e^{-2ct}}{2ct} + q\,\frac{1 - e^{-ct}}{ct}\right]^k =$$
$$= e^{-bt}\left[\frac{1}{2ct}\left(1 - e^{-ct}\right)\left(2 - p(1 - e^{-ct})\right)\right]^k.$$

Finally,

$$P(\lambda > t) = \sum_{k=0}^{\infty} P(\pi(t) = k)P(\lambda > t \,|\, \pi(t) = k) =$$

$$= \sum_{k=0}^{\infty} \frac{t^k}{k!} e^{-t} \cdot e^{-bt} \left[\frac{1}{2ct} \left(1 - e^{-ct}\right)\left(2 - p(1 - e^{-ct})\right) \right]^k =$$

$$= \exp\left(-(1+b)t + \frac{1}{2c}\left(1 - e^{-ct}\right)\left(2 - p(1 - e^{-ct})\right) \right). \qquad \blacksquare$$

Corollary 4.1.

$$\mu(t) = \frac{1+p}{c} \int_0^{1-e^{-ct}} (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{u(2 - pu)}{2c} \right) du.$$

Moreover, the mean lifetime is

$$E(\lambda) = \frac{1}{c} \int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{u(2 - pu)}{2c} \right) du.$$

Proof. As we have already seen, $\mu(t) = (1 + p)E(\lambda \wedge t)$. Here $E(\lambda \wedge t) = \int_0^t [1 - L(s)]\,ds$, and substitution $u = 1 - e^{-cs}$ on the right hand side leads to the expression above. For $t \to \infty$ we get $\mu(\infty) = (1 + p)E(\lambda)$. $\blacksquare$

Next, we compute the joint probability generating function of $\pi(\lambda)$ and $\xi(\lambda) = \xi(\infty)$, defined as

$$g_{\pi,\xi}(x, y) = E\left(x^{\pi(\lambda)} y^{\xi(\lambda)} \right) = \sum_{i=0}^{\infty} \sum_{j=i}^{2i} P(\pi(\lambda) = i,\, \xi(\lambda) = j)\, x^i y^j,$$

for $x, y \in [-1, 1]$.

Theorem 4.2.

$$g_{\pi,\xi}(x, y)$$
$$= 1 - \frac{1 - qxy - pxy^2}{c} \int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{qxy + pxy^2}{c} u - \frac{pxy^2}{2c} u^2 \right) du$$

For the sake of convenience, we first focus on the bivariate generating function of another, closely related sequence with double indices.

Lemma 4.1. *For integers $0 \le i \le j$ let*

$$w_{i,j} = P(\pi(\lambda) = i,\, \xi(\lambda) = j), \quad v_{i,j} = \frac{w_{i,j}}{b + jc},$$

and for $x, y \in [-1, 1]$ *define*

$$G(x, y) = \sum_{i=0}^{\infty} \sum_{j=0}^{i} v_{i,i+j}\, x^i y^j.$$

Then

$$(4.1) \quad G(x, y) = \frac{1}{c} \exp\left(\frac{qx}{c} + \frac{pxy}{2c}\right) \int_0^1 s^{\frac{1+b}{c}-1} \exp\left(-\frac{qx}{c}s - \frac{pxy}{2c}s^2\right)ds =$$

$$(4.2) \qquad = \frac{1}{c} \int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{qx+pxy}{c}u - \frac{pxy}{2c}u^2\right)du.$$

Proof. The probability that a live edge of biological age j dies before the next reproduction event is $(b+cj)/(1+b+cj)$. Hence,

$$P(\pi(\lambda) = i,\, \xi(\lambda) = j) = P(\exists t < \lambda : \pi(t) = i,\, \xi(t) = j)\frac{b+cj}{1+b+cj}\,.$$

On the other hand,

$$P(\exists t < \lambda : \pi(t) = i,\, \xi(t) = j)$$
$$= P(\exists t < \lambda : \pi(t) = i-1,\, \xi(t) = j-1)\frac{q}{1+b+c(j-1)} +$$
$$+\, P(\exists t < \lambda : \pi(t) = i-1,\, \xi(t) = j-2)\frac{p}{1+b+c(j-2)}\,,$$

where the probability on the left hand side is decomposed according to the size of the last litter. From that we obtain the following recursion for $v_{i,i+j}$:

$$[1+b+c(i+j)]v_{i,i+j} = qv_{i-1,(i-1)+j} + pv_{i-1,(i-1)+(j-1)},$$

with initial condition $v_{0,0} = 1/(1+b)$, $v_{0,j} = 0$ for $j \geq 1$. Multiplying this equality with $x^i y^j$, then adding up for $i \geq 1$ and $j \geq 1$ one gets

$$(4.3)\ (1+b)\left(G(x,y) - \frac{1}{1+b}\right) + c\left(xG'_x(x,y) + yG'_y(x,y)\right) = (qx+pxy)G(x,y),$$

with $G(0, y) = 1/(1+b)$. Let $h(t) = G(tx, ty)$, $0 \leq t \leq 1$. Then h satisfies the following ODE:

$$(1+b-qxt-pxyt^2)h(t) + cth'(t) = 1, \quad h(0) = \frac{1}{1+b}\,.$$

The solution is

$$h(t) = \frac{1}{c}\, t^{-\frac{1+b}{c}} \exp\left(\frac{qx}{c}t + \frac{pxy}{2c}t^2\right) \int_0^t s^{\frac{1+b}{c}-1} \exp\left(-\frac{qx}{c}s - \frac{pxy}{2c}s^2\right)ds,$$

which immediately implies (4.1) for $G(x, y) = h(1)$. Substituting $u = 1 - s$ in the integral we get (4.2). ∎

Proof of Theorem 4.2. Clearly,

$$\sum_{i=0}^{\infty} \sum_{j=0}^{i} w_{i,i+j}\, x^i y^j = \sum_{i=0}^{\infty} \sum_{j=0}^{i} [b + c(i+j)] v_{i,i+j}\, x^i y^j$$

$$= bG(x, y) + c\big(xG'_x(x, y) + yG'_y(x, y)\big).$$

By (4.3) we have

$$c\big(xG'_x(x, y) + yG'_y(x, y)\big) = 1 - (1 + b - qx - pxy)G(x, y),$$

consequently,

$$\sum_{i=0}^{\infty} \sum_{j=0}^{i} w_{i,i+j}\, x^i y^j = 1 - (1 - qx - pxy)G(x, y).$$

The desired generating function can be obtained by plugging xy in place of x:

$$g_{\pi,\xi}(x, y) = 1 - (1 - qxy - pxy^2)G(xy, y).$$

Now the proof can be completed by applying Lemma 4.1. ∎

5. Life history of the graph process

From Theorem 4.2 one can immediately compute the probability of extinction. Extinction of our branching process means that eventually all edges die: the graph becomes empty. This probability is equal to 1 if $E\xi(\infty) = (1 + p)E(\lambda) = \leq 1$ (subcritical and critical regime). In the supercritical case, i.e., when

$$(5.1) \qquad E\xi(\infty) = \frac{1+p}{c} \int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{u}{c} - \frac{pu^2}{2c}\right) du > 1,$$

the extinction probability is less than 1, and it can be obtained as follows.

Theorem 5.1. *When (5.1) holds, the probability y of extinction is the smallest nonnegative root of the equation*

$$(5.2) \qquad 1 = \frac{1 + py}{c} \int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{qy + py^2}{c}u - \frac{py^2}{2c}u^2\right) du.$$

Note that the right hand side is an increasing continuous function of y. It is equal to $(1+b)^{-1} \leq 1$ at $y = 0$, and greater than 1 at $y = 1$, by (5.1).

Proof. The extinction probability is the smallest nonnegative root of the equation $g_\xi(y) = y$, where g_ξ stands for the probability generating function of $\xi(\infty) = \xi(\lambda)$, the total number of children of the ancestor. Clearly, $g_\xi(y) = g_{\pi,\xi}(1, y)$, hence by Theorem 4.2,

$$1 - y = \frac{1 - qy - py^2}{c} \int_0^1 (1 - u)^{\frac{1+b}{c} - 1} \exp\left(\frac{qy + py^2}{c} u - \frac{py^2}{2c} u^2\right) du.$$

Here $1 - qy - py^2 = (1 - y)(1 + py)$, thus one can divide by $1 - y$ on both sides. ∎

The Malthusian parameter α is the only solution of the equation

$$\int_0^\infty e^{-\alpha t} \mu(dt) = 1.$$

In our case, by Theorem 4.1, this equation takes shape in the following form:

$$1 = \int_0^\infty e^{-\alpha t} \mu(dt) = (1 + p) \int_0^\infty e^{-\alpha t}[1 - L(t)] \, dt =$$

$$= (1 + p) \int_0^\infty e^{-\alpha t} \exp\left(-(1 + b)t + \frac{1}{2c}(1 - e^{-ct})(2 - p(1 - e^{-ct}))\right) dt.$$

Similarly to what we have done during the computation of $E(\lambda)$, let us substitute $u = 1 - e^{-ct}$ again. It leads to the equation

$$(5.3) \qquad \frac{1 + p}{c} \int_0^1 (1 - u)^{\frac{\alpha+1+b}{c} - 1} \exp\left(\frac{u(2 - pu)}{2c}\right) du = 1.$$

Remark. The Malthusian parameter α satisfies $p - b < \alpha < 1 + p - b$, since from Theorem 4.1 it follows that

$$\exp(-(1 + b)t) < 1 - L(t) < \exp\left(-(1 + b)t + \frac{1 - e^{-ct}}{c}\right) \leq \exp(-bt),$$

and consequently,

$$(1 + p) \int_0^\infty e^{-(\alpha+1+b)t} \, dt < 1 < (1 + p) \int_0^\infty e^{-(\alpha+b)t} \, dt,$$

that is,

$$\frac{1 + p}{\alpha + 1 + b} < 1 < \frac{1 + p}{\alpha + b}.$$

The next theorem describes the asymptotic behaviour of $Z(t)$, the number of edges.

Theorem 5.2. *As $t \to \infty$, $e^{-\alpha t} Z(t)$ converges almost surely and in L^1 to $Y_\infty m_\infty$, where Y_∞ is a nonnegative random variable with expectation 1, positive on the event of non-extinction, and*

$$m_\infty = \left[(1+p)^2 \int_0^\infty t\, e^{-\alpha t} [1 - L(t)]\, dt \right]^{-1} =$$

$$= \left[\frac{(1+p)^2}{c^2} \int_0^1 [-\log(1-u)](1-u)^{\frac{\alpha+1+b}{c}-1} \exp\left(\frac{u(2-pu)}{2c} \right) du \right]^{-1},$$

with α defined by equation (5.3).

Proof. We want to apply Proposition 2.1. Let us check its conditions. Obviously,

$$M = \int_0^\infty e^{-\mu t} \xi(dt) = \sum_{\tau_i < \lambda} \varepsilon_i e^{-\mu \tau_i} \leq 2 \sum_{i=1}^\infty e^{-\mu \tau_i} = M'.$$

Using that the distribution of τ_i is Gamma$(i, 1)$, we have

$$E(M') = 2 \sum_{i=1}^\infty E\left(e^{-\mu \tau_i}\right) = 2 \sum_{i=1}^\infty \frac{1}{(1+\mu)^i} = \frac{2}{\mu}.$$

On the other hand, the distribution of M' coincides with that of $e^{-\mu \tau}(2 + M')$, where τ is exponentially distributed with unit mean, and independent of M'. Hence

$$E(M'^2) = E(e^{-2\mu \tau})\left[4 + 4E(M') + E(M'^2)\right] = \frac{1}{1+2\mu}\left[4 + \frac{8}{\mu} + E(M'^2)\right],$$

implying

$$E(M'^2) = \frac{2(2+\mu)}{\mu^2}.$$

The conditions imposed on ϕ are obviously met for $\phi(t) = I(0 \leq t < \lambda)$. By (2.1) we now have

(5.4) $$e^{-\alpha t} Z(t) \to Y_\infty \frac{\int_0^\infty e^{-\alpha t}[1 - L(t)]\, dt}{\int_0^\infty t\, e^{-\alpha t} \mu(dt)}$$

a.s. and in L^1, as $t \to \infty$. Here the numerator is equal to $1/(1+p)$ by the Malthusian equation, and the denominator is

$$(1+p) \int_0^\infty t\, e^{-\alpha t}[1 - L(t)]\, dt.$$

Again, substitution $u = 1 - e^{-ct}$ leads to the second equality. ∎

Next we deal with the number of vertices. At time t it can be obtained as $V(t) = 2 + Z^\phi(t)$ for $\phi(t) = \pi(t \wedge \lambda)$.

Theorem 5.3.

$$\lim_{t \to \infty} \frac{V(t)}{Z(t)} = \frac{1}{\alpha}$$

almost everywhere on the event of non-extinction.

Proof. The conditions of Proposition 2.1 are satisfied, because by Wald's identity we have

$$E\phi(t) = E\pi(\lambda \wedge t) = E(\lambda \wedge t) = \int_0^t [1 - L(s)]\, ds,$$

which is bounded and continuous. Let us compute the numerator of m_∞^ϕ (the denominator does not depend on ϕ; it is the same as for the number of edges). By interchanging the order of integrations we get

$$\int_0^\infty e^{-\alpha t} E\phi(t)\, dt = \int_0^\infty e^{-\alpha t} \int_0^t [1 - L(s)]\, ds\, dt =$$
$$= \int_0^\infty [1 - L(s)] \int_s^\infty e^{-\alpha t} dt\, ds = \frac{1}{\alpha} \int_0^\infty e^{-\alpha s}[1 - L(s)]\, ds,$$

which, in virtue of (5.4), completes the proof. ∎

Finally, we will study $B(t)$, the growth rate of the total sum of biological ages of all edges at time t, i.e., the total number of offspring, dead or alive, born by individuals alive at time t. Clearly,

$$B(t) = \sum_e \xi_e(t - \sigma_e)I(t - \sigma_e < \lambda_e),$$

thus $B(t) = Z^\phi(t)$ with $\phi(t) = \xi(t)I(t < \lambda)$.

Theorem 5.4.

$$\lim_{t \to \infty} \frac{B(t)}{Z(t)} = \frac{1+p}{c^2} \int_0^1 u(1 + p - pu)(1 - u)^{\frac{\alpha+1+b}{c}-1} \exp\left(\frac{u(2 - pu)}{2c}\right) du.$$

almost everywhere on the event of non-extinction.

Proof. Following the proof of Theorem 4.1 we see that

$$P(\lambda > t \mid \pi(t) = k, \varepsilon_1, \dots, \varepsilon_k) =$$
$$= E\left(\exp\left(-bt + ct \sum_{i=1}^k \varepsilon_i(U_i^{(k)} - 1) \right) \bigg| \varepsilon_1, \dots, \varepsilon_k \right),$$

where $U_1^{(k)}$, ..., $U_k^{(k)}$ is an ordered sample of size k from the uniform distribution $U(0,1)$. Therefore, by the law of total expectation,

$$E\big(\xi(t)I(t<\lambda)\,\big|\,\pi(t)=k\big) = E\big(S_k I(t<\lambda)\,\big|\,\pi(t)=k\big) =$$
$$= E\big(S_k P(\lambda>t\,|\,\pi(t)=k,\varepsilon_1,\ldots,\varepsilon_k)\,\big|\,\pi(t)=k\big) =$$
$$= E\Big[E\Big(S_k\exp\Big(-bt+ct\sum_{i=1}^{k}\varepsilon_i(U_i^{(k)}-1)\Big)\,\Big|\,\varepsilon_1,\ldots,\varepsilon_k\Big)\Big] =$$
$$= E\Big(e^{-bt}S_k\prod_{i=1}^{k}\exp\Big(ct\varepsilon_i(U_i^{(k)}-1)\Big)\Big).$$

The right hand side is invariant under permutations of $(\varepsilon_1,\ldots,\varepsilon_k)$, hence the ordered sample can be replaced with iid $(U_1,\ldots,U_k)$.

$$E\big(\xi(t)I(t<\lambda)\,\big|\,\pi(t)=k\big) =$$
$$= E\Big(e^{-bt}S_k\prod_{i=1}^{k}\exp\Big(ct\varepsilon_i(U_i-1)\Big)\Big) =$$
$$= E\Big(e^{-bt}\sum_{j=1}^{k}\varepsilon_j\prod_{i=1}^{k}\exp\Big(ct\varepsilon_i(U_i-1)\Big)\Big) =$$
$$= e^{-bt}k\,E\big[\varepsilon_1\exp(ct\varepsilon_1(U_1-1))\big]\big[E\big(\exp(ct\varepsilon_1(U_1-1))\big)\big]^{k-1} =$$
$$= e^{-bt}k\,E\Big(\frac{1-e^{-ct\varepsilon_1}}{ct}\Big)\Big[E\Big(\frac{1-e^{-ct\varepsilon_1}}{ct\varepsilon_1}\Big)\Big]^{k-1}.$$

Hence,

$$E\big(\xi(t)I(t<\lambda)\big) = \sum_{k=1}^{\infty}e^{-bt}k\,E\Big(\frac{1-e^{-ct\varepsilon_1}}{ct}\Big)\Big[E\Big(\frac{1-e^{-ct\varepsilon_1}}{ct\varepsilon_1}\Big)\Big]^{k-1}\frac{t^k}{k!}e^{-t} =$$
$$= E\Big(\frac{1-e^{-ct\varepsilon_1}}{c}\Big)\exp\Big(-(1+b)t+E\Big(\frac{1-e^{-ct\varepsilon_1}}{c\varepsilon_1}\Big)\Big) =$$
$$= \frac{1}{c}\big(1-pe^{-2ct}-qe^{-ct}\big)\big[1-L(t)\big] =$$
$$= \frac{1}{c}(1-e^{-ct})(1+pe^{-ct})\big[1-L(t)\big].$$

Let us apply Proposition 2.1. In the numerator of m_∞^ϕ we have

$$\frac{1}{c}\int_0^\infty e^{-\alpha t}(1-e^{-ct})(1+pe^{-ct})\big[1-L(t)\big]\,dt,$$

where $1-L(t)$ can be taken from Theorem 4.1. Substituting $u=1-e^{-ct}$ we arrive at the formula to be proved. ∎

Remark. As we have seen in the proof,

$$E(\xi(t) \mid \lambda > t) = \frac{1}{c}(1 - pe^{-2ct} - qe^{-ct}) < \frac{1}{c}.$$

This appears counter-intuitive, because the compound Poisson process $\xi(t)$ grows linearly before it is stopped at λ, hence one may think that if t is large but $\lambda > t$ is still supposed, then $\xi(t)$ is also large, at least not bounded. But look at that from the other side: since the hazard rate of λ is a linear function of $\xi(t)$, condition $\lambda > t$ indicates that $\xi(t)$ is unusually small, in spite of the large value of t.

6. Life history of a vertex

In this section, we investigate how the degree of a fixed vertex is evolving.

When a vertex is added to the graph, its degree is 2 with probability p and 1 with probability q. Suppose the latter, i.e., there is only one initial edge. It starts a new CMJ process, where reproduction is driven by the same dynamics as in the original edge process, but of its children we only count those who are connected to the monitored vertex. When an edge in this process gives birth to two edges, the degree of the monitored vertex increases by 1, and when there is a single offspring, it only contributes to the degree with probability $1/2$. However, the biological age of an edge in consideration grows by its not counted children, too.

Let us denote the degree reproduction process by $\eta(\cdot)$. Then, up to time t, the number of litters of size 2, resp. 1, is $\xi(t) - \pi(t \wedge \lambda)$, resp. $2\pi(t \wedge \lambda) - \xi(t)$, hence

$$\eta(t) = \xi(t) - \pi(t \wedge \lambda) + \sum_{i=1}^{2\pi(t\wedge\lambda)-\xi(t)} \delta_i,$$

where the random variables $\delta_1, \delta_2, \ldots$ are iid with $P(\delta_i = 0) = P(\delta_i = 1) = = 1/2$, and they are independent of $\pi(\cdot)$, $\xi(\cdot)$, and λ.

When the monitored vertex is born with initial degree 2, its degree process is the sum (superposition) of two independent processes $(\eta(\cdot), \lambda)$ described above.

Theorem 6.1. *The degree process of a vertex is supercritical if and only if*

$$(6.1) \qquad E\eta(\infty) = \frac{1+p}{2c} \int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{u(2-pu)}{2c}\right) du > 1.$$

In the supercritical case the Malthusian parameter β is the only positive root of the equation

$$(6.2) \qquad \frac{1+p}{2c} \int_0^1 (1-u)^{\frac{\beta+1+b}{c}-1} \exp\left(\frac{u(2-pu)}{2c}\right) du = 1,$$

and the probability of extinction (i.e., the monitored vertex eventually becomes isolated) is equal to pz^2+qz, where z is the smallest positive root of the equation

$$(6.3) \qquad \frac{1+p}{2c} \int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{1+p}{2c} u(1-u)z\right) du = 1.$$

Proof. In the process $\eta(\cdot)$, the expectation of the total number of children of an initial edge up to time t can be computed by the law of total expectation:

$$E\eta(t) = E\big[E(\eta(t)\,|\,\pi(t\wedge\lambda), \xi(t))\big] =$$
$$= E\big(\xi(t) - \pi(t\wedge\lambda) + \tfrac{1}{2}[2\pi(t\wedge\lambda) - \xi(t)]\big) =$$
$$= \tfrac{1}{2} E\xi(t).$$

The result is plausible, because now the expected number of children at a birth event is $p + \tfrac{1}{2}q = \tfrac{1}{2}(1+p)$, which is just the half of the mean litter size in the process $\xi(.)$. Now, (5.1) implies (6.1), and (6.2) follows from (5.3).

Finally, let us compute the probability generating function of $\eta(\infty) = \eta(\lambda)$. Again, by the law of total expectation and Theorem 4.2 we have

$$g_\eta(z) = E\big(z^{\eta(\lambda)}\big) = E\big[E\big(z^{\eta(\lambda)}\,|\,\pi(\lambda), \xi(\lambda)\big)\big] =$$
$$= E\left(z^{\xi(\lambda)-\pi(\lambda)}\left(\frac{1+z}{2}\right)^{2\pi(\lambda)-\xi(\lambda)}\right) =$$
$$= g_{\pi,\xi}\left(\frac{(1+z)^2}{4z}, \frac{2z}{1+z}\right) =$$
$$= 1 - \frac{1+p}{2c}(1-z)\int_0^1 (1-u)^{\frac{1+b}{c}-1} \exp\left(\frac{1+p}{2c} u(1-u)z\right) du.$$

Starting with initial degree 1, the degree process eventually dies out with probability $z \in (0,1)$ satisfying $z = g_\eta(z)$. After rearranging and dividing by $1-z$ on both sides we get (6.3).

If the initial degree is random with probability generating function ψ, it is easy to see that the probability of extinction is just $\psi(z)$. ∎

It can happen that the edge process is supercritical, while the degree process is not. If both processes are supercritical, they grow at different rates: $\beta < \alpha$, and the extinction probability is greater for the degree process. Let $\deg(t)$ denote the degree of a fixed vertex at time t, then $\deg(t) = O(e^{\beta t}) = O\big(V(t)^{\beta/\alpha}\big)$ as $t \to \infty$.

7.   A slowed down discrete version of the model

In this section, we introduce a discrete time version of our graph process. Again, we initially have a single edge. The graph evolves by discrete steps. At every step the graph changes in one of the following ways: either an edge is deleted, or a new vertex is added, which then gets connected to one or both endpoints of an old edge. This is called edge reproduction, and the new edge or edges are considered the children of the old one. The biological age of an edge is defined as the number of its children.

Let E_n denote the edge set after step n. If $E_n \neq \emptyset$, then at the next step exactly one of the events $\{A_e, B_e : e \in E_n\}$ occurs, where $A_e =$ $= \{e$ becomes deleted$\}$, $B_e = \{e$ reproduces$\}$, with probabilities $P(A_e) = \kappa$ and $P(B_e) = \kappa(b + c\,\xi_e)$, resp. Here b, c are positive constants, ξ_e is the biological age of edge e, and the multiplier $\kappa = \kappa_n$ makes the sum of these probabilities be equal to 1.

This discrete model is exactly the same which is found embedded in the continuous time model of Section 3 at the moments of events (birth or death). Thus, we can easily transfer our earlier results to the discrete model.

Clearly, the probability of extinction is the same for both processes (Theorem 5.1), and the limiting vertex to edge ratio also remains valid (Theorem 5.3). For the growth rate we only have to find the asymptotic number of events up to time t.

Theorem 7.1. *Let $W(t)$ denote the number of events up to t. Then on the set of non-extinction*

$$\lim_{t\to\infty} \frac{W(t)}{Z(t)} = \frac{2+p}{\alpha} - 1,$$

where α is the Malthusian parameter defined in (5.3).

Proof. Note that $W(t) = Z^\phi(t)$ for the random characteristic $\phi(t) = \pi(t \wedge \lambda) + I(\lambda \leq t)$. Here the first term counts the number of birth events, while the second one the deaths. Let us apply Proposition 2.1. Now,

$$E\phi(t) = E\pi(t \wedge \lambda) + L(t),$$

hence in the numerator of m_∞^ϕ we obtain

$$\int_0^\infty e^{-\alpha t}\, E\phi(t)\, dt = \frac{1}{\alpha} \int_0^\infty e^{-\alpha t}\, [1 - L(t)]\, dt +$$

$$+ \int_0^\infty e^{-\alpha t}\, dt - \int_0^\infty e^{-\alpha t}\, [1 - L(t)]\, dt =$$

$$= \frac{1}{\alpha} + \left(\frac{1}{\alpha} - 1\right) \int_0^\infty e^{-\alpha t}\, [1 - L(t)]\, dt =$$

$$= \frac{1}{\alpha} + \left(\frac{1}{\alpha} - 1\right) \frac{1}{1 + p},$$

from the Malthusian equation (5.3). The proof can be completed by comparing this with Theorem 5.2. ∎

Corollary 7.1. *In the discrete model, let V_n and Z_n denote the numbers of vertices and edges, resp., after the n-th step. Then*

$$\lim_{n\to\infty} \frac{Z_n}{n} = \lim_{t\to\infty} \frac{Z(t)}{W(t)} = \frac{\alpha}{2 + p - \alpha}, \quad \lim_{n\to\infty} \frac{V_n}{n} = \lim_{t\to\infty} \frac{V(t)}{W(t)} = \frac{1}{2 + p - \alpha}$$

almost surely on the event of non-extinction.

Corollary 7.2. *By Theorem 5.4, the following asymptotic expression holds for the normalizing factors $\kappa = \kappa_n$:*

$$\lim_{n\to\infty} n\kappa_n = \lim_{t\to\infty} \frac{W(t)}{(1 + b)Z(t) + cB(t)} = \left(\frac{2 + p}{\alpha} - 1\right)\left[1 + b+\right.$$

$$\left. + \frac{1 + p}{c} \int_0^1 u(1 + p - pu)(1 - u)^{\frac{\alpha + 1 + b}{c} - 1} \exp\left(\frac{u(2 - pu)}{2c}\right) du\right]^{-1}.$$

almost surely on the event of non-extinction.

Finally, our last assertion immediately follows from the studied properties of the continuous time model.

Theorem 7.2. *Let v be a fixed vertex, and let $\deg_n(v)$ denote its degree after step n. If the degree process is supercritical (i.e., $\beta > 0$), then almost surely*

$$\lim_{n\to\infty} n^{-\beta/\alpha} \deg_n(v) = \zeta_v,$$

where the random variable ζ_v is positive except on the set where $\deg_n(v)$ eventually becomes zero (i.e., on the event of extinction of the degree process).

8.   Particular cases

In this section, we pay closer attention to graphs obtained by extremal choices of parameter p. In both cases the integrals in our formulae (5.1)–(5.3), (6.1), and (6.2) can be expressed in terms of the confluent hypergeometric function of the first kind. It is defined as

$$M(a, b, z) = \sum_{n=0}^{\infty} \frac{a^{(n)}}{b^{(n)}} \frac{z^n}{n!},$$

where $a^{(n)}$ is the Pochhammer symbol or rising factorial: $a^{(0)} = 1$, and $a^{(n)} = a(a + 1) \cdots (a + n - 1)$ for $n > 0$. It has the following integral representation if both $\operatorname{Re} a$ and $\operatorname{Re} b$ are positive.

$$M(a, b, z) = \frac{\Gamma(b)}{\Gamma(a)\Gamma(b - a)} \int_0^1 u^{a-1}(1 - u)^{b-a-1}e^{zu}\, du.$$

Since the confluent hypergeometric function is implemented in many scientific software packages, e.g., `Hypergeometric1F1[a,b,z]` in Mathematica®, `kummer(a,b,z)` in MATLAB®, or `kummerM(a,b,z)` in the R package 'fAsianOptions', such a representation makes numerical computations easier. Besides, there are several online calculators at hand, e.g., the Keisan Online Calculator [12].

First, let $p = 0$. In this case the new vertex joins to the graph with a single edge, thus the graph will never contain any cycles. If there were no edge deaths, we would get the so called Barabási–Albert tree: choosing an edge at random, then one of its endpoints with equal probabilities leads to the preferential attachment rule, i.e., every vertex is selected with probability proportional to its degree (see [16], [17] for selected properties of the Barabási tree). When edges are aging, the graph ceases to be connected, it becomes a forest with many isolated vertices. With the confluent hypergeometric notation, the condition for supercriticality is that

(8.1) $$\frac{1}{1 + b} M\left(1, \frac{1 + b}{c} + 1, \frac{1}{c}\right) > 1,$$

and the probability y of extinction is the smallest nonnegative root of the equation

$$\frac{1}{1 + b} M\left(1, \frac{1 + b}{c} + 1, \frac{y}{c}\right) = 1.$$

Note that the mean life span $E(\lambda)$ is just the left hand side of (8.1). The Malthusian parameter α is the positive root of the equation

$$\frac{1}{\alpha + 1 + b} M\left(1, \frac{\alpha + 1 + b}{c} + 1, \frac{1}{c}\right) = 1.$$

The degree process of a vertex is supercritical if

$$\frac{1}{1 + b} M\left(1, \frac{1 + b}{c} + 1, \frac{1}{c}\right) > 2,$$

and the corresponding Malthusian parameter β is the positive root of the equation

$$\frac{1}{\beta + 1 + b} M\left(1, \frac{\beta + 1 + b}{c} + 1, \frac{1}{c}\right) = 2.$$

Secondly, let $p = 1$. Then the new vertex is connected to both ends of the selected old edge, i.e., a 2-star is added to the graph. A 2-star is sometimes called a cherry, and the graph built of cherries a cherry tree (although it is not a tree in the usual, cycle-free sense). Thus, in the particular case $p = 1$ a random cherry tree emerges with aging edges. Properties of random cherry trees and their generalizations are dealt with in [18]. Let us substitute $v = (1 - u)^2$ in the integrals of (5.1)–(5.3), (6.1), and (6.2). Now, the graph process is supercritical if and only if

$$\frac{2}{1 + b} M\left(1, \frac{1 + b}{2c} + 1, \frac{1}{2c}\right) > 1,$$

and the probability y of extinction is the smallest nonnegative root of the equation

$$\frac{1 + y}{1 + b} M\left(1, \frac{1 + b}{2c} + 1, \frac{y^2}{2c}\right) = 1.$$

The Malthusian parameter α is the positive root of the equation

$$\frac{2}{\alpha + 1 + b} M\left(1, \frac{\alpha + 1 + b}{2c} + 1, \frac{1}{2c}\right) = 1.$$

The degree process of a vertex is supercritical if

$$\frac{1}{1 + b} M\left(1, \frac{1 + b}{2c} + 1, \frac{1}{2c}\right) > 1,$$

and the corresponding Malthusian parameter β is the positive root of the equation

$$\frac{1}{\beta + 1 + b} M\left(1, \frac{\beta + 1 + b}{2c} + 1, \frac{1}{2c}\right) = 1.$$

9.   Closing remark

A referee called our attention to the possibility of the following generalization. If the branching parameter p can depend on t, that is, the distribution of the offspring size at a birth event can depend on the physical age of the parent, what kind of conditions should $p(t)$ satisfy so that one can prove similar statements?

May it be somewhat surprising, in this more general model our computations can still be saved. E.g., in the proof of Theorem 4.1, the litter sizes $\varepsilon_1, \ldots, \varepsilon_k$ are neither exchangeable, nor independent of $U_1^{(k)}, \ldots, U_k^{(k)}$ anymore. However,

$$P(\lambda > t \,|\, \pi(t) = k) = E\bigg(\exp\Big(-bt + ct \sum_{i=1}^{k} \varepsilon_i(tU_i^{(k)})(U_i^{(k)} - 1) \Big) \bigg),$$

where $\varepsilon_i(tU_i^{(k)})$, $1 \leq i \leq k$, are conditionally independent, given $U_1^{(k)}, \ldots, U_k^{(k)}$, with (conditional) distribution $P\big(\varepsilon_i(tU_i^{(k)}) = 2\big) = p(tU_i^{(k)})$, hence we can get rid of the ordered sample $U_1^{(k)}, \ldots, U_k^{(k)}$, namely,

$$P(\lambda > t \,|\, \pi(t) = k) = E\bigg(\exp\Big(-bt + ct \sum_{i=1}^{k} \varepsilon_i(tU_i)(U_i - 1) \Big) \bigg) =$$

$$= e^{-bt}\Big[E\big(\exp\big(ct\,\varepsilon_1(tU_1)(U_1 - 1) \big) \big) \Big]^{k} =$$

$$= e^{-bt}\bigg[\int_0^1 \Big(p(tu)e^{2ct(u-1)} + q(tu)e^{ct(u-1)} \Big) du \bigg]^{k}.$$

Thinking over how this affects our formulae is left to the reader.

References

[1] **Athreya, K.B., A.P. Ghosh, and S. Sethuraman** Growth of preferential attachment random graphs via continuous-time branching processes. *Proc. Indian Acad. Sci. Math. Sci.*, **118** (2008), 473–494.

[2] **Biggins, J.D., and D.R. Grey,** A note on the growth of random trees. *Statist. Probab. Lett.*, **32** (1997), 339–342.

[3] **Bollobás, B., O. Riordan, J. Spencer, and G. Tusnády,** The degree sequence of a scale free random graph process. *Random Structures Algorithms*, **18** (2001), 279–290.

[4] **Bukszár, J., and A. Prékopa,** Probability bounds with cherry trees. *Math. Oper. Res.*, **26** (2001), 174–192.

[5] **Devroye, L.,** Branching processes in the analysis of the heights of trees. *Acta Inform.*, **24** (1987), 277–298.

[6] **Devroye, L.,** Branching Processes and Their Applications in the Analysis of Tree Structures and Tree Algorithms. In: M. Habib, C. McDiarmid, J. Ramirez-Alfonsin, B. Reed (Eds) *Probabilistic Methods for Algorithmic Discrete Mathematics*. Springer Berlin Heidelberg, 1998, pp 249–314.

[7] **Garavaglia, L., R. van der Hofstad, and G. Woeginger,** The dynamics of power laws: Fitness and aging in preferential attachment trees. https://arxiv.org/pdf/1703.05943 (2017)

[8] **Haccou, P., P. Jagers, and V.A. Vatunin,** *Branching Processes: Variation, Growth, and Extinction of Populations*, Cambridge University Press, 2005.

[9] **Holmgren, C., and S. Janson,** Fringe trees, Crump–Mode–Jagers branching processes and m-ary search trees. *Probab. Surveys*, **14** (2017), 53–154.

[10] **Jagers, P.,** *Branching Processes with Biological Applications*, Wiley, London, 1975.

[11] **Jog, V., and P.L. Loh,** Analysis of centrality in sublinear preferential attachment trees via the Crump-Mode-Jagers branching process. *IEEE Trans. Network Sci. Engrg.*, **4** (2017), 1–12.

[12] *Confluent hypergeometric function of the 1st kind Calculator*, Keisan Online Calculator, ©Casio Computer Co., Ltd., 2017 http://keisan.casio.com/exec/system/1349143651 (Retrieved 18 May 2017)

[13] **Krapivsky, P.L., and S. Redner,** Organization of growing random networks. *Phys. Rev. E (3)*, **63** (2001), 066123.

[14] **Krapivsky, P.L., S. Redner, and F. Leyvraz,** Connectivity of growing random networks. *Phys. Rev. Lett.*, **85** (2000), 4629–4632.

[15] **Mahmoud, H.M.,** A strong law for the height of random binary pyramids. *Ann. Appl. Probab.*, **4** (1994), 923–932.

[16] **Móri, T.F.,** On random trees. *Studia Sci. Math. Hungar.*, **39** (2003), 143–155.

[17] **Móri, T.F.,** The maximum degree of the Barabási–Albert random tree. *Combin. Probab. Comput.*, **14** (2005), 339–348.

[18] **Móri, T.F.,** Random multitrees. *Studia Sci. Math. Hungar.*, **47** (2010), 59–80.

[19] **Nerman, O.,** On the convergence of supercritical general (C-M-J) branching processes. *Z. Wahrscheinlichkeit.*, **57** (1981), 365–395.

[20] **Oliveira, R., and J. Spencer,** Connectivity transitions in networks with super-linear preferential attachment. *Internet Math.*, **2** (2005), 121–163.

[21] **Pittel, B.,** Note on the heights of random recursive trees and random m-ary search trees. *Random Structures Algorithms*, **5** (1994), 337–348.

[22] **Rosengren, S.,** A Multi-type Preferential Attachment Model. https://arxiv.org/pdf/1704.03256 (2017)

[23] **Rudas, A., B. Tóth,** Random Tree Growth with Branching Processes — A Survey. In: B. Bollobás, R. Kozma, D. Miklós (Eds) *Handbook of Large-Scale Random Networks,* Bolyai Society Mathematical Studies, Vol. 18, Springer Berlin Heidelberg, 2008, pp 171–202.

[24] **Rudas, A., B. Tóth, and B. Valkó,** Random trees and general branching processes. *Random Structures Algorithms*, **31(2)** (2007), 186–202.

T.F. Móri and S. Rokob
Department of Probability Theory and Statistics
Faculty of Science
Eötvös Loránd University (ELTE)
H-1117 Budapest
Pázmány Péter sétány 1/A
Hungary
mori@math.elte.hu
sk8tersanyi@gmail.com