Random cherry graphs

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Abstract. Due to the popularity of randomly evolving graph processes, there exists a randomized version of many recursively defined graph models. This is also the case with the cherry tree, which was introduced by Bukszár and Prékopa to improve Bonferroni type upper bounds on the probability of the union of random events. Here we consider a substantially extended random analogue of that model, embedding it into a general time-dependent branching process.

1. Introduction

In [3], BUKSZÁR and PRÉKOPA introduced the following recursively defined graph model, called cherry tree. Initially, there is only an adjacent pair of vertices, the only cherry tree on exactly two vertices. From a cherry tree one can obtain another cherry tree by adding a new vertex and two new edges connecting this new vertex to two already existing vertices. This new, length 2 path between the two already existing vertices is called cherry. Note that, in spite of their name, cherry trees are not trees in the usual graph theoretic sense, as they generally contain cycles.

Their purpose was to improve the Hunter–Worsley second-order upper bound on the probability of union of random events (see, e.g., [14]). The main idea behind their reasoning was to extend the spanning tree in the Hunter–Worsley

inequality to a cherry tree. In fact, the extension they used was the so-called t-cherry tree, a particular type of cherry trees where the cherries are always added to adjacent old vertices.

Apart from its use for constructing probability bounds, the graph model itself was not further studied. A few years later a randomized generalization of this model was introduced in [10], where random evolving m-ary trees were introduced and examined. In the case $m = 2$, this model reduces to a random t-cherry tree.

A slightly related model is analysed with martingale methods in [1], [2] and [7]. In the particular case where the parameters of the model are appropriately set $(p = 1)$, it also defines a kind of random evolving cherry tree.

Here we consider a more general version of the random t-cherry tree. For the sake of convenience, this generalized model will also be called cherry tree or cherry graph. The main direction on the generalization is twofold: firstly, an edge is allowed to grow randomly many cherries at the same time; secondly, the possibility of edge deletion is introduced. This breaks the monotonicity of growth, making the analyis much harder, but we hope it will be much easier to find real life applications for the generalized model.

The paper is organized as follows. First we gave a precise definition of the generalized version of the random cherry tree. Then we introduce the continuous time version of the model, completed with a well-known stochastic process, namely, the Crump–Mode–Jagers process, which then constitutes the backbone of the analysis hereafter. Using this continuous version, we establish several properties of the model, such as the probability of extinction, the asymptotic number of vertices or edges, the evolution of the degree of a fixed vertex, and so on.

2. Model

In this section, we introduce the basic notations and define our model of interest. Before setting up the model, we need some definitions.

2.1. Discrete time. Assume we have a graph with only one edge connecting two vertices. Now, add a new vertex to this graph. If it is connected to both endpoints of the given edge, these new edges (and the new middle vertex) are called *a cherry (of the existing edge)*. Alternatively, if the new vertex is joined to only one randomly chosen endpoint of the existing edge, the new edge (and the new vertex) is called *a semi-cherry* or *cherry stem (of the existing edge)*.

Now, we have everything to describe the main object of our further examinations.

Definition 2.1. The random cherry tree is a graph process evolving in discrete time steps in the following way.

(1) Initially, there is only one edge with two vertices.

(2) In a general step, the current graph changes in exactly one way of the following options:

  (a) A randomly chosen edge is deleted.

  (b) A random number of cherries or semi-cherries are joined to a randomly chosen edge (reproduction event).

To get a well-defined model, we have to specify what randomly means. For this purpose we need some more notations. Let $\mathcal{E}_n$ and $\mathcal{V}_n$ denote the sets of edges and vertices of the graph after n steps, resp. At the n-th step, let $D_n(e)$ denote the event that $e \in \mathcal{E}_n$ becomes deleted, and $C_n(e)$ denote that cherries and semi-cherries are joined to $e \in \mathcal{E}_n$ (reproduction). Note that these notations are meaningful only in the case when $\mathcal{E}_n$ is not empty. In a reproduction event, let κ_n and ε_n denote the random number of new vertices and edges added to the graph, resp. The pairs $(\kappa_1, \varepsilon_1)$, $(\kappa_2, \varepsilon_2), \ldots$ are iid copies of a generic pair of positive integer-valued random variables (κ, ε), where

$$\varepsilon = \sum_{i=1}^{\kappa} \varphi_i,$$

with iid summands $\varphi_1, \varphi_2, \ldots$, independent of κ, that represent the amounts of new edges connecting the new vertices to the existing graph. Thus,

$$\mathbb{P}(\varphi_i = 2) = p \qquad \text{and} \qquad \mathbb{P}(\varphi_i = 1) = 1 - p.$$

We will suppose that κ has an everywhere finite probability generating function $g_\kappa(z) = \mathbb{E}(z^\kappa)$. Then $g_\varepsilon(z) = \mathbb{E}(z^\varepsilon) < \infty$ for every $z \in \mathbb{R}$ as well; more precisely, $g_\varepsilon(z) = g_\kappa(pz^2 + (1 - p)z)$.

Finally, let $\xi_n(e)$ denote the number of cherries and semi-cherries attached to edge $e \in \mathcal{E}_n$ *before* the n-th step (regardless that they still are in the graph or got deleted at an earlier stage). This will be called *the biological age* of edge e at the n-th step.

Using these notations, we are able to define the probabilities of the events $D_n(e)$ and $C_n(e)$:

$$\mathbb{P}(D_n(e)) = q_n(b + c\,\xi_n(e)) \qquad \text{and} \qquad \mathbb{P}(C_n(e)) = q_n,$$

where b, c are positive constants, and q_n is a normalizing multiplier in order that the sum of probabilities of all these events be equal to 1.

An alternative formulation can be given by introducing weights of edges. When an edge is added to the graph, initially it has weight $1 + b$. Every cherry and semi-cherry connected to an edge increases the edge's weight by $2c$ and c, resp. At each step, we first select an existing edge with probability proportional to its weight w, then either we delete it with probability $1 - 1/w$, or reproduction takes place, with probability $1/w$.

So far we have given the mathematically rigorous definition of our random cherry graph, although it does not seem easy to treat. An obvious, and, as we will see, useful, idea is to change the time from discrete to continuous, examine the new continuous version, and then draw the appropriate conclusions on the original, embedded model. So, in the next subsection we will define this continuous version of our randomly evolving graph.

2.2. Continuous time. First of all, ignore the fact that the time elapsed between consecutive events is considered as unit, and take a look at the role of the edges. After a new edge is drawn between a new and a previously existing vertex, it grows a random number of cherries and semi-cherries at the same time, on a random number of occasions before its deletion, which happens with probability proportional to a linear function of the number of these new edges. Hence, whenever new cherries and semi-cherries are joined to an edge, these new edges can be interpreted as descendants of the selected edge.

Accepting this approach, it is much easier to introduce the corresponding continuous time version of the previuosly defined random cherry graph. Furthermore, it can give the reader the idea, how our analysis will be performed in the forthcoming sections.

Definition 2.2. The continuous random cherry tree is a graph process which is evolving in continuous time, as described below.

(1) Initially, there is only one edge, joining two vertices, called the ancestor.

(2) An edge produces possibly more than one new edges, as its children, at different birth events, which form a homogeneous Poisson process of unit density. Formally:

   (a) At every birth event a random number κ of new vertices are added to the current graph. Their numbers are iid random variables.

   (b) Each of these new vertices is connected to either a randomly chosen

endpoint of the selected edge with probability $1 - p$, or both of its endpoints with probability p.

(3) To consider the deletion (or death) of an edge, let us call the time elapsed from its birth *the edge's physical age*, and let the number of new edges born up to physical age t be denoted by $\xi(t)$ (this is the edge's biological age). The edge is deleted at physical age t with hazard rate $b + c\xi(t)$, a linear function of its biological age. This means that the (conditional to the reproducing process) probability of surviving physical age t is equal to

$$\exp\left(- \int_0^t (b + c\xi(s)) ds \right).$$

Life histories of the different edges are assumed to be independent.

Looking at this continuous time model, one can ask how can this take us closer to the analysis of our original cherry graph. The answer is somehow hidden in the phrasing of its definition. Indeed, we used the words ancestor, children, birth and death to suggest that, in spite of its derivation, the described graph, looking at the process from the viewpoint of the edges, is nothing else than a *Markov branching process*. Though the Markov property is a strong and profitable feature that a stochastic process can have, here we will only use the fact that this is just a special case of the so-called *general time-dependent branching process*, or *Crump–Mode–Jagers (CMJ) process*.

2.3. General branching processes. Since there are several monographs discussing the properties of general branching processes (see, e.g., [4]–[6], [13], or [8]–[9]), here we only summarize how our model fits the theory of CMJ processes, borrowing the notations from [11] and [13].

Consider an arbitrary edge in our graph. Denote the Poisson process of its birth events by $(\pi(t))_{t \geq 0}$, and its life span by λ, with survival function $S(t) = \mathbb{P}(\lambda > t)$. At the consecutive birth events τ_i $(i = 1, 2, \dots)$ this edge gives birth to ε_i $(i = 1, 2, \dots)$ random edges, which are connected to its endpoints forming cherries or cherry stems. Hence the number of descendants of this parent edge up to the i-th birth event is equal to the sum $B_i = \varepsilon_1 + \varepsilon_2 + \cdots + \varepsilon_i$, thus its biological age at physical age t is given by the random sum $\xi(t) = B_{\pi(t \wedge \lambda)}$. This defines a compound Poisson process. In the theory of general branching processes, the process $(\xi(t))_{t \geq 0}$ is called *the reproduction process*.

Although all individuals e in the general branching process can be characterized by the pairs (λ_e, ξ_e), which are iid copies of $(\lambda, \xi(.))$ defined above, the

popularity of this model is due to a third process joined to these two. This stochastic process, often denoted by $\phi(.)$, is called *a random characteristic*. It somehow takes the history of an individual into consideration. In most cases it is assumed that $\phi(t) = 0$ if $t \leq 0$, and $\phi(t) \equiv \phi(\lambda)$ whenever $t \geq \lambda$, but it is not necessarily required.

Complete the previously defined pairs with iid copies of the random characteristic and denote the birth time of edge e by σ_e. Then, summing up $\phi_e(t - \sigma_e)$ over all edges, namely, taking the sum

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

only those individuals are counted who are alive and possess the property measured by $\phi(\cdot)$ at the given moment. Accordingly, the process $(Z^\phi(t))_{t \geq 0}$ is called *a (time-dependent) branching process counted by a random characteristic*. To enlighten this notion, consider the random characteristic $\phi(t) = \mathbb{1}_{\{0 \leq t < \lambda\}}$ as an example. Then the branching process $(Z^\phi(t))_{t \geq 0}$ counted by this characteristic is nothing else than the number of living individuals at time t.

Using the notations introduced above, it is obvious that edge e is deleted at time $\sigma_e + \lambda_e$. It is possible that our graph process dies out, i.e., eventually all the edges get erased. Furthermore, it is well-known (see [9]), that the reproduction mean $\mathbb{E}\xi(\infty)$ plays crucial role in the characterization of extinction (similarly to the discrete-time Galton–Watson processes). Indeed, if this mean is less than or equal to 1 (subcritical and critical regimes), then the process dies out almost surely. On the other hand, when $\mathbb{E}\xi(\infty) > 1$ (supercritical case), the extinction probability is strictly less than 1. From now on, we only deal with the latter case, restricting ourselves to the event where the process does not get extinct.

In the continuous model the underlying branching process grows exponentially fast on the event of non-extinction, and the growth rate is characterized by the *Malthusian parameter*, denoted by α. This is the only positive solution of the equation

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

where μ is the so-called *intensity measure*, defined by $\mu(t) = \mathbb{E}\xi(t)$. With these concepts and notations, we have everything needed to cite the theorem proved by NERMAN in [13], which shows the asymptotic properties of a general branching process counted by a random characteristic. Since we do not need the most general form, here we only cite the form stated in [11].

Theorem 2.3. *Suppose the random characteristic ϕ satisfies the following conditions:*

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

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

(iii) $\mathbb{E}[\sup_t \phi(t)] < \infty$.

Furthermore, with the definition

$$_{\alpha}\xi(t) = \int_0^t e^{-\alpha s}\, \xi(ds),$$

we have $_{\alpha}\xi(\infty) \in L \log^+ L$. Then

$$\lim_{t \to \infty} e^{-\alpha t} Z^{\phi}(t) = Y_{\infty} m_{\infty}^{\phi} \tag{2}$$

almost surely, where

$$m_{\infty}^{\phi} = \frac{\int_0^{\infty} e^{-\alpha t} \mathbb{E}\phi(t)\, dt}{\int_0^{\infty} t\, e^{-\alpha t} \mu(dt)}, \tag{3}$$

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.

In addition, if the random characteristics ϕ and ψ are both satisfying the conditions above, then, almost everywhere on the event of non-extinction,

$$\lim_{t \to \infty} \frac{Z^{\phi}(t)}{Z^{\psi}(t)} = \frac{\int_0^{\infty} e^{-\alpha t} \mathbb{E}\phi(t)\, dt}{\int_0^{\infty} e^{-\alpha t} \mathbb{E}\psi(t)\, dt} \tag{4}$$

holds.

Using the statements of this theorem, we will be able to rigorously formulate the connection between the discrete and the continuous models. Then, it will be relatively easy – again with the help of Theorem 2.3 – to describe certain properties of the discrete time graph, by proving results for the continuous one.

3. Properties

The section is organized as follows. First of all, we show how the growth rate in the discrete modell is connected to that of the continuous one. After that, taking only the latter model into consideration, we can deduce results on

the original random cherry tree. This upcoming collection of propositions will include the probability of extinction, the asymptotic number of vertices, and other properties.

Before examinig the two models' connection, let us make some remarks. In Theorem 2.3 we introduced the intensity measure μ. By definition, $\mu(t)$ is the mean reproduction at time t. By applying Wald's identity, we can express it in terms of the lifespan's survival function:

$$\mu(t) = \mathbb{E}\xi(t) = \mathbb{E}(\varepsilon)\mathbb{E}(\lambda \wedge t) = \mathbb{E}(\varepsilon) \int_0^t S(u)\, du.$$

Thus, the equation for the Malthusian parameter takes the following shape:

$$\mathbb{E}(\varepsilon) \int_0^\infty e^{-\alpha t} S(t)\, dt = 1. \tag{5}$$

The idea of the present random cherry tree model comes from the continuous-time random graph model considered in [12]. Though there we "*did not fix how many new edges should be added to the graph, or how the subgraph they form should look like*", some important properties could be proved without further specification. Here we cite them merged into one theorem.

Theorem 3.1 ([12, Corollaries 3.1, 3.2 and 3.3])**.**

Survival function: *The survival function of the lifespan satisfies*

$$S(t) = P(\lambda > t) = \exp\left\{ -(1+b)t + \frac{1}{c} \int_{e^{-ct}}^1 \frac{g_\varepsilon(v)}{v}\, dv \right\}. \tag{6}$$

Supercriticality: *The random cherry tree is supercritical ($\mathbb{E}\xi(\infty) > 1$) if and only if*

$$\frac{\mathbb{E}(\varepsilon)}{c} \int_0^1 u^{\frac{1+b}{c}-1} \exp\left\{ \frac{1}{c} \int_u^1 \frac{g_\varepsilon(v)}{v}\, dv \right\} du > 1. \tag{7}$$

Malthusian parameter: *The Malthusian parameter α of the continuous-time random cherry tree is determined by the equation*

$$\frac{\mathbb{E}(\varepsilon)}{c} \int_0^1 u^{\frac{\alpha+1+b}{c}-1} \exp\left\{ \frac{1}{c} \int_u^1 \frac{g_\varepsilon(v)}{v}\, dv \right\} du = 1. \tag{8}$$

3.1. From discrete to continuous. As mentioned before, the original random cherry tree model is embedded into the continuous one. Indeed, if one takes 'snapshots' of the continuous random cherry tree at the moments of events (which

can be birth or death) and looks at these photographs one by one in chronological order, then the resulted process is just the discrete-time cherry tree process.

As a consequence, it is obvious that the probability of extinction is the same for both processes. However, so as to transfer the asymptotic results that will be obtained for the continuous case, we need to compare the growth rates of the two processes. In order to do so, as a first step, we will calculate the asymptotics of the number of edges in the continuous model.

Recall the definition

$$_\alpha\xi(t) = \int_0^t e^{-\alpha s}\,\xi(ds),$$

where α is the Malthusian-parameter, and $(\xi(t))_{t\geq 0}$ is the biological age process of an edge.

Proposition 3.2.
$$\mathbb{E}\big[_\alpha\xi^2(\infty)\big] < \infty,$$

and hence the condition $_\alpha\xi(\infty) \in L\log^+ L$ is statisfied.

PROOF. By definition we have

$$_\alpha\xi(\infty) = \int_0^\infty e^{-\alpha t}\,\xi(dt) = \sum_{\tau_i<\lambda} \varepsilon_i e^{-\alpha\tau_i} \leq \sum_{i=1}^\infty \varepsilon_i e^{-\alpha\tau_i}.$$

Note that the random variables ε_i and τ_i are independent for every $i = 1, 2, \dots$. Hence, for the L^2 norm we get

$$\|_\alpha\xi(\infty)'\|_2 \leq \sum_{i=1}^\infty \|\varepsilon_i e^{-\alpha\tau_i}\|_2 = \|\varepsilon\|_2 \sum_{i=1}^\infty \frac{1}{(1+2\alpha)^{i/2}} < \infty,$$

using the fact that in a homogeneous Poisson process with unit density, the birth times τ_i are distributed as $\Gamma(i, 1)$. □

Proposition 3.3. *Denote the number of living edges in the continuous model at time t by $E(t)$. Then*

$$\lim_{t\to\infty} e^{-\alpha t} E(t) = \left[\mathbb{E}^2(\varepsilon)\int_0^\infty t\,e^{-\alpha t} S(t)\,dt\right]^{-1} Y_\infty$$

almost surely, where Y_∞ is the same as in Theorem 2.3.

PROOF. Since $E(t) = Z^\phi(t)$ with the random characteristic $\phi(t) = \mathbb{1}_{\{0 \le t < \lambda\}}$, it is plausible to use Theorem 2.3. Hence the proof of the statement is conducted by showing that all assumptions imposed on $(\phi(t))_{t \ge 0}$ hold, and then calculating the constant m_∞^ϕ. However, since this random characteristic is just an indicator, the conditions are trivially satisfied, so it is enough to determine the constant, which, by the definitions and the previous remark on the intensity measure, is equal to

$$m_\infty^\phi = \frac{\int_0^\infty e^{-\alpha t}\mathbb{E}\phi(t)\,dt}{\int_0^\infty t\,e^{-\alpha t}\mu(dt)} = \frac{\int_0^\infty e^{-\alpha t}S(t)\,dt}{\mathbb{E}(\varepsilon)\int_0^\infty t\,e^{-\alpha t}S(t)\,dt} = \left[\mathbb{E}^2(\varepsilon)\int_0^\infty t\,e^{-\alpha t}S(t)\,dt\right]^{-1}. \quad \square$$

In order to transfer this result to the original discrete time cherry tree, we have to deal with the asymptotic growth rate of the number of events in the continuous time model.

Theorem 3.4. *Introduce the notation $H(t)$ for the number of events (birth or death) up to time t. Then, on the event of non-extinction,*

$$\lim_{t \to \infty} \frac{H(t)}{E(t)} = \frac{\mathbb{E}(\varepsilon) + 1 - \alpha}{\alpha}$$

almost everywhere.

PROOF. We want to use (4) from Theorem 2.3. Since the asymptotics of $E(t)$ is known from Proposition 3.3, it is enough to find an adequate random characteristic $\psi(t)$ for which $H(t) = Z^\psi(t)$ holds. It is obvious that $\psi(t) = \pi(t \wedge \lambda) + \mathbb{1}_{\{\lambda \le t\}}$ will do (note that $\pi(t) = 0$ for negative t).

To compute the numerator of (4), recall that $(\pi(t))_{t \ge 0}$ is a Poisson process with unit intensity, hence

$$\mathbb{E}(\pi(t \wedge \lambda)) = \mathbb{E}(t \wedge \lambda) = \int_0^t S(u)\,du.$$

Reversing the order of integrations, we get

$$\int_0^\infty e^{-\alpha t}\mathbb{E}(t \wedge \lambda) = \int_0^\infty \int_u^\infty e^{-\alpha t}\,dt\,S(u)\,du = \frac{1}{\alpha}\int_0^\infty e^{-\alpha u}S(u)\,du. \quad (9)$$

This, by (5) and (1), implies that

$$\int_0^\infty e^{-\alpha t}\mathbb{E}(\psi(t))\,dt = \frac{1}{\alpha}\int_0^\infty e^{-\alpha t}S(t)\,dt + \int_0^\infty e^{-\alpha t}(1 - S(t))\,dt =$$

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

$$= \frac{1}{\alpha} + \left(\frac{1}{\alpha} - 1\right) \frac{1}{\mathbb{E}(\varepsilon)} \int_0^\infty e^{-\alpha t}\, \mu(dt) = \frac{1}{\alpha} + \left(\frac{1}{\alpha} - 1\right) \frac{1}{\mathbb{E}(\varepsilon)}$$

holds. Plugging this, and the result of Proposition 3.3 into (4), we get

$$\frac{\int_0^\infty e^{-\alpha t} \mathbb{E}\big[\mathbb{1}_{\{\lambda \le t\}} + \pi(t \wedge \lambda)\big]\, dt}{\int_0^\infty e^{-\alpha t} \mathbb{E}\big[\mathbb{1}_{\{0 \le t < \lambda\}}\big]\, dt} = \frac{\frac{1}{\alpha} + \left(\frac{1}{\alpha} - 1\right)\frac{1}{\mathbb{E}(\varepsilon)}}{\int_0^\infty e^{-\alpha t} S(t)\, dt} = \frac{\mathbb{E}(\varepsilon) + 1 - \alpha}{\alpha},$$

as needed. □

It is evident that we can obtain results on the original discrete time cherry tree if we normalize a quantity of the continuous one with the number of events $H(t)$. For example, Theorem 3.4 immediately yields the following asymptotic property of the number E_n of living edges in the discrete time cherry tree.

Corollary 3.5. *Almost everywhere on the event of non-extinction,*

$$\lim_{n \to \infty} \frac{E_n}{n} = \lim_{t \to \infty} \frac{E(t)}{H(t)} = \frac{\alpha}{\mathbb{E}(\varepsilon) + 1 - \alpha},$$

where $E_n = |\mathcal{E}_n|$ denotes the number of edges after the n-th step. □

3.2. Probability of extinction. Inequality (7) contains a necessary and sufficient condition for our evolving graph process to be supercritical. In this case, the probability of extinction (when all edges die out) is strictly less than 1. Since there is an embedded Galton–Watson process with offspring size $\xi(\infty) = \xi(\lambda)$ in every general branching process, this probability can be obtained as the smallest nonnegative solution of the equation $g_{\xi(\lambda)}(z) = z$, where

$$g_{\xi(\lambda)}(z) = \mathbb{E}\big(z^{\xi(\lambda)}\big).$$

Hence, for the extinction probability, we need to compute this probability generating function. In the next lemma we derive a general formula, from which the requested generating function can easily be obtained. To that end, we first introduce the process $(\pi'(t))_{t \ge 0}$ that counts the number of vertices added to the graph by an edge up to and including its physical age t. This is a compound Poisson process having jumps exactly when so does $\pi(t)$. The jump sizes are κ_i (iid copies of κ).

Lemma 3.6. *Define the joint probability generating function of $\pi'(\lambda)$ and $\xi(\lambda)$ as*

$$f(x,y) = \mathbb{E}\big(x^{\pi'(\lambda)}y^{\xi(\lambda)}\big) = \sum_{i=0}^{\infty}\sum_{j=i}^{2i}\mathbb{P}(\pi'(\lambda)=i,\,\xi(\lambda)=j)x^i y^j.$$

Then

$$f(x,y) = 1 - \frac{1-g_{\kappa,\varepsilon}(x,y)}{m}\int_0^1 u^{\frac{1+a}{m}-1}\exp\left\{\int_u^1 g_{\kappa,\varepsilon}(x,sy)\,ds\right\}du,$$

where $g_{\kappa,\varepsilon}(x,y) = \mathbb{E}\big(x^\kappa y^\varepsilon\big)$ is the joint probability generating function of (κ,ε).

Remark 3.7. Using the well-known formula for the generating function of the binomial distribution and the connection between κ and ε, we obtain

$$g_{\kappa,\varepsilon}(x,y) = \mathbb{E}\big(x^\kappa\,\mathbb{E}(y^\varepsilon|\kappa)\big) = \mathbb{E}(x^\kappa(py^2+(1-p)y)^\kappa) = g_\kappa\big(xy(py+(1-p))\big)$$

for the joint probability generating function of (κ,ε).

PROOF OF LEMMA 3.6. First, consider the generating function

$$G(x,y) = \sum_{i=0}^{\infty}\sum_{j=0}^{i}\frac{\mathbb{P}(\exists\,t<\lambda:\pi'(t)=i,\,\xi(t)=i+j)}{1+b+c(i+j)}x^i y^j.$$

Since $\pi'(t) \le \xi(t) \le 2\pi'(t)$, it seems reasonable to deal with events of the form $\{\exists\,t<\lambda:\pi'(t)=i,\,\xi(t)=i+j\}$. For the sake of convenience, denote the coefficient of $x^i y^j$ by $v_{i,i+j}$. Note that $v_{i,i+j}=0$ for $j>i$. By the definition of our process $v_{0,0}=\frac{1}{b+1}$ and $v_{0,j}=0$ $(j\ge 1)$. Since

$$\mathbb{P}(\exists\,t<\lambda:\ \pi'(t)=i,\,\xi(t)=i+j)$$

$$=\sum_{\ell=1}^{i}\sum_{k=0}^{j}\mathbb{P}(\exists\,t<\lambda:\pi'(t)=i-\ell,\,\xi(t)=i-\ell+j-k)\times\frac{\mathbb{P}(\kappa=\ell,\,\varepsilon=\ell+k)}{1+b+c(i-\ell+j-k)},$$

with the notation introduced above we have the following recursion:

$$(1+b+c(i+j))v_{i,i+j} = \sum_{\ell=1}^{i}\sum_{k=0}^{j}v_{i-\ell,(i-\ell)+(j-k)}\mathbb{P}(\kappa=\ell,\varepsilon=\ell+k).$$

Multiply both sides by $x^i y^j$ and add up for $i\ge 1$, $0\le j\le i$ to get

$$(1+b)\left[G(x,y) - \frac{1}{1+b}\right] + c(x\,\partial_x G(x,y) + y\,\partial_y G(x,y))$$

$$= \sum_{i=1}^{\infty}\sum_{j=0}^{i}\sum_{\ell=1}^{i}\sum_{k=0}^{j} v_{i-\ell,(i-\ell)+(j-k)}\mathbb{P}(\kappa = \ell, \varepsilon = \ell + k)x^i y^j$$

$$= \sum_{\ell=1}^{\infty}\sum_{k=0}^{\ell}\mathbb{P}(\kappa = \ell, \varepsilon = \ell + k)x^\ell y^k \sum_{i=\ell}^{\infty}\sum_{j=k}^{i} v_{i-\ell,(i-\ell)+(j-k)}x^{i-\ell}y^{j-k}$$

$$= g_{\kappa,\varepsilon}\left(\tfrac{x}{y},\, y\right)G(x,y).$$

After rearrangement, we obtain the following partial differential equation:

$$\begin{cases} \left[1 + b - g_{\kappa,\varepsilon}\left(\tfrac{x}{y},\, y\right)\right]G(x,y) + c(x\,\partial_x G(x,y) + y\,\partial_y G(x,y)) = 1; \\ G(0,y) = \frac{1}{1+b}\,. \end{cases}$$

To solve this equation, we introduce the function $h(t) = G(tx, ty)$, which then satisfies the following linear ODE:

$$\begin{cases} \left[1 + b - g_{\kappa,\varepsilon}\left(\tfrac{x}{y},\, ty\right)\right]h(t) + cth'(t) = 1; \\ h(0) = \frac{1}{1+b}\,. \end{cases}$$

Such an ODE is a routine problem to solve, and its solution is

$$h(t) = \frac{1}{c}\, t^{-\frac{1+b}{c}} \int_0^t u^{\frac{1+b}{c}-1} \exp\left\{ \int_u^t g_{\kappa,\varepsilon}\left(\tfrac{x}{y},\, sy\right) ds \right\} du.$$

The correspondence between $h(t)$ and $G(x,y)$ yields

$$G(x,y) = h(1) = \frac{1}{c}\int_0^1 u^{\frac{1+b}{c}-1} \exp\left\{ \int_u^1 g_{\kappa,\varepsilon}\left(\tfrac{x}{y},\, sy\right) ds \right\} du.$$

Let us turn to the bivariate generating function f we are interested in. Clearly,

$$f\left(\frac{x}{y},\, y\right) = \sum_{i=0}^{\infty}\sum_{j=0}^{i} \mathbb{P}(\pi'(\lambda) = i, \xi(\lambda) = i + j)x^i y^j.$$

The probability that an edge of biological age j dies before the next reproduction event is

$$\frac{b + cj}{1 + b + cj}\,,$$

therefore

$$\mathbb{P}(\pi'(\lambda) = i, \, \xi(\lambda) = i + j)$$

$$= \mathbb{P}(\exists \, t < \lambda : \pi'(t) = i, \, \xi(t) = i + j) \, \frac{b + c(i + j)}{1 + b + c(i + j)} = [b + c(i + j)] v_{i,i+j}.$$

Consequently,

$$f\left(\frac{x}{y}, \, y\right) = \sum_{i=0}^{\infty} \sum_{j=0}^{i} [b + c(i+j)] v_{i,i+j} x^i y^j = b \, G(x, y) + c\big(x \, \partial_x G(x, y) + y \, \partial_y G(x, y)\big).$$

As we have already seen,

$$c\big(x \, \partial_x G(x, y) + y \, \partial_y G(x, y)\big) = 1 - \left[1 + b - g_{\kappa,\varepsilon}\left(\tfrac{x}{y}, \, y\right)\right] G(x, y),$$

which implies

$$f\left(\frac{x}{y}, \, y\right) = 1 - \left[1 - g_{\kappa,\varepsilon}\left(\tfrac{x}{y}, \, y\right)\right] G(x, y).$$

Finally, so as to get the generating function $f(x, y)$, we simply have to replace x with xy. Then we conclude with

$$f(x, y) = 1 - [1 - g_{\kappa,\varepsilon}(x, y)] G(xy, y). \qquad \square$$

Substituting 1 for x, we get the generating function of $\xi(\lambda)$. Note that $g_{\kappa,\varepsilon}(1, y) = g_\varepsilon(y)$.

Corollary 3.8. *The probability generating function of $\xi(\lambda)$ is*

$$g_{\xi(\lambda)}(z) = 1 - \frac{1 - g_\varepsilon(z)}{c} \int_0^1 u^{\frac{1+b}{c} - 1} \exp\left\{ \int_u^1 g_\varepsilon(sy) \, ds \right\} du. \qquad \square$$

Turning back to the theory of general branching proesses, we can determine the probability that our random cherry tree eventually dies out when the reproduction mean $\mathbb{E}(\xi(\lambda))$ is greater than 1.

Corollary 3.9. *Assume that (7) holds. Then the probability that the random cherry tree process becomes extinct is equal to the smallest nonnegative root of the equation*

$$\frac{1 - g_\varepsilon(z)}{c} \int_0^1 u^{\frac{1+b}{c} - 1} \exp\left\{ \int_u^1 g_\varepsilon(sy) \, ds \right\} du = 1 - z.$$

PROOF. The probability of extinction is the smallest nonnegative root of the fixpoint equation $g_{\xi(\lambda)}(z) = z$. $\qquad \square$

3.3. Asymptotics of vertices. This section focuses on the vertices in the cherry tree. First we consider the number of vertices, then turn our attention to how the degree of a fixed vertex changes in time. We deal with the former question in a similar way as in the proof of Proposition 3.3, meanwhile the latter one needs a slightly more work.

Proposition 3.10. *Let $V_n = |\mathcal{V}_n|$. Almost everywhere on the event of non-extinction,*

$$\lim_{n \to \infty} \frac{V_n}{n} = \frac{\mathbb{E}(\kappa)}{\mathbb{E}(\varepsilon) + 1 - \alpha} \,.$$

PROOF. It is obvious that

$$\lim_{n \to \infty} \frac{V_n}{n} = \lim_{t \to \infty} \frac{V(t)}{H(t)}$$

holds. Furthermore, from the proof of Theorem 3.4 we know that $H(t) = Z^\phi(t)$, where

$$\phi(t) = \pi(t \wedge \lambda) + \mathbb{1}_{\{0 \le t < \lambda\}},$$

for which

$$\int_0^\infty e^{-\alpha t} \mathbb{E}\phi(t)\, dt = \frac{1}{\alpha} + \left(\frac{1}{\alpha} - 1\right) \frac{1}{\mathbb{E}(\varepsilon)} = \frac{\mathbb{E}(\varepsilon) + 1 - \alpha}{\alpha \mathbb{E}(\varepsilon)} \,.$$

Hence, we only need to find a characteristic ψ that counts the vertices in the graph and then compute the corresponding integral $\int_0^\infty e^{-\alpha t} \mathbb{E}\psi(t)\, dt$. Set $\psi(t) = \pi'(\lambda \wedge t)$ (the compound Poisson process $\pi'(\cdot)$ was introduced in Subsection 3.2), then $Z^\psi(t)$ is less than $V(t)$ by the two initial nodes, whose significance asymptotically vanishes. Now we get

$$\mathbb{E}\psi(t) = \mathbb{E}(\kappa)\mathbb{E}\pi(t \wedge \lambda) = \mathbb{E}(\kappa) \int_0^t S(u)\, du,$$

and consequently,

$$\int_0^\infty e^{-\alpha t} \mathbb{E}\psi(t)\, dt = \frac{\mathbb{E}(\kappa)}{\alpha} \int_0^\infty e^{-\alpha t} S(t)\, dt = \frac{1}{\alpha(1 + p)},$$

using (1). Applying that $\mathbb{E}(\varepsilon) = (1 + p)\mathbb{E}(\kappa)$, by Theorem 2.3 we obtain

$$\lim_{t \to \infty} \frac{V(t)}{H(t)} = \frac{\mathbb{E}(\kappa)}{\mathbb{E}(\varepsilon) + 1 - \alpha} \,,$$

as requested.   □

It is obvious (or, using the random characteristic $\xi(t) - \pi'(t)$, easy to check) that the asymptotic proportion of vertices born with two edges is equal to p. In this way, we can get the asymptotic number of triangles ever created in the graph. However, if we wanted to examine the number of *living* triangles only, the resulting formula would be much more complicated.

Next, let us turn to the behaviour of the degree process of a fixed vertex. To handle this problem, we need to define a new branching process, closely related to the original one constructed on the edges, which only takes the edges joined to the given vertex into consideration. To this end, suppose that the fixed vertex is born with a single initial edge and introduce the following notations.

Whenever an edge, joined to the vertex under consideration, gives birth to κ cherries and semi-cherries, each can increase the degree of the monitored vertex by 1; namely, a cherry will always increase, but a semi-cherry only with probability $1/2$. Let ϕ_i be equal to 2 if the contribution of the i-th new vertex is a cherry, and 1, if it is a semi-cherry. Let $\gamma_1, \gamma_2, \ldots$ be iid with conditional distribution

$$P(\gamma_i = 1 | \varphi_i = 2) = 1; \quad P(\gamma_i = 1 | \varphi_i = 1).$$

Then the increase of the degree at a birth event is

$$\delta = \sum_{i=1}^{\kappa} \gamma_i.$$

Introduce the notation

$$\Delta_n = \sum_{i=1}^{n} \delta_i,$$

where the random variables δ_i are iid copies of δ. Then the reproduction process of the monitored vertex's degree is $\eta(t) = \Delta_{\pi(t \wedge \lambda)}$, where $(\pi(t))_{t \geq 0}$ and λ are the same as before. Note that the biological age of an edge still grows by every birth, even though it is not considered in the degree process.

In order to find the condition of supercriticality and formulate the equation for the Malthusian parameter, we can argue as follows. By the definition, $\mathbb{E}(\gamma) = \mathbb{E}(\phi)/2$, $\mathbb{E}(\delta) = \mathbb{E}(\varepsilon)/2$, and as a consequence we have

$$\mathbb{E}\eta(\lambda) = \mathbb{E}(\Delta_{\pi(\lambda)}) = \mathbb{E}(\delta)\mathbb{E}(\lambda) = \frac{1}{2}\mathbb{E}(\varepsilon)\mathbb{E}(\lambda) = \frac{1}{2}\mathbb{E}\xi(\infty).$$

Referring to (7), one can immediately see that the degree process is supercritical if $\mathbb{E}\eta(\infty) = \mathbb{E}\xi(\infty)/2 > 1$, that is,

$$\frac{\mathbb{E}(\varepsilon)}{c} \int_0^1 u^{\frac{1+b}{c} - 1} \exp\left\{ \frac{1}{c} \int_u^1 \frac{g_\varepsilon(v)}{v} \, dv \right\} du > 2.$$

Similarly, the intensity measure of the degree process of a fixed vertex is just
the half of the edge process' intensity measure, from which it follows that the
Malthusian parameter $\beta > 0$ of the former one satisfies the equation

$$\frac{\mathbb{E}(\varepsilon)}{c} \int_0^1 u^{\frac{\beta+1+b}{c}-1} \exp\left\{\frac{1}{c}\int_u^1 \frac{g_\varepsilon(v)}{v}\,dv\right\} du = 2.$$

It is clear that $\beta < \alpha$.

For the probability that the vertex becomes isolated, i.e., the corresponding
degree process extincts, we need to compute the probability generating function
of $\eta(\infty)$, for which we can use Lemma 3.6. In fact, this is only valid in the case
when the initial degree of the vertex is 1. When the initial degree of the observed
vertex is 2, its degree process is the superposition of two independent copies of
$(\eta(\cdot), \lambda)$.

Proposition 3.11. *The probability generating function of $\eta(\lambda)$ is*

$$1 - \frac{1 - g_{\kappa,\varepsilon}\left(\frac{(1+z)^2}{4z}, \frac{2z}{1+z}\right)}{c} \int_0^1 u^{\frac{1+b}{c}-1} \exp\left\{\int_u^1 g_{\kappa,\varepsilon}\left(\frac{(1+z)^2}{4z}, \frac{2sz}{1+z}\right) ds\right\} du.$$

*Hence, if $\mathbb{E}\eta(\lambda) > 1$, the probability that a fixed vertex eventually gets isolated
is equal to $pz^2 + (1-p)z$, where z is the smallest positive root of the equation*

$$\frac{1 - g_{\kappa,\varepsilon}\left(\frac{(1+z)^2}{4z}, \frac{2z}{1+z}\right)}{c} \int_0^1 u^{\frac{1+b}{c}-1} \exp\left\{\int_u^1 g_{\kappa,\varepsilon}\left(\frac{(1+z)^2}{4z}, \frac{2sz}{1+z}\right) ds\right\} du = 1 - z.$$

PROOF. By the law of total expectation,

$$g_{\eta(\lambda)}(z) = \mathbb{E}\left(z^{\eta(\lambda)}\right) = \mathbb{E}\left[\mathbb{E}\left(z^{\eta(\lambda)}\big|\pi'(\lambda), \xi(\lambda)\right)\right],$$

therefore it is sufficient to deal with the conditional expectation

$$\mathbb{E}\left(z^{\eta(\infty)}\big|\pi'(\lambda) = \ell, \xi(\lambda) = k\right)$$

where $0 \le \ell \le k \le 2\ell$. Clearly, if k new edges are added with ℓ new vertices, then
the increment is composed of $k - \ell$ cherries and $2\ell - k$ semi-cherries. Thus the
conditional distribution of $\eta(\lambda) - (k - \ell)$ is Binomial$(2\ell - k, 1/2)$. Hence,

$$\mathbb{E}\left(z^{\eta(\lambda)}\big|\pi'(\lambda) = \ell, \xi(\lambda) = k\right) = z^{k-l}\left(\frac{1+z}{2}\right)^{2\ell-k}.$$

Consequently, by Lemma 3.6 we get

$$g_{\eta(\lambda)}(z) = \mathbb{E}\left[z^{\xi(\lambda)-\pi'(\lambda)}\left(\frac{1+z}{2}\right)^{2\pi'(\lambda)-\xi(\lambda)}\right] = f\left(\frac{(1+z)^2}{4z}, \frac{2z}{1+z}\right)$$

$$= 1 - \frac{1 - g_{\kappa,\varepsilon}\left(\frac{(1+z)^2}{4z}, \frac{2z}{1+z}\right)}{c} \int_0^1 u^{\frac{1+b}{c}-1} \exp\left\{\int_u^1 g_{\kappa,\varepsilon}\left(\frac{(1+z)^2}{4z}, \frac{2sz}{1+z}\right) ds\right\} du,$$

completing the proof.   □

3.4. Further properties. The first proposition of the section is about the asymptotic proportion of living edges without any descendants.

Proposition 3.12. *Let us denote the number of childless edges after n steps by O_n, then*

$$\lim_{n\to\infty} \frac{O_n}{E_n} = \frac{\mathbb{E}(\varepsilon)}{1+b+\alpha}$$

almost everywhere on the event of non-extinction.

PROOF. Similarly to what we did in the proofs of previous results, we will introduce the notation $O(t)$ for the number of living childless edges at time t in the continuous time model, and since

$$\lim_{t\to\infty} \frac{O_n}{E_n} = \lim_{n\to\infty} \frac{O(t)}{E(t)}$$

holds, we can rely on Proposition 3.3 and Theorem 2.3 with the appropriate random characteristic. It is easy to see that the right choice is

$$\phi(t) = \mathbb{1}_{\{0 \le t < \tau_1 \wedge \lambda\}},$$

where τ_1 is the first birth time in the Poisson process $(\pi(t))_{t\ge 0}$.

To calculate the corresponding limit fraction, we first need to compute the mean $\mathbb{E}\phi(t) = \mathbb{P}(\tau_1 \wedge \lambda > t)$. The distribution of τ_1 is exponential with mean 1, and up to τ_1, the hazard rate of the edge lifetime is constant b, that is, λ behaves like an exponential random variable, which is independent of τ_1. Therefore $\tau_1 \wedge \lambda$ is exponentially distributed with parameter $1+b$, thus $\mathbb{E}\phi(t) = e^{-(1+b)t}$.

By Theorem 2.3 we have

$$\lim_{t\to\infty} \frac{O(t)}{E(t)} = \frac{\int_0^\infty e^{-\alpha t} e^{-(1+b)t}\, dt}{\int_0^\infty e^{-\alpha t} S(t)\, dt} = \frac{\mathbb{E}(\varepsilon)}{1+b+\alpha}\,. \qquad \square$$

So far we could easily utilize the direct connection between the discrete and the continuous models. The next example will show a case where the transfer of results is not so straightforward.

Consider the continuous cherry tree and define

$$T(t) = \big|\{e : \sigma_e \le t\}\big|;$$

this is the number of edges born up to time t, irrespectively that they are still present or already deleted. Moreover, let

$$J(t) = \int_0^t E(s)\, ds,$$

where $E(s)$ is the number of living edges at time s. Clearly,

$$J(t) = \int_0^t \sum_e \mathbb{1}_{\{\sigma_e \leq s < \sigma_e + \lambda_e\}}\, ds = \sum_e \int_0^t \mathbb{1}_{\{\sigma_e \leq s < \sigma_e + \lambda_e\}}\, ds = \sum_e (t - \sigma_e)^+ \wedge \lambda_e,$$

thus $J(t)$ is the sum of the lengths of time the edges spent in the graph up to time t. In the statistical analysis of survival data, this quantity is called *the total time on test*. The summands can also be considered a censored sample from the lifetime distribution λ, hence the mean lifetime $\mathbb{E}(\lambda)$ can be estimated by $\hat{\lambda}_1(t) = J(t)/T(t)$. As a result of censoring, this estimation is underbiased. One might reduce the bias by leaving censored observations out of consideration. This leads to the estimator $\hat{\lambda}_2(t) = \widetilde{J}(t)/\widetilde{T}(t)$, where

$$\widetilde{J}(t) = \sum_{e\,:\,\sigma_e + \lambda_e \leq t} \lambda_e, \qquad \widetilde{T}(t) = \left|\{e : \sigma_e + \lambda_e \leq t\}\right|.$$

We should remark that this second estimator is still underbiased, because the exponential growth of the continuous cherry tree imples that a non-negligible proportion of the edges born so far entered the graph in the recent past, and they are only counted if died at an unusually young age.

Let us compute their limits as $t \to \infty$.

Proposition 3.13. *Almost everywhere on the event of non-extinction,*

$$\lim_{t\to\infty} \hat{\lambda}_1(t) = \frac{1}{\mathbb{E}(\varepsilon)}, \qquad \lim_{t\to\infty} \hat{\lambda}_2(t) = \frac{1 - \alpha\mathbb{E}(\varepsilon)\int_0^\infty t\, e^{-\alpha t} S(t)\, dt)}{\mathbb{E}(\varepsilon) - 1}.$$

PROOF. All four quantities can be expressed as $Z^\phi(t)$ by the help of suitable random characteristics ϕ as Table 1 shows.

$J(t)$	$\phi_1(t) = (t \wedge \lambda)\, \mathbb{1}_{\{t \geq 0\}}$
$T(t)$	$\phi_2(t) = \mathbb{1}_{\{t \geq 0\}}$
$\widetilde{J}(t)$	$\phi_3(t) = \lambda\, \mathbb{1}_{\{\lambda \leq t\}}$
$\widetilde{T}(t)$	$\phi_4(t) = \mathbb{1}_{\{\lambda \leq t\}}$

Table 1. Statistics and the corresponding random characteristics

First, we have to compute $\mathbb{E}\phi_i(t)$, $i = 1, 2, 3, 4$, $t \geq 0$.

$$\mathbb{E}\phi_1(t) = \mathbb{E}(t \wedge \lambda) = \int_0^t S(s)\,ds, \qquad\qquad \mathbb{E}\phi_2(t) = 1,$$

$$\mathbb{E}\phi_3(t) = \mathbb{E}(\lambda\,\mathbb{1}_{\{\lambda \leq t\}}) = \int_0^t [S(s) - S(t)]\,ds, \qquad \mathbb{E}\phi_4(t) = 1 - S(t).$$

Therefore, by (9) and (5) we have

$$\int_0^\infty e^{-\alpha t}\mathbb{E}\phi_1(t)\,dt = \frac{1}{\alpha}\int_0^\infty e^{-\alpha t}S(t)\,dt = \frac{1}{\alpha\mathbb{E}(\varepsilon)}\,.$$

Obviously,

$$\int_0^\infty e^{-\alpha t}\mathbb{E}\phi_2(t)\,dt = \frac{1}{\alpha},$$

$$\int_0^\infty e^{-\alpha t}\mathbb{E}\phi_4(t)\,dt = \int_0^\infty e^{-\alpha t}(1 - S(t))\,dt = \frac{1}{\alpha} - \frac{1}{\alpha\mathbb{E}(\varepsilon)}\,,$$

and

$$\begin{aligned}
\int_0^\infty e^{-\alpha t}\mathbb{E}\phi_3(t)\,dt &= \int_0^\infty e^{-\alpha t}\int_0^t [S(s) - S(t)]\,ds\,dt \\
&= \int_0^\infty e^{-\alpha t}\mathbb{E}\phi_1(t)\,dt - \int_0^\infty t\,e^{-\alpha t}S(t)\,dt \\
&= \frac{1}{\alpha\mathbb{E}(\varepsilon)} - \int_0^\infty t\,e^{-\alpha t}S(t)\,dt = \frac{1}{\alpha\mathbb{E}(\varepsilon)}\left(1 - \alpha\int_0^\infty t\,e^{-\alpha t}\mu(dt)\right),
\end{aligned}$$

using that $\mathbb{E}(\varepsilon)S(t)\,dt = \mu(dt)$. Application of Theorem 2.3 will complete the proof. $\qquad\square$

Remark 3.14. Unfortunately, the last integral cannot be transformed into a closed form, but we find the following connection between $T(t)$ and $\widetilde{J}(t)$:

$$\lim_{t\to\infty} e^{-\alpha t}T(t) = Y_\infty + \mathbb{E}(\varepsilon)\lim_{t\to\infty} e^{-\alpha t}\widetilde{J}(t)$$

almost everywhere on the event of non-extinction.

Next, let us turn to the discrete time cherry tree. Though the number T_n of edges born up to time t is of order n, the total time on test statistic $J_n = E_0 + E_1 + \cdots + E_n$ exhibits a completely different behaviour. By Corollary 3.5 we have

$$J_n \sim \frac{\alpha}{\mathbb{E}(\varepsilon) + 1 - \alpha}\sum_{i=0}^n i \sim \frac{\alpha n^2}{2(\mathbb{E}(\varepsilon) + 1 - \alpha)}\,, \tag{10}$$

thus J_n/T_n tends to infinity on the event of non-extinction. This is not at all surprising, because the correspondence of the discrete and continuous time models is based on a time transform, by which the discrete time model is a slowed down version of the continuous one. The later an edge is born, the longer its life will last. If we want to infer from a continuous counterpart, time has to be measured by the number of events; that is, instead of $J(t)$ we should use $\int_0^t E(s)\,dH(s)$. Using Corollary 3.5 and integrating by parts, we get

$$\int_0^t E(s)\,dH(s) \sim \int_0^t e^{-\alpha(t-s)}E(t)\,dH(s)$$
$$= E(t)\left(\left[e^{-\alpha(t-s)}H(s) \right]_{s=0}^t - \int_0^t \alpha e^{-\alpha(t-s)}H(s)\,ds \right)$$
$$\sim E(t)\left(H(t) - \int_0^t \alpha e^{-2\alpha(t-s)}H(t)\,ds \right) \sim \tfrac{1}{2}E(t)H(t),$$

which already corresponds to (10).

In the discrete model it seems more adequate to measure an edge's lifetime by the number of birth events, which is not affected by time transformations. The mean number of litters during the life of an edge can be estimated by the statistic B_n/T_n, where B_n is the number of reproduction events in the first n steps. The corresponding quantity in the continuous model can be counted by the random characteristic $\phi(t) = \pi(t \wedge \lambda)$. Hence,

$$\lim_{n\to\infty} \frac{B_n}{T_n} = \lim_{t\to\infty} \frac{\int_0^t e^{-\alpha t}\mathbb{E}(t \wedge \lambda)\,dt}{\int_0^\infty e^{-\alpha t}\,dt} = \frac{1}{\mathbb{E}(\varepsilon)};$$

this coincides with the limit of $\hat{\lambda}_1(t)$.

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