# Perfect simulation for a continuous one-dimensional loss network

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**Abstract** Sufficient conditions for ergodicity of a one-dimensional loss networks on $\mathbb{R}$ with length distribution $G$ and cable capacity $C$ are found. These processes are spatial birth-and-death processes with an invariant measure which is absolutely continuous with respect to a Poisson process and we implement the perfect simulation scheme based on the clan of ancestors introduced by Fernández, Ferrari and Garcia (2002) to obtain perfect samples viewed in a finite window of the *infinite-volume* invariant measure. Moreover, by a better understanding of the simulation process it is possible to get a better condition for ergodicity.

**Key words:** clan of ancestors, branching process, Peron-Frobenius root, perfect simulation

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## 1 Introduction

Kelly (1991) introduced a continuous unbounded loss network described as follows. Imagine that users are arranged along an infinitely long cable and that a call between two points on the cable

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$s_1,\ s_2 \in \mathbb{R}$ involves just that section of the cable between $s_1$ and $s_2$. Past any point along its length the cable has the capacity to carry simultaneously up to $C$ calls: a call attempt between $s_1$, $s_2 \in \mathbb{R}$, $s_1 < s_2$, is lost if past any point of the interval $[s_1, s_2]$ the cable is already carrying $C$ calls. Suppose that calls are attempted at points in $\mathbb{R}$ following a homogeneous Poisson process with rate $\lambda$. Assume that the section of the cable demanded by a call has distribution $\pi$ with finite mean $\rho_1$ and the duration of a call has exponential distribution with mean one. Assume that the location of a call, the cable section needed and its duration are independent. Let $m(s,t)$ be the number of calls in progress past point $s$ on the cable at time $t$. Kelly (1991) conjectured that $((m(s,t), s \in \mathbb{R}), t \geq 0)$ has a unique invariant measure, given by a stationary $M/G/\infty$ queue (Markov arrivals, general service time and infinite servers) conditioned to have at most $C$ clients at all times. Ferrari and Garcia (1998) used a continuous (non-oriented) percolation argument to prove the above conjecture whenever $\pi$ has finite third moment and the arrival rate $\lambda$ is sufficiently small. Fernández, Ferrari and Garcia (2002) using an oriented percolation argument improved this bound to

$$\lambda(\rho_2 + \rho_1 + 1) < 1 \tag{1.1}$$

where $\rho_1$ and $\rho_2$ are the first and second moment of distribution $\pi$ respectively. This argument is based on a graphical representation of the birth and death process and it is the basis for the perfect simulation scheme "*Backward-Forward Algorithm*", described in Fernández, Ferrari and Garcia (2002). This algorithm involves the "thinning" of a marked Poisson process —the *free process*— which dominates the birth-and-death process, and it involves a time-backward and a time-forward sweep. The initial stage of the construction is done *toward the past*, starting with a finite window and retrospectively looking to *ancestors*, namely to those births in the past that could have (had) an influence on the current birth. The construction of the *clan of ancestors* constitutes the time-backward sweep of the algorithm. Once this clan is completely constructed, the algorithm proceeds in a time-forward fashion "cleaning up" successive generations according to appropriate penalization schemes. The relation "being ancestor of" induces a backward in time *contact/oriented percolation* process. The algorithm is applicable as long as this oriented percolation process is sub-critical.

In this work, using the Peron-Frobenius theory for sub-criticality of branching process we obtain

a new bound given by

$$\lambda(\sqrt{\rho_2} + \rho_1) < 1. \tag{1.2}$$

However, studying the characteristics of the clan of ancestors through simulation in Section 9 it is clear that the domination by the branching process is not sharp. That is, the number of ancestors is much smaller than the total number of the population in the branching process and the clan of ancestors can be finite even though the branching is supercritical. By studying the perfect simulation algorithm it is possible to improve bound (1.2) to

$$\lambda < \frac{2}{\rho_1 + b_1/2 + \sqrt{\rho_2 + a_1 + b_1^2/4}} \tag{1.3}$$

where $a_1$ and $b_1$ are positive constants related to higher moments of the $\pi$ distribution.

# 2 Space processes of interest

## 2.1 Point processes

A point process models the random distribution of indistinguishable points in some space, for concreteness we take this space to be $\mathbb{R}^d$. We identify a point process $N$ with the counting measure $N$ given by assigning unit mass to each point, that is, $N(A)$ is the number of points in a set $A$. The latter assumption implies that such a process $N$ is determined by the probability distribution of the random variables $N(A)$ = number of points in $A \in \mathcal{B}(\mathbb{R}^d)$, the bounded subsets of $\mathbb{R}^d$. With this identification in mind, consider $\mathcal{N}(\mathbb{R}^d)$ be the set of counting measures on $\mathbb{R}^d$. For a more general discussion, see Daley and Vere-Jones (1988).

### 2.1.1 Poisson point processes

The Poisson point process is one of the most popular models for counting problems. Besides being a good description of many natural phenomena, it is very simple from the computational point of view. Furthermore, or perhaps relatedly, it is used as a reference measure to define other types of processes. Its general definition is as follows.

**Definition 2.1** *Let $\nu$ be a Radon measure on $\mathbb{R}^d$. A point process $N_\nu$ on $\mathbb{R}^d$ is a* Poisson process *with mean measure $\nu$ if its state space is $\{N \in \{0,1\}^{\mathbb{R}^d} : N(x) = 1$ for only a countable number of $x \in \mathbb{R}^d\}$, and defining $N_\nu(A) = \int_A N_\nu(dx)$,*

*(i) For any disjoint $A_1, A_2, \ldots, A_k \in \mathcal{B}(\mathbb{R}^d)$ the random variables $N_\nu(A_1), N_\nu(A_2), \ldots, N_\nu(A_k)$ are independent, and*

*(ii) For each $A \in \mathcal{B}(\mathbb{R}^d)$ and $k \geq 0$*

$$\mathbb{P}[N_\nu(A) = k] \;=\; \frac{e^{-\nu(A)}\nu(A)^k}{k!}\,. \tag{2.2}$$

We can think the process $N_\nu$ either as a random counting measure or as the random set of points $\{x \in \mathbb{R}^d : N_\nu(x) = 1\}$.

A $\lambda$-*homogeneous Poisson process* is a process with $\nu = \lambda\, m_d$, where $\lambda$ is a constant and $m_d$ the Lebesgue measure on $\mathbb{R}^d$. The simulation of such a process is simple:

- For each finite window $W$, generate $R \sim \text{Poisson}\Big(\lambda\, m_d(W)\Big)$;
- Given $R = r$ generate $U_1, \ldots, U_r$ independently distributed according to the uniform distribution in $W$.
- Repeat independently for disjoint windows.

More general Poisson processes in which $\nu$ is absolutely continuous with respect to the Lebesgue measure in $\mathbb{R}^d$ with density $f$, can be simulated using the *projection method* described by Garcia (1995). Consider the set

$$C_f \;=\; \Big\{(x,s); x \in \mathbb{R}^d, s \in \mathbb{R}, 0 \leq s \leq f(x)\Big\}\,, \tag{2.3}$$

and the Poisson process $N_{m_{d+1}}$ on $\mathbb{R}^{d+1}$ with Lebesgue mean measure $m_{d+1}$. Then the process $N_{C_f}$ on $\mathbb{R}^d$ defined by

$$N_{C_f}(A) = N_{m_{d+1}}\Big(C_f \cap (A \times \mathbb{R})\Big) \tag{2.4}$$

is Poisson with mean $\nu$. In words, it is enough to simulate $N_{m_{d+1}}$ as above, and then take the points that lie in $C_f$ and project them onto $\mathbb{R}^d$. More generally, this scheme can be used for Poisson processes whose measure $\nu$ has the form

$$\nu(A) \;=\; m_{d+1}\Big(C \cap (A \times \mathbb{R})\Big) \tag{2.5}$$

for some $C \in \mathbb{R}^{d+1}$.

# 3 Marked Poisson processes

Sometimes it is convenient to allow each point of the process to have a mark belonging to a set $\mathcal{M}$. That is, a *marked point process* is a point process $M$ on $\mathbb{R}^d \times \mathcal{M}$ such that the marginal process of locations $M(\cdot \times \mathcal{M})$ is a point process on $\mathbb{R}^d$.

Notice that not all point processes on a product space are marked point processes, for example a $\lambda$-homogeneous Poisson process on $\mathbb{R}^2$ cannot be represented as a marked point process on $\mathbb{R} \times \mathbb{R}$.

An important example is the *completely independent marked point process*. Let $N$ be a marked point process on $\mathbb{R}^d \times \mathcal{M}$ with the property that the $n$ random variables of the set

$$\{N(A_i \times B_i) :\ \text{bounded } A_i \in \mathcal{B}_{\mathbb{R}^d}, B_i \in \mathcal{B}_{\mathcal{M}},\ i = 1, 2, \ldots, n\} \tag{3.1}$$

are mutually independent whenever $A_i$ are disjoint. It is easy to see Daley and Vere-Jones (1988) that a marked point process with the complete independence property is fully specified by two components:

(i) a Poisson process of locations $N(\cdot \times \mathcal{M})$; and

(ii) a family of probability distributions $\{P(\cdot \mid x), x \in \mathbb{R}^d\}$ giving the distribution of the mark in $\mathcal{M}$.

A very important example of a completely independent marked point process is the so called Boolean model. Let $N$ be a $\lambda$-homogeneous Poisson point process in $\mathbb{R}^d$, represent it by the location of its points as

$$N = \{\xi_1, \xi_2, \ldots\}. \tag{3.2}$$

Let $S_1, S_2, \ldots$ be a collection of independent $\mathcal{B}_{\mathbb{R}^d}$-valued random variables. That is, $S_i$ is a random Borel set on $\mathbb{R}^d$ and construct the marked point process

$$M = \{(\xi_1, S_1), (\xi_2, S_2), \ldots\} \tag{3.3}$$

or represent it as a coverage process on $\mathbb{R}^d$ given by

$$\mathcal{C} = \{\xi_i + S_i, i = 1, 2, \ldots\} \tag{3.4}$$

where $\xi + S = \{\xi + z; z \in S\}$. Boolean models have the property that the number of sets $C \in \mathcal{C}$ that cover a fixed point $x \in \mathbb{R}^d$ is a Poisson random variable with mean $\lambda\mathbb{E}(\mathrm{vol}(S))$. For more details about coverage processes see Hall (1988).

## 3.1 Spatial birth-and-death processes (in $\mathbb{R}^d$)

A spatial birth-and-death process is a continuous time Markovian process. Its state space $\mathcal{N} := \mathcal{N}(\mathbb{R}^d)$ is the family of point configurations in $\mathbb{R}^d$. The evolution of these processes in time are given either by the *birth* of a new point to be added to the actual configuration or by the *death* of an existing point that will be eliminated from the actual configuration. Moreover, they have the Markovian property in time that, the probability of a change depends only on the actual configuration of the system. Births are controlled by a *birth rate* $\mathbf{b}$, a non-negative measurable function

$$\mathbf{b} : \mathbb{R}^d \times \mathcal{N} \to [0, \infty)$$

satisfying

$$\int_B \mathbf{b}(x, \eta)dx < \infty$$

for each $B$, bounded Borel set, and for all $\eta \in \mathcal{N}$. The probability of a birth to occur in the set $B$, during $[t, t + s)$, given the configuration at time $t$ to be $\eta$ $t$, is

$$s \int_B \mathbf{b}(x, \eta)dx + o(s).$$

The *death rate* $\mathbf{d}$ is also a non-negative measurable function

$$\mathbf{d} : \mathbb{R}^d \times \mathcal{N} \to [0, \infty).$$

The probability of a point from $x \in \eta$ be eliminated during the time interval $[t, t + s)$, given that $\eta$ is the configuration of the process at $t$ is:

$$s \cdot \mathbf{d}(x, \eta) + o(s).$$

These functions $\mathbf{b}$ and $\mathbf{d}$ characterize the birth-and-death process whose infinitesimal generator is given by:

$$Af(\eta) = \int \mathbf{b}(x,\eta)[f(\eta \cup \{x\}) - f(\eta)]dx + \int \mathbf{d}(x,\eta\backslash\{x\})[f(\eta\backslash\{x\}) - f(\eta)]\eta(dx). \tag{3.5}$$

for "suitable" functions $f$.

We are going to consider a particular class of birth-and-death processes. Let $\mathcal{G}$ be a family of objects $\gamma$ ($\gamma \subseteq \mathbb{R}^d$), which we will call *individuals*, and consider a state space $\mathcal{S} = \{\xi \in \mathbb{N}^{\mathcal{G}} \ : \ \xi(\gamma) \neq 0$ only for a countable set of $\gamma \in \mathcal{G}\}$. A birth-and-death process $\eta_t$ is defined by a marked Poisson process characterized by non-negative measurable function $\mathbf{b}(\gamma,\eta)$ (same sense as before) The marks include a life-time exponentially distributed with mean one and the length of the call. If the rate densities are independent of the actual configuration there exists $\omega : \mathbf{G} \to [0,\infty)$ such that

$$\mathbf{b}(\gamma,\eta) = \omega(\gamma) \tag{3.6}$$

we call the process a *free process*. Such a process is just a space-time marked Poisson process. It exists and is ergodic whichever the choice of $w$. In the particular case where $\omega(\gamma) = \lambda$ the invariant measure is the $\lambda$-homogeneous Poisson process. If the birth rate is uniformly bounded, it can be decomposed as

$$\mathbf{b}(\gamma,\eta) = \omega(\gamma)M(\gamma,\eta) \tag{3.7}$$

where, $0 \leq M(\gamma,\eta) \leq 1$. The first factor represents a basic birth-rate density due to an "internal" Poissonian clock and the last factor acts as an unnormalized probability for the individual to be actually born once the internal clock has rang. The birth is hindered or reinforced according to the configuration $\eta$.

We introduce a function $I : \mathbf{G} \times \mathbf{G} \to \{0,1\}$

$$I(\gamma,\theta) = \mathbf{1}\{sup_\eta\{|M(\gamma,\eta) - M(\gamma,\eta+\delta_\theta)\}| > 0\}. \tag{3.8}$$

where $\delta_\theta(\gamma) = \mathbf{1}\{\gamma = \theta\}$ is the configuration having unique individual $\theta$ and the supremum is taken over the set of all configurations $\xi$ such that $\xi$ and $\xi + \delta_\theta$ are in the set of allowed configurations (either $\{0,1\}^{\mathbf{G}}$ or $\mathbb{N}^{\mathbf{G}}$). The function $I(\gamma,\theta)$ indicates which individuals $\theta$ may have an influence in the birth-rate of the individual $\gamma$, that is if $I(\gamma,\theta)$ =1, the presence (or absence) of $\theta$ modifies the birth rate of $\gamma$ and then we say that $\theta$ is *incompatible* to $\gamma$.

# 4 Graphical construction for the loss networks

Loss networks are spatial birth and death processes, the individuals are *calls* ($\gamma = (x, x+u), x, u \in \mathbb{R}$) and births are regulated by the exclusion principle, depending on the capacity ($C$) of the network. The generator of the process is given by

$$Af(\eta) = \int (f(\eta + \delta_\gamma) - f(\eta))b(\gamma, \eta)d\gamma + \int (f(\eta - \delta_\gamma) - f(\eta))\eta(d\gamma) \tag{4.1}$$

where $\eta \in \{0,1\}^{\mathcal{B}(\mathbb{R})}$. The death rate 1 is included in the second expression. In the rate of the associated free process, we get the factor $\pi(u)$ (following the notation of Section 3.1):

$$\omega((x, x+u)) = \lambda\pi(u) \tag{4.2}$$

The birth rate, according to (3.7) is:

$$\mathbf{b}((x, x+u), \eta) = \lambda\ \pi(u)\ M((x, x+u), \eta). \tag{4.3}$$

where, for capacity $C = 1$,

$$M(\gamma, \eta) = \prod_{\theta:\eta(\theta)\neq 0} (1 - I(\gamma, \theta)) \tag{4.4}$$

$$I(\gamma, \theta) = \begin{cases} 1 & \gamma \cap \theta \neq \emptyset \\ 0 & \text{otherwise} \end{cases} \tag{4.5}$$

where $\gamma, \theta$ are of the form $(x, x+u)$. For $C > 1$, the expression is less simple

$$M((x, x+u), \eta) = \begin{cases} 1 & \text{otherwise} \\ 0 & \text{there exists } y \in (x, x+u) \ \textit{and} \\ & \theta_1, ..., \theta_C \text{ such that } \eta(\theta_i) = 1 \\ & \text{and } y \in \theta_i \ \text{ for all } i = 1, ..., C. \end{cases}$$

Observe that

$$\mathbf{b}((x, x+u), \eta) \leq \lambda, \text{ for all } x, u, \eta \Rightarrow sup_{x,u,\eta}\mathbf{b}((x, x+u), \eta) \leq \lambda. \tag{4.6}$$

Let $N = \{ (\xi_1, T_1), (\xi_2, T_2), ...\}$ be a homogeneous Poisson Process with rate $\lambda$ in $\mathbb{R} \times [0, \infty)$, and let $S_1, S_2, ...$ be i.i.d. random variables exponentially distributed with mean one and let $U_1, U_2, ...$ be i.i.d. random variables with common distribution $\pi$. Assume the family of variables $\{S_1, S_2, \ldots\}$, $\{U_1, U_2, \ldots\}$ and the Poisson process are all independent. Consider the random rectangles

$$R_i = \{(x, y); \xi_i \leq x \leq \xi_i + U_i, T_i \leq y \leq T_i + S_i\}.$$

Then $\{R_i, i \geq 1\} = \{(\xi_i, T_i) + D_i, i \geq 1\}$ is a Boolean model in $\mathbb{R}^2$ where $D_i = [0, U_i] \times [0, S_i]$ and represents the free process of calls.

Now, for each rectangle $R_i$ we associate an independent mark $Z_i \sim U(0, 1)$, and each marked rectangle we identify with the marked point $(\xi_i, T_i, S_i, U_i, Z_i)$. We recognize in the marked point process $\mathbf{R} = \{(\xi_i, T_i, S_i, U_i, Z_i),\ i = 1, 2, \ldots\}$ a graphical representation of the birth and death process with constant birth rate $\lambda$, and constant death rate, equal to 1. We call this free process $\alpha$ and $Z_i$ will serve as a flag of allowed births. Calling $R = (\xi, \tau, s, u, z)$, we use the notation

$$\text{Basis(R)}= (\xi, \xi + u), \quad \text{Birth(R)}= \tau, \quad \text{Life(R)}= [\tau, \tau+\text{s}], \quad \text{Flag(R)}= \text{z}.$$

We also define, for two rectangles $R$ and $R'$,

$$R' \nsim R, \text{ if } R' \cap R \neq \emptyset$$
$$R' \sim R, \text{ otherwise.}$$

We need a series of definitions:

- For an arbitrary point $(x, t) \in \mathbb{R}^2$ define the collection of all rectangles in $\mathbf{R}$ that contain this point
$$A_1^{(x,t)} = \{R \in \mathbf{R} |\ x \in Basis(R), t \in Life(R)\} \tag{4.7}$$

- For each rectangle $R$ define its ancestor set
$$A_1^R = \{R' \in \mathbf{R} |\ Birth(R') \leq Birth(R),\ R' \nsim R\} \tag{4.8}$$

- Define recursively the generations ($n > 1$) of the above sets that is, the $n$th generation of ancestors:
$$A_n^{(x,t)} = \{R'' | R'' \in A_1^{R'} \text{ for some } R' \in A_{n-1}^{(x,t)}\} \tag{4.9}$$
$$A_n^R = \{R'' | R'' \in A_1^{R'} \text{ for some } R' \in A_{n-1}^R\} \tag{4.10}$$

We say that there is *backward oriented percolation* if there exists one point $(x,t)$ such that $A_n^{(x,t)} \neq \emptyset$ for all $n$, that is, if there exists one point with an infinite number of ancestors. Call *clan of ancestors* of $(x,t)$ the union of all its ancestors:

$$A^{(x,t)} = \bigcup_{n\geq 1} A_n^{(x,t)} \tag{4.11}$$

and $\mathbf{R}[0,\mathrm{t}] = \{\mathrm{R} \in \mathbf{R} |\ \mathrm{Birth(R)} \in [0,\mathrm{t}]\}$.

To estimate the size of the clan $A^{(x,t)}$ we will use two random variables associated to the free process: the time-length and space-width of the clan:

$$TL(A^{(x,t)}) = t - \sup\{s | s \in Life(R) \text{ for some } R \in A^{(x,t)}\} \tag{4.12}$$

$$SW(A^{(x,t)}) = m_1(\cup_{R\in A^{(x,t)}} Basis(R)) \tag{4.13}$$

The existence of the process in infinite volume for any time interval is guaranteed as long as the process do not explode, that is, no rectangle has an infinite number of ancestors in a finite time. The following theorem is proved in Fernández, Ferrari and Garcia (2001).

**Theorem 4.14** *If $A^{(x,t)} \cap \mathbf{R}[0,\mathrm{t}]$ is finite with probability one, for any $x \in \mathbb{R}$ and $t \geq 0$, then for all $\Lambda \subseteq \mathbb{R}$ the loss network process defined in $\Lambda$ is well-defined and has at least one invariant measure $\mu^\Lambda$.*

For the existence of the process in infinite time, it is needed that the clan of ancestors of all rectangles are finite with probability one, that is, there is no backward oriented percolation. In order to construct the invariant measure for stationary Markov processes it is usual to construct the process beginning at $-\infty$ with an arbitrary configuration and look at the process at time 0. If the configuration at time 0 does not depend on the initial configuration then we have a sample of invariant measure. The graphical construction described above allow us to construct the process $\eta_t$ by a thinning of the free process $\alpha_t$ for all $t \in \mathbb{R}$. Moreover, the same argument shows that the distribution of $\eta_0$ does not depend on the initial configuration. The next theorem summarizes the results about the process, see Fernández et al. (2001, 2002) and Garcia (2000).

**Theorem 4.15** *If with probability one there is no backward oriented percolation in $\mathbf{R}$, then the loss network process can be constructed in $(-\infty,\infty)$ in such a way that the marginal distribution of $\eta_t$ is invariant. Moreover, this distribution is unique and the velocity of convergence is exponential.*

One way of determining the lack of percolation is the domination through a branching process. Establishing sub-criticality conditions for the branching process we obtain sufficient conditions for lack of percolation. Looking backward, the ancestors will be the branches. The time of the death will be the birth time for the branching process. The clan of ancestors in itself is not a branching process because the lack of independence.

# 5 Dominating the clan of ancestors by a branching process. Critical value.

Let $R$ be a rectangle with basis $\gamma = (x, x+u)$ with length $u$, born at time 0. Define $\tilde{b}_n^u(v)$ as the number of rectangles in the $n$th generation of ancestors of $R$ having basis with length $v$:

$$\tilde{b}_n^u(v) = |\{R^{'} \in A_n^R| \ |Basis(R^{'})| = v\}|. \tag{5.1}$$

The process $\tilde{b}_n$ is not a Galton-Watson process but it can be dominated by one (call it $b_n$) as described by Fernández et al. (2001), where each call length represents a type. The number of types can fe finite, countable or uncountable depending upon the distribution $\pi$.

**Lemma 5.2** *The offspring distribution of $b_n$ is Poisson distributed with mean*

$$m(u,v) = \lambda \ \pi(v) \ (u+v) \tag{5.3}$$

*where $m(u,v)$ is the mean number of children type $v$ for parents type $u$.*

**Proof.** In the proof we use the terms "parent" and "ancestor" in the original sense. If $\gamma = (0,u)$ and we consider the rectangle $R$ born at time 0 such that $Basis(R) = \gamma$, it is easy to see that a rectangle $(x, x+v) \times (y, y+s)$ can be a parent of $R$ if, and only if, $x \in (-v, u)$ and $y + s > 0$.

Let $\beta_{uv}(t)$ the number of parents of $R$ type $v$ born after time $-t$. Then

$$b_1^u(v) = \lim_{t\to\infty} \beta_{uv}(t) \quad \text{a.s.} \tag{5.4}$$

Let us call $\Delta$ the set $[-v, u] \times [-t, 0]$, and $N(\Delta)$ the homogeneous Poisson process with rate $\lambda$ in $\Delta$. Then, for $k = 0, 1, ...$

$$P(\beta_{uv}(t) = k) = \sum_{n \geq k} P(N(\Delta) = n \text{ and among } n \text{ rectangles } k \text{ are parents of } R \text{ type } v) \tag{5.5}$$

Let $(x_1, y_1), \ldots, (x_n, y_n)$ a realization of $N(\Delta)$. To each point we associate two independent marks– $w$, the call length $\pi$ distributed and $s$ time length exponentially distributed with mean one. Given $N(\Delta) = n$, the points $(x_i, y_i)$ are uniformly distributed in $\Delta$, that is, $x_i \sim U(-v, u)$ and $y_i \sim U(-t, 0)$. Consider the rectangles $R_i = [x_i, x_i + w_i] \times [y_i, y_i + s_i]$. Thus,

$$P(R_i \text{ is a parent of } R \text{ type } v) = \pi(v)\ P(y_i + s_i > 0). \tag{5.6}$$

and we have

$$P(y_i + s_i > 0) = \int_{-t}^{0} P(s_i > -y)\frac{1}{t}dy = \frac{1 - e^{-t}}{t}. \tag{5.7}$$

To clarify the computations we use the following notation:

$$\alpha_t = \lambda\ (u + v)\ t, \qquad p_t = \pi(v)\ (1 - e^{-t})/t.$$

From (5.5),(5.6) and (5.7) we have

$$\mathbb{P}(\beta_{uv}(t) = k) = \sum_{n \geq k} \left( \begin{array}{c} n \\ k \end{array} \right) (p_t)^k (1 - p_t)^{n-k} e^{-\alpha_t} \frac{(\alpha_t)^n}{n!} = e^{-p_t \alpha_t} \frac{(p_t \alpha_t)^k}{k!}. \tag{5.8}$$

Observe that

$$\lim_{t \to \infty} p_t \alpha_t = \lim_{t \to \infty} \lambda \pi(v)(u + v)(1 - e^{-t}) = \lambda \pi(v)(u + v). \tag{5.9}$$

From (5.4) it follows that $\beta_{uv}(t)$ converges to $b_1^u(v)$ in distribution

$$\mathbb{P}(b_1^u(v) = k) = \lim_{t \to \infty} P(\beta_{uv}(t) = k), \quad k = 0, 1, ... \tag{5.10}$$

Therefore we conclude that $b_1^u(v)$ has Poisson distribution with mean $\lambda \pi(v)(u + v)$. □

We are interested to find conditions under which the process $b_n$ is sub-critical and a sufficient condition for this is that the mean of the total number of children in all generations when the initial parent is of type $u$ is finite for all $u$. Thus we are interested in the convergence of the series

$$\sum_{n \geq 1} \sum_{v} m^{(n)}(u, v) \tag{5.11}$$

where $m^{(n)}(u, v)$ is the mean offspring number of type $v$ from a parent type $u$ in the $n$th generation and it is given inductively by

$$m^{(n)}(u, v) = \sum_{w} m^{(n-1)}(u, w) m(w, v). \tag{5.12}$$

Thus,

$$\sum_v m^{(n)}(u,v) = \sum_v \sum_{v_1} \dots \sum_{v_{n-1}} \lambda^n \pi(v_1)(u+v_1)\pi(v_2)(v_1+v_2)\dots\pi(v)(v_{n-1}+v). \tag{5.13}$$

In order to simplify the reading, recall that $\rho_1$ and $\rho_2$ are the first and second moment of the distribution $\pi$ respectively, that is $\rho_1 = \mathbb{E}_\pi u$ and $\rho_2 = \mathbb{E}_\pi u^2$.

Observe that

$$\sum_v \pi(v)(v_{n-1}+v) = v_{n-1}\sum_v \pi(v) + \sum_v \pi(v)v = v_{n-1} + \rho = f_1 + v_{n-1}g_1 \tag{5.14}$$

where $f_1 = \rho_1$, $g_1 = 1$. Also,

$$\begin{aligned}
&\sum_{v_{n-1}} \pi(v_{n-1})(v_{n-2}+v_{n-1})(f_1+v_{n-1}g_1) = \sum_{v_{n-1}} \pi(v_{n-1})(v_{n-2}+v_{n-1})(v_{n-1}+\rho_1) \\
= &\sum_{v_{n-1}} v_{n-1}^2\pi(v_{n-1}) + v_{n-1}\pi(v_{n-1})(v_{n-2}+\rho_1) + \pi(v_{n-1})(v_{n-2}\rho_1) \\
= &\ \rho_2 + \rho_1(v_{n-2}+\rho_1) + v_{n-2}\rho_1 = \rho_2 + \rho_1^2 + v_{n-2}2\rho_1 = f_2 + v_{n-2}g_2
\end{aligned} \tag{5.15}$$

where $f_2 = \rho_2 + \rho_1^2$, $g_2 = 2\rho_1$.

Let us establish the relationship among $f_j, g_j e f_{j+1}, g_{j+1}$:

$$\begin{aligned}
&\sum_{v_{n-j}} \pi(v_{n-j})(v_{n-j-1}+v_{n-j})(f_j+v_{n-j}g_j) &(5.16)\\
= &\sum_{v_{n-j}} g_j v_{n-j}^2\pi(v_{n-j}) + v_{n-j}\pi(v_{n-j})(f_j+v_{n-j-1}g_j) + \pi(v_{n-j})(v_{n-j-1}f_j) \\
= &\ g_j\rho_2 + f_j\rho_1 + v_{n-j-1}(g_j\rho_1+f_j) = f_{j+1} + v_{n-j-1}g_{j+1}. &(5.17)
\end{aligned}$$

Then

$$f_{j+1} = \rho_1 f_j + \rho_2 g_j, \quad g_{j+1} = f_j + \rho_1 g_j \tag{5.18}$$

or written in matricial form

$$\begin{bmatrix} f_{j+1} \\ g_{j+1} \end{bmatrix} = \begin{bmatrix} \rho_1 & \rho_2 \\ 1 & \rho_1 \end{bmatrix} \cdot \begin{bmatrix} f_j \\ g_j \end{bmatrix} = \begin{bmatrix} \rho_1 & \rho_2 \\ 1 & \rho_1 \end{bmatrix}^j \cdot \begin{bmatrix} \rho_1 \\ 1 \end{bmatrix} \tag{5.19}$$

From (5.13) it follows

$$\sum_v m^{(n)}(u,v) = \lambda^n(f_n + u\ g_n). \tag{5.20}$$

**Computation of $f_n$ and $g_n$**

We need to find $T^n$, where $T = \begin{bmatrix} \rho_1 & \rho_2 \\ 1 & \rho_1 \end{bmatrix}$. Consider the eigenvalues $(\epsilon_1, \epsilon_2)$ and the corresponding eigenvectors $(\mathbf{x_1}, \mathbf{x_2})$ in order to factor $T$. We have

$$det(T - \epsilon\ I) = \epsilon^2 - 2\rho_1\epsilon + \rho_1^2 - \rho_2 \tag{5.21}$$

and the eigenvalues are

$$\epsilon_1 = \rho_1 + \sqrt{\rho_2}, \quad \epsilon_2 = \rho_1 - \sqrt{\rho_2}. \tag{5.22}$$

Solving the equation $T\mathbf{x} = \epsilon\mathbf{x}$ we find the right normalized eigenvectors which are

$$\mathbf{x_1} = \frac{1}{\sqrt{\rho_2 + 1}} \begin{bmatrix} \sqrt{\rho_2} \\ 1 \end{bmatrix}, \quad \mathbf{x_2} = \frac{1}{\sqrt{\rho_2 + 1}} \begin{bmatrix} \sqrt{\rho_2} \\ -1 \end{bmatrix}. \tag{5.23}$$

Let $Q = [\mathbf{x_1}\ \mathbf{x_2}]$ and $D$ be a diagonal matrix with elements $\epsilon_1$ and $\epsilon_2$. Thus,

$$T^n = Q\ D^n\ Q^{-1}. \tag{5.24}$$

Explicitly,

$$Q = \frac{1}{\sqrt{\rho_2 + 1}} \begin{bmatrix} \sqrt{\rho_2} & \sqrt{\rho_2} \\ 1 & -1 \end{bmatrix}, \quad D = \begin{bmatrix} \epsilon_1 & 0 \\ 0 & \epsilon_2 \end{bmatrix}, \quad Q^{-1} = \frac{\sqrt{\rho_2 + 1}}{2\sqrt{\rho_2}} \begin{bmatrix} 1 & \sqrt{\rho_2} \\ 1 & -\sqrt{\rho_2} \end{bmatrix}. \tag{5.25}$$

Then

$$\begin{aligned} T^n &= \frac{1}{2\sqrt{\rho_2}} \begin{bmatrix} \sqrt{\rho_2} & \sqrt{\rho_2} \\ 1 & -1 \end{bmatrix} \cdot \begin{bmatrix} \epsilon_1^n & 0 \\ 0 & \epsilon_2^n \end{bmatrix} \cdot \begin{bmatrix} 1 & \sqrt{\rho_2} \\ 1 & -\sqrt{\rho_2} \end{bmatrix} \\ T^n &= \frac{1}{2\sqrt{\rho_2}} \begin{bmatrix} \sqrt{\rho_2}(\epsilon_1^n + \epsilon_2^n) & \rho_2(\epsilon_1^n - \epsilon_2^n) \\ \epsilon_1^n - \epsilon_2^n & \sqrt{\rho_2}(\epsilon_1^n + \epsilon_2^n) \end{bmatrix}. \end{aligned} \tag{5.26}$$

Now

$$\begin{aligned} \begin{bmatrix} f_n \\ g_n \end{bmatrix} = T^{n-1} \cdot \begin{bmatrix} \rho_1 \\ 1 \end{bmatrix} &= \frac{1}{2\sqrt{\rho_2}} \begin{bmatrix} \rho_1\sqrt{\rho_2}(\epsilon_1^{n-1} + \epsilon_2^{n-1}) + \rho_2(\epsilon_1^{n-1} - \epsilon_2^{n-1}) \\ \rho_1(\epsilon_1^{n-1} - \epsilon_2^{n-1}) + \sqrt{\rho_2}(\epsilon_1^{n-1} + \epsilon_2^{n-1}) \end{bmatrix} \\ &= \frac{1}{2\sqrt{\rho_2}} \begin{bmatrix} \sqrt{\rho_2}\epsilon_1^{n-1}(\rho_1 + \sqrt{\rho_2}) + \sqrt{\rho_2}\epsilon_2^{n-1}(\rho_1 - \sqrt{\rho_2}) \\ \epsilon_1^{n-1}(\rho_1 + \sqrt{\rho_2}) - \epsilon_2^{n-1}(\rho_1 - \sqrt{\rho_2}) \end{bmatrix}. \end{aligned} \tag{5.27}$$

Finally,

$$f_n = \frac{1}{2}(\epsilon_1^n + \epsilon_2^n), \qquad g_n = \frac{1}{2\sqrt{\rho_2}}(\epsilon_1^n - \epsilon_2^n). \tag{5.28}$$

Returning to expression (5.11) we verify the convergence of the series

$$\sum_n \sum_v m^{(n)}(u,v) = \sum_n \lambda^n (f_n + u\ g_n). \tag{5.29}$$

The radius of convergence of this series, given by the Cauchy-Hadamard formula, is

$$R = \frac{1}{\overline{\lim}_{n\to\infty}(f_n + u g_n)^{1/n}}. \tag{5.30}$$

In order to find $R$, notice

$$f_n + u g_n = \frac{1}{2}[(1 + \frac{u}{\sqrt{\rho_2}})\epsilon_1^n + (1 - \frac{u}{\sqrt{\rho_2}})\epsilon_2^n] \tag{5.31}$$

$$= \epsilon_1^n \frac{1}{2}[(1 + \frac{u}{\sqrt{\rho_2}}) + (1 - \frac{u}{\sqrt{\rho_2}})(\frac{\epsilon_2}{\epsilon_1})^n]. \tag{5.32}$$

We know that $\epsilon_1 = \rho_1 + \sqrt{\rho_2}$ is positive since $\pi([0,\infty)) = 1$ and if we had $\rho_1 = 0$ then $\pi(\{0\}) = 1$ which can be excluded. Also $\epsilon_2$ is non-positive, since $\rho_1 \leq \sqrt{\rho_2}$.
Moreover, $\epsilon_2 + \epsilon_1 = 2\rho_1 \ > \ 0$ and we get $\frac{\epsilon_2}{\epsilon_1} \in [-1, 0]$.

Therefore,

$$\frac{1}{2}\ 2\min(1, \frac{u}{\sqrt{\rho_2}}) \leq \frac{1}{2}\ [(1 + \frac{u}{\sqrt{\rho_2}}) + (1 - \frac{u}{\sqrt{\rho_2}})(\frac{\epsilon_2}{\epsilon_1})^n] \leq \frac{1}{2}\ 2\max(1, \frac{u}{\sqrt{\rho_2}}). \tag{5.33}$$

From (5.33) and (5.32) we get

$$\epsilon_1(\min(1, \frac{u}{\sqrt{\rho_2}}))^{1/n} \leq (f_n + u g_n)^{1/n} \leq \epsilon_1(\max(1, \frac{u}{\sqrt{\rho_2}}))^{1/n} \tag{5.34}$$

where both bounds go to $\epsilon_1$ when $n \to \infty$. Then,

$$\lim_{n\to\infty} (f_n + u g_n)^{1/n} = \epsilon_1 \tag{5.35}$$

and

$$R = \frac{1}{\epsilon_1} \ = \ \frac{1}{\rho_1 + \sqrt{\rho_2}}. \tag{5.36}$$

Since, $\lambda > 0$, we obtain

1. If

$$\lambda < \frac{1}{\rho_1 + \sqrt{\rho_2}} \tag{5.37}$$

then the series (5.29) converges absolutely and consequently $b_n$ is sub-critical.

2. If $\lambda > \frac{1}{\rho_1+\sqrt{\rho_2}}$ the series (5.29) is divergent and the process $b_n$ can be supercritical.

Call *lambda critical* for $b_n$, the following

$$\lambda_c^* = \frac{1}{\rho_1 + \sqrt{\rho_2}}. \tag{5.38}$$

In the general case, we can have an uncountable number of types. Let $V$ be the set of all possible types and we observe that

$$\sum_{n\geq 1} \int_V m^{(n)}(u, dv) \tag{5.39}$$

where

$$m^{(n)}(u, dv) = \int_V m^{(n-1)}(u, dw) m(w, dv) \tag{5.40}$$

can be obtained inductively. Then,

$$\int_V m^{(n)}(u, dv) = \int_V \int_V \dots \int_V m(u, dv_1) m(v_1, dv_2) \dots m(v_{n-1}, dv). \tag{5.41}$$

Suppose that the distribution of the length of the calls is absolutely continuous with respect to the Lebesgue measure and $\pi$ is its density. We can write

$$m(u, dv) = \lambda(u + x)\pi(x)dx. \tag{5.42}$$

Then,

$$\int_V m(v_{n-1}, dv) = \int_0^\infty \lambda(v_{n-1} + x)\pi(x)dx = \lambda(v_{n-1} + \rho_1) = \lambda(f_1 + v_{n-1}g_1) \tag{5.43}$$

and

$$\begin{aligned} &\int_V m(v_{n-2}, dv_{n-1}) \cdot \lambda(f_1 + v_{n-1}g_1) && (5.44)\\ &= \int_0^\infty \lambda(v_{n-2} + x)\pi(x) \cdot \lambda(x + \rho_1)dx \\ &= \lambda^2 \int_0^\infty x^2\pi(x) + x(v_{n-2} + \rho_1)\pi(x) + v_{n-2}\rho_1\pi(x)dx \\ &= \lambda^2(\rho_2 + \rho_1(v_{n-2} + \rho_1) + v_{n-2}\rho_1) = \lambda^2(\rho_2 + \rho_1^2 + v_{n-2}2\rho_1) = \lambda^2(f_2 + v_{n-2}g_2) && (5.45) \end{aligned}$$

where $f_1, g_1, f_2, g_2, ...$ are given by (5.19). Therefore, the computation is completely analogous to the discrete case and

$$\int_V m^{(n)}(u, dv) = \lambda^n (f_n + u g_n) \tag{5.46}$$

and the process is sub-critical if the series (5.29) is convergent.

*Remark: If $\pi$ is the density of the $U(0,1)$ distribution then $\lambda_c^* \approx 0.9282$.*

Fernández et al. (2002) obtained a sufficient condition for sub-criticality of the branching process which can be written as

$$\alpha = \sup_G \frac{1}{\mu(G)} \int_{\mathbb{R}} \lambda dx \int_{G_x} \pi_x(dH)\mu(H) I(H, G) < 1 \tag{5.47}$$

where $G_x$ is the possible set of calls beginning at $x$ and $I$ is defined by (4.5). Due to the translation invariance property of the process, we can consider, without loss of generality, a call $G = (0, L)$, beginning at the origin. Its ancestors would be rectangles, with sufficient long lives, with basis that intersect the call $G$. This includes any call beginning at any point inside the call $G$ and also all calls beginning before the origin but with sufficient large length to intersect the call $G$. If we choose, $\mu(v) = c$, where $c$ is an arbitrary constant $\geq 1$ we obtain

$$\alpha = \sup_G \lambda \int_{\mathbb{R}} dx \int_{G_x} I(G, H)\pi(dH). \tag{5.48}$$

Then,

$$\alpha = \lambda \sup_L \left( \int_{-\infty}^{0} P(|H| > -x)dx + \int_0^L dx \right) \tag{5.49}$$

$$= \lambda \sup_L (\rho_1 + L) = \lambda(\rho_1 + \sup_L L). \tag{5.50}$$

When the length of the call is uniformly bounded a.s. and $M = \inf\{y \geq 0 | P(|H| \leq y) = 1\}$, condition (5.48) turns out to be

$$\lambda \, (\rho_1 + M) \; < \; 1 \quad \Leftrightarrow \quad \lambda \; < \; \frac{1}{\rho_1 + M} \quad . \tag{5.51}$$

And this coincides with (5.37) only in the case of fixed length call, for all other cases it is weaker than(5.37) since $\sqrt{\rho_2} \leq M$. For the particular case, $U(0,1)$, this condition guarantees the sub-criticality of the process for $\lambda < \frac{2}{3} \approx 0.6667$ while our condition gives $\lambda < 0.9282$.

# 6 Backward-Forward Algorithm (BFA) applied to loss networks

# 7 Backward-Forward Algorithm (BFA)

The BFA was introduced by Fernández, Ferrari e Garcia (2002) to perfect simulate from spatial point processes which are absolutely continuous with respect to a Poisson point process and that are invariant measures of spatial birth and death processes.

The algorithm does involve the "thinning" of a marked Poisson process —the *free process*— which dominates the birth-and-death process, and it involves a time-backward and a time-forward sweep. But these procedures are performed in a form quite different from previous algorithms. The initial stage of our construction is done *toward the past*, starting with a finite window and retrospectively looking to *ancestors*, namely to those births in the past that could have (had) an influence on the current birth. The construction of the *clan of ancestors* constitutes the time-backward sweep of the algorithm. Once this clan is completely constructed, the algorithm proceeds in a time-forward fashion "cleaning up" successive generations according to appropriate penalization schemes.

The relation "being ancestor of" induces a backward in time *contact/oriented percolation* process. The algorithm is applicable as long as this oriented percolation process is sub-critical.

# 8 Application to loss networks

To simplify the implementation of BFA to the loss network process we are going to assume that $\pi$ have compact support. This assumption is not necessary and can be removed with a little modification on the generation of the free process. Define $M = \inf\{y \mid \pi((0,y)) = 1\}$.

## 8.1 Construction of the clan of ancestors of a finite window $\Lambda = [a,b] \subset \mathbb{R}$

We are interested in sampling a finite window $\Lambda = [a,b]$ of the equilibrium measure in *infinite-volume*.

C1. Generate the free process $\alpha_0 = \{\xi_1^0, ..., \xi_m^0\}$; a homogeneous Poisson process with rate $\lambda$ in the

interval $[a-M, b]$.

$s_L^0 = a$; $s_R^0 = b$.

C2. Generate $U_1^0, ..., U_m^0$ iid random variables with common distribution $\pi$ and let $\eta = \emptyset$.

For each $i$ from 1 to $m$

$$\text{if } (\xi_i^0, \xi_i^0 + U_i^0) \cap [a, b] \neq \emptyset \text{ then } \eta = \eta \cup (\xi_i^0, \xi_i^0 + U_i^0) \tag{8.1}$$

We are simply generating rectangles with basis intersecting $[a, b]$. We have $n_0 = |\eta| \leq N$ basis.

C3. Generate $S_1^0, ..., S_{n_0}^0$ iid exponential random variables with mean one and construct the rectangles

$$\mathbf{R}_0 = \{(\xi_i^0, \xi_i^0 + U_i^0) \times [-S_i^0, 0]; i = 1, ..., n\}. \tag{8.2}$$

Consider now the following subset of $\mathbb{R} \times (-\infty, 0]$

$$\Lambda_0 = \bigcup_{i=1}^{n} (\xi_i^0 - M, \xi_i^0 + U_i^0) \times [-S_i^0, 0] \tag{8.3}$$

C4. $k = 1$; $\Delta = \Lambda_0$;

C5. $s_L^k = \min(s_L^{k-1}, \min_{i \leq n_{k-1}} (\xi_i^{k-1} - M))$
$s_R^k = \max(s_R^{k-1}, \max_{i \leq n_{k-1}} (\xi_i^{k-1} + U_i^{k-1}))$

C6. Generate a $\lambda$-homogeneous Poisson process $\{(\xi_1^k, \tau_1^k), ..., (\xi_{n_k}^k, \tau_{n_k}^k)\}$ on $\Delta \cup [s_L^k, s_L^{k-1}) \cup (s_R^{k-1}, s_R^k]$.

C7. Generate $U_1^k, ..., U_{n_k}^k$ iid random variables with distribution $\pi$ and $S_1^k, ..., S_{n_k}^k$ iid exponential random variables with mean one and construct the rectangles

$$\mathbf{R}_k = \{(\xi_i^k, \xi_i^k + U_i^k) \times [\tau_i^k - S_i^k, \tau_i^k]; i = 1, ..., n_k\}. \tag{8.4}$$

Consider

$$\Lambda_k = \bigcup_{i=1}^{n_k} (\xi_i^k - M, \xi_i^k + U_i^k) \times [\tau_i^k - S_i^k, 0]. \tag{8.5}$$

C8. – if $n_k = 0$ then construct the clan of ancestors of $\eta$

$$A^\eta := \bigcup_{i=0}^{k-1} \mathbf{R}_i \tag{8.6}$$

and STOP.

– otherwise, do

$\Delta = \Lambda_k \backslash \Lambda_{k-1}$;

k=k+1;

return to C5;

In order to improve the performance of the algorithm we suggest at step C6. to exclude the rectangles satisfying

$$\tau_i^k - S_i^k < \min_{j=1,\ldots,n_{k-1}} (\tau_i^{k-1} - S_i^{k-1})$$

.

We finish performing the *BACKWARD* step of the algorithm: the construction of the clan of ancestors. The *FORWARD* step corresponds to move to the beginning of the clan of ancestors and decide which rectangles are going to be kept and which ones are going to be erased. Once these clans are perfectly simulated, it is only necessary to apply the *deterministic* "cleaning procedure", based on the capacity $C$ of the network , to obtain a perfect sample of the interacting process. In this case, if a point $(x,t)$ belongs to more than $C$ rectangles, keep the $C$ rectangles born first and erase the others.

## 8.2 The cleaning algorithm

Call $\mathbf{T}$ the set of rectangles to be tested and $\mathbf{K}$ the set of kept rectangles.

L1. $\mathbf{K}=\emptyset$; $\mathbf{T}= A^\eta$;

L2. If $\mathbf{T} = \emptyset$ go to L4.

otherwise, order $\mathbf{T}$ by birth time. Let $R_1$ be the first rectangle following such ordering.

$\mathbf{K} = \mathbf{K} \cup \mathrm{R}_1$; $\mathbf{T} = \mathbf{T} \backslash \mathrm{R}_1$

L3. Depending upon $C$

1. If $C = 1$; For all $R \in \mathbf{T}$ such that $R \nsim R_1$, $\mathbf{T} = \mathbf{T} \backslash \mathrm{R}$.

   return to L2.

2. Se $C > 1$;

   *para i=1 até* $|\mathbf{T}| - \mathrm{C}$

   $R_i \in \mathbf{T}$, if $R_i \nsim R_1$ call $Area{=}R_i \cap R_1$, $C(Area){=}2$ and $\mathbf{K} = \mathbf{K} \cup \mathrm{R_i}$; $\mathbf{T} = \mathbf{T} \backslash \mathrm{R_i}$;

   *for j=1 to* $|\mathbf{T}|$

   if $R_j \cap Area \neq \emptyset$ take $C(Area) = C(Area) + 1$, if $C(Area) > C$ then $\mathbf{T} = \mathbf{T} \backslash \mathrm{R_j}$

   return to L2.

L4. Take $\mathbf{K}^\eta = \mathbf{K}$ and STOP.

Obtaining $\mathbf{K}^\eta$, we define

$$\eta^*(\gamma) = \begin{cases} 1 & \eta(\gamma) = 1 \text{ and } \exists R \in \mathbf{K}^\eta \text{ such that Basis(R)} = \gamma \\ 0 & \text{otherwise} \end{cases} \tag{8.7}$$

Theorem 3.18 of Fernández et al. (2002) guarantees that $\eta^*$ is a perfect sample from the invariant measure of the loss network described above.

## 8.3 Simulation results

In this section we present some of the simulation results for several values of $\lambda$, $C$ ( network capacity) and window $\Lambda$. The distribution $\pi$ is taken to be $\mathbf{U}(\mathbf{0}, \mathbf{1})$. In this case, by (5.37), $\lambda < 0.9282$ is a sufficient condition for the simulation. The programs were written in MATLAB 5.0. For easiness of reading the results are presented in two steps: the clan of ancestors and the cleaning result. The basis of the rectangles kept at time $t = 0$ constitutes the perfect sample.

Figure 8.1: Clan of ancestors for $U(0,1)$, $\lambda = 0.5$, $\Lambda = [0, 10]$.

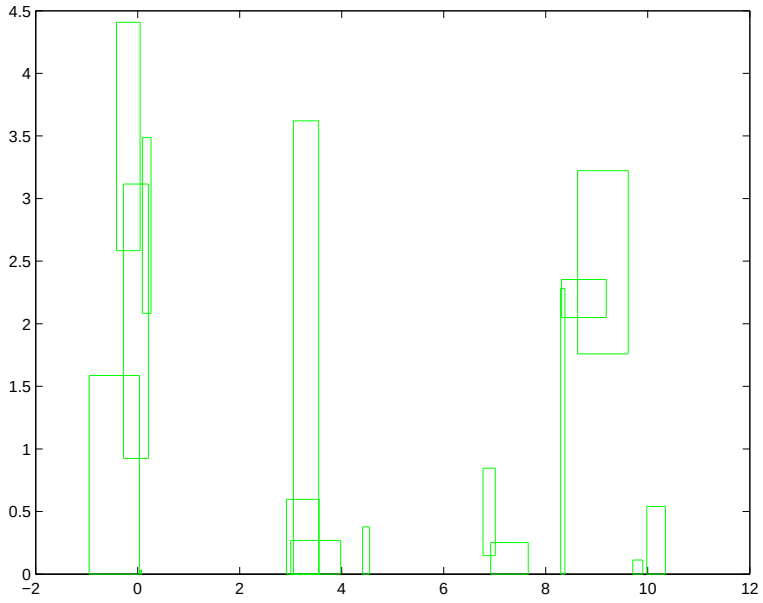



Figure 8.2: Cleaning procedure $C = 1$ for the clan presented in Figure 8.1

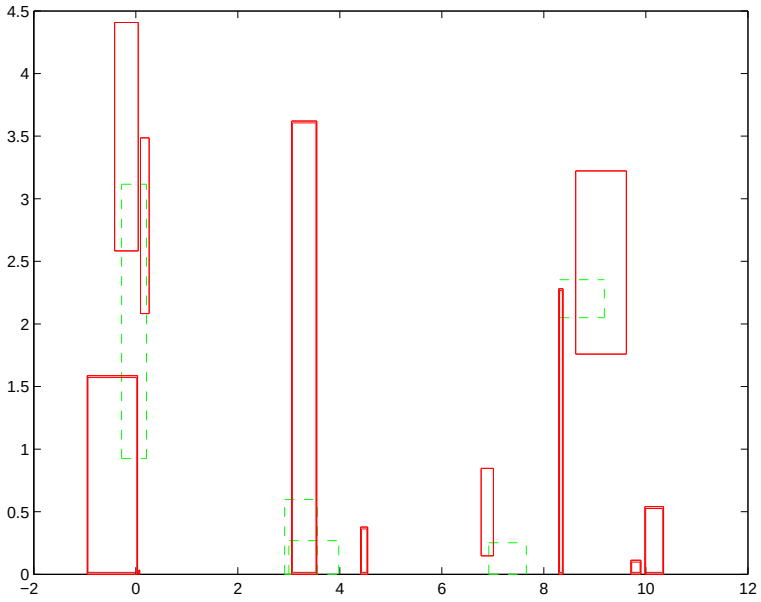


Figure 8.3: Clan of ancestors for $U(0,1)$, $\lambda = 0.9$, $\Lambda = [0, 10]$.

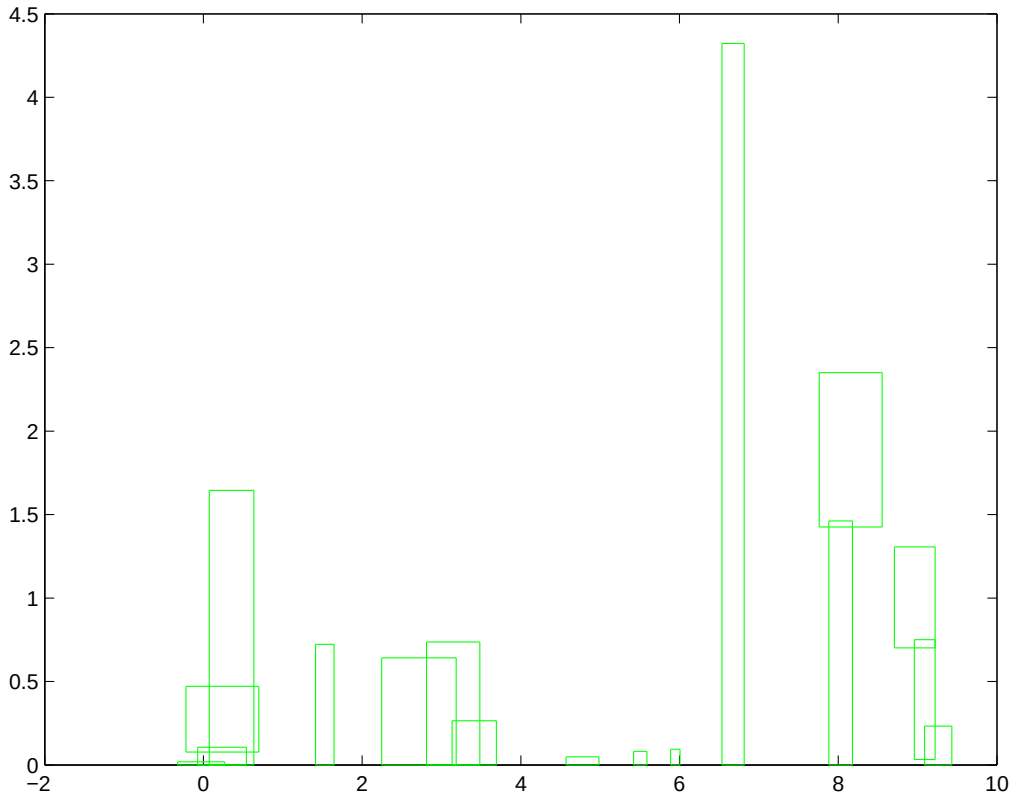


Figure 8.4: Cleaning procedure for the clan presented in Figure 8.3. a) $C = 1$ b) $C = 2$.

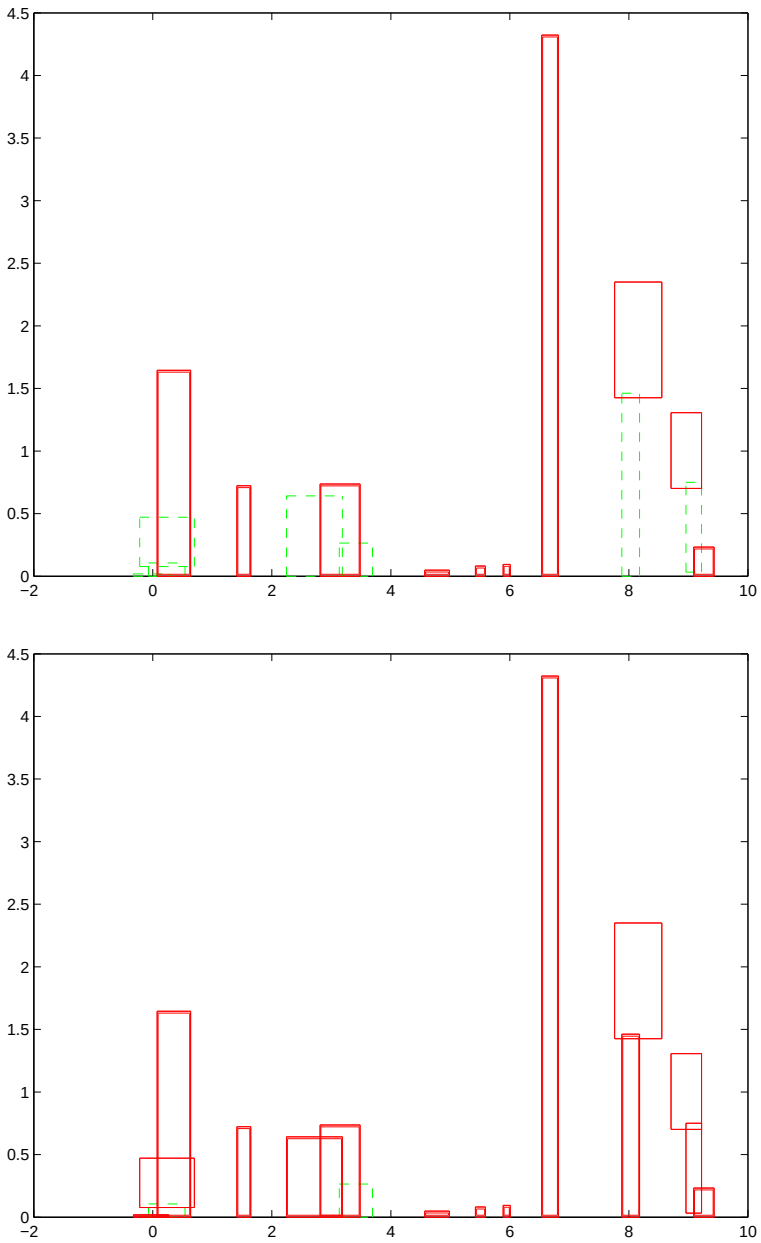


Figure 8.5: Clan of ancestors for $U(0,1)$, $\lambda = 1$, $\Lambda = [0, 10]$.

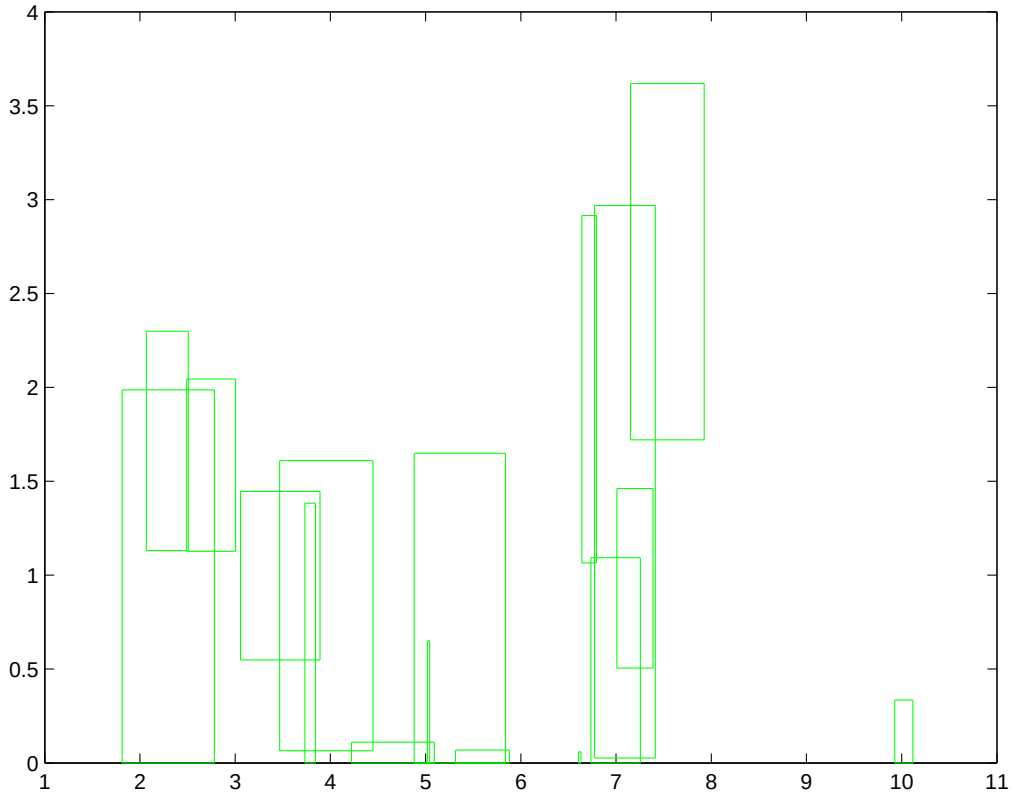


Figure 8.6: Cleaning procedure for the clan presented in Figure 8.5. a) $C = 1$ b) $C = 2$.

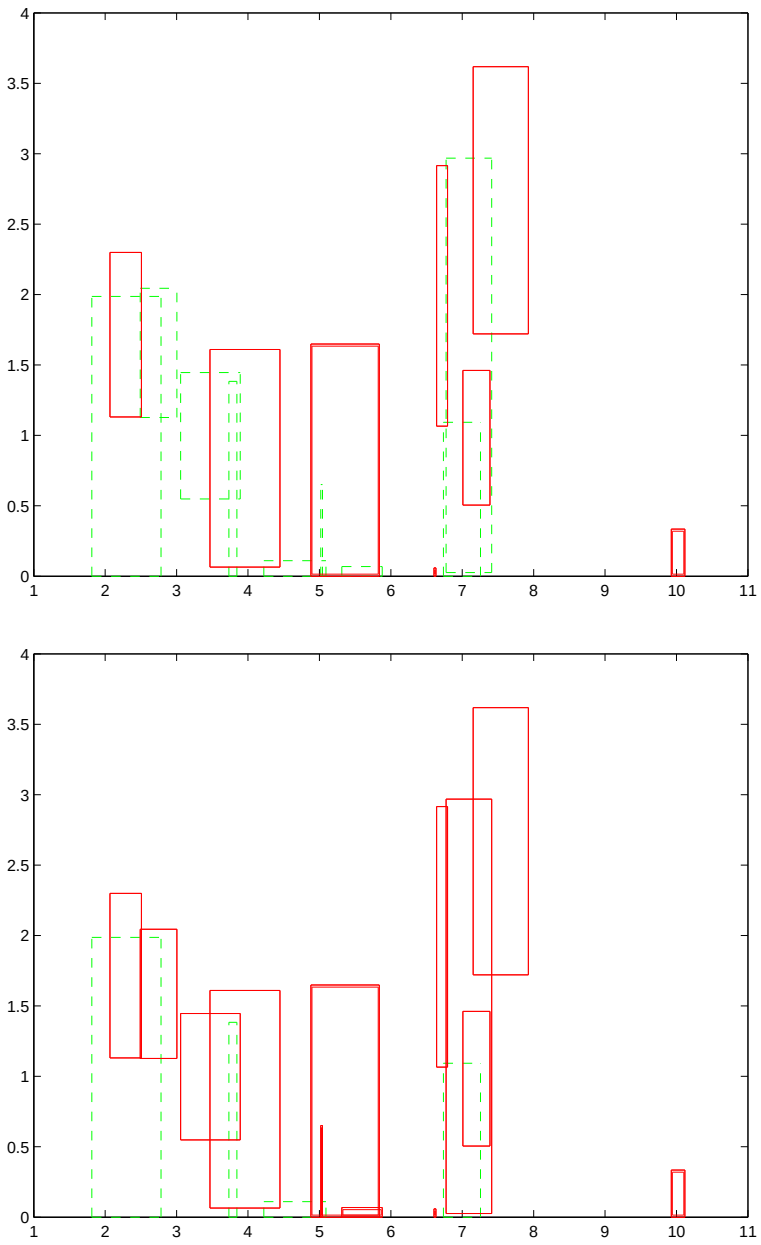


Figure 8.7: Clan of ancestors for $U(0,1)$, $\lambda = 1.2$, $\Lambda = [0,8]$.

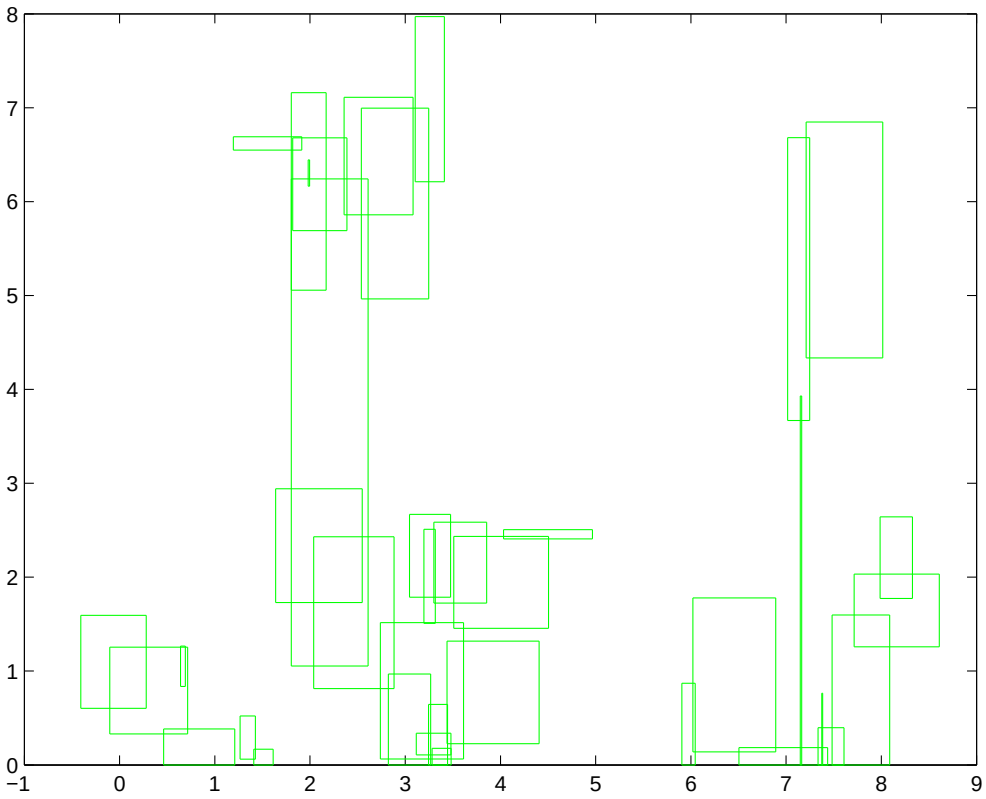
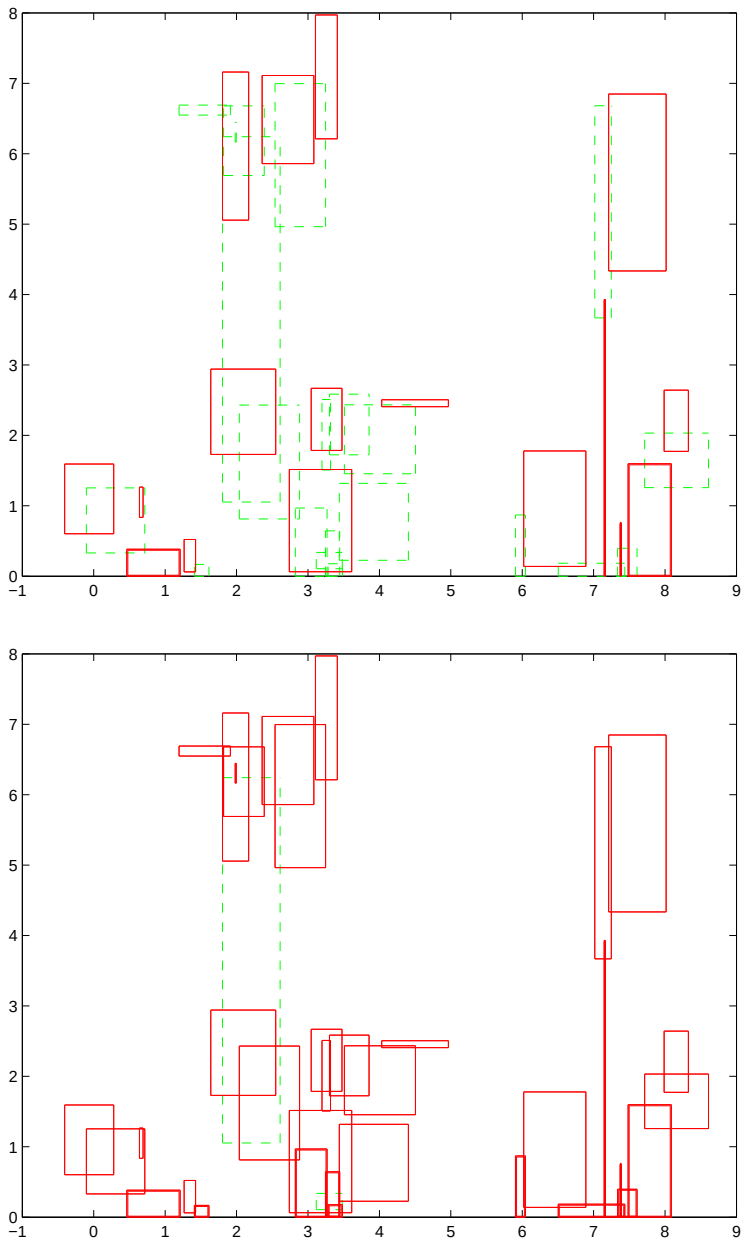


Figure 8.8: Cleaning procedure for the clan presented in Figure 8.7. a) $C = 1$ b) $C = 3$.



# 9 Studying the characteristics of the clan of ancestors through simulation results

We perform a 1,000 simulations for several values of $\lambda < \lambda_c^*$. Conditioned on the event "the point $(x, 0)$ is present at the free process" (which has probability $1 - \exp\{-\lambda\rho\}$), we observed the values of the following random variables related to the clan of ancestors:

1. $SW(A^{(x,0)})$ – space width of the clan of the point $(x, t)$, defined by (4.12);
2. $TL(A^{(x,0)})$ – time length of the clan of the point $(x, t)$ defined by (4.13); and
3. $N(A^{(x,0)})$ – total number of rectangles present in the clan.

The expectation of these variables were estimated through the sample mean and compared then to the expected values for the associated branching process used to find the sub-criticality condition.

The simulations were performed in two cases, when $\pi$ is the $U(0, 1)$ distribution and when $\pi$ is concentrated in one point (fixed call length). From (5.38), the critical value for $\lambda$ to assure sub-criticality is

- When $\pi = U(0, 1)$

$$\lambda_c^* = \frac{1}{\frac{1}{2} + \sqrt{\frac{1}{3}}} \approx 0.9282 \tag{9.1}$$

- When $\pi(d) = 1$

$$\lambda_c^* = \frac{1}{2d} \tag{9.2}$$

Figures 9.9, 9.10 and 9.11 show that the branching process dominated the clan of ancestors (we constructed then this way). However, it is amazing to see that as $\lambda$ increases, the number of rectangles of the branching process is much bigger that the number of rectangles of the clan of ancestors. We can see also, that this difference occurs also for the time-length and space-width but less noticeable. This is a consequence of the fact that in the branching process we can have subsequent generations of rectangles to be born in the same area as the predecessor generations.

The distribution of these random variables are not known in this case. Hall (1988) have a derivation of the "time length" of a coverage process of intervals in $\mathbb{R}$, but nothing is known in the

Figure 9.9: Expected total number of rectangles in the branching process and the clan of ancestors. a) $U(0,1)$ b) $d = 0.5$

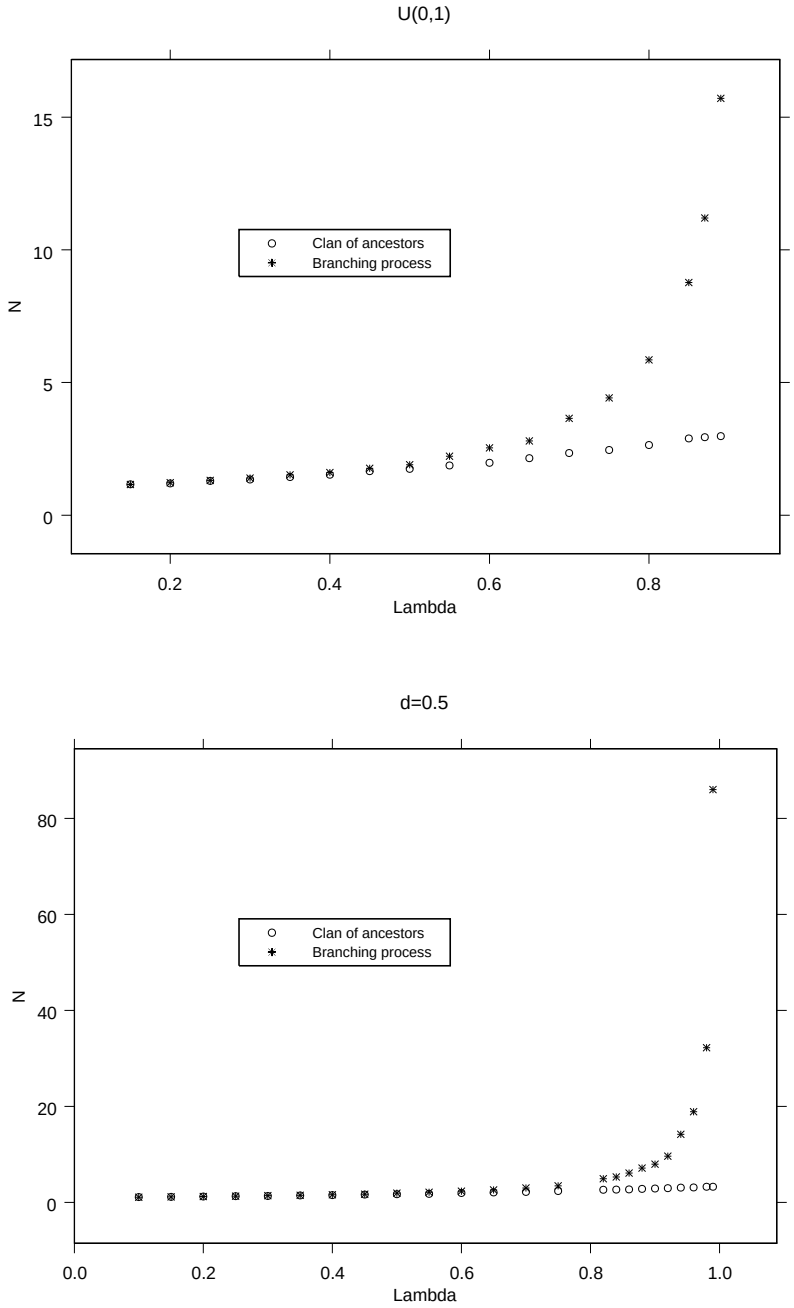


Figure 9.10: Expected time length ($\mathbb{E}(TL)$) for the branching process and the clan of ancestors. a) $U(0,1)$ b) $d = 0.5$

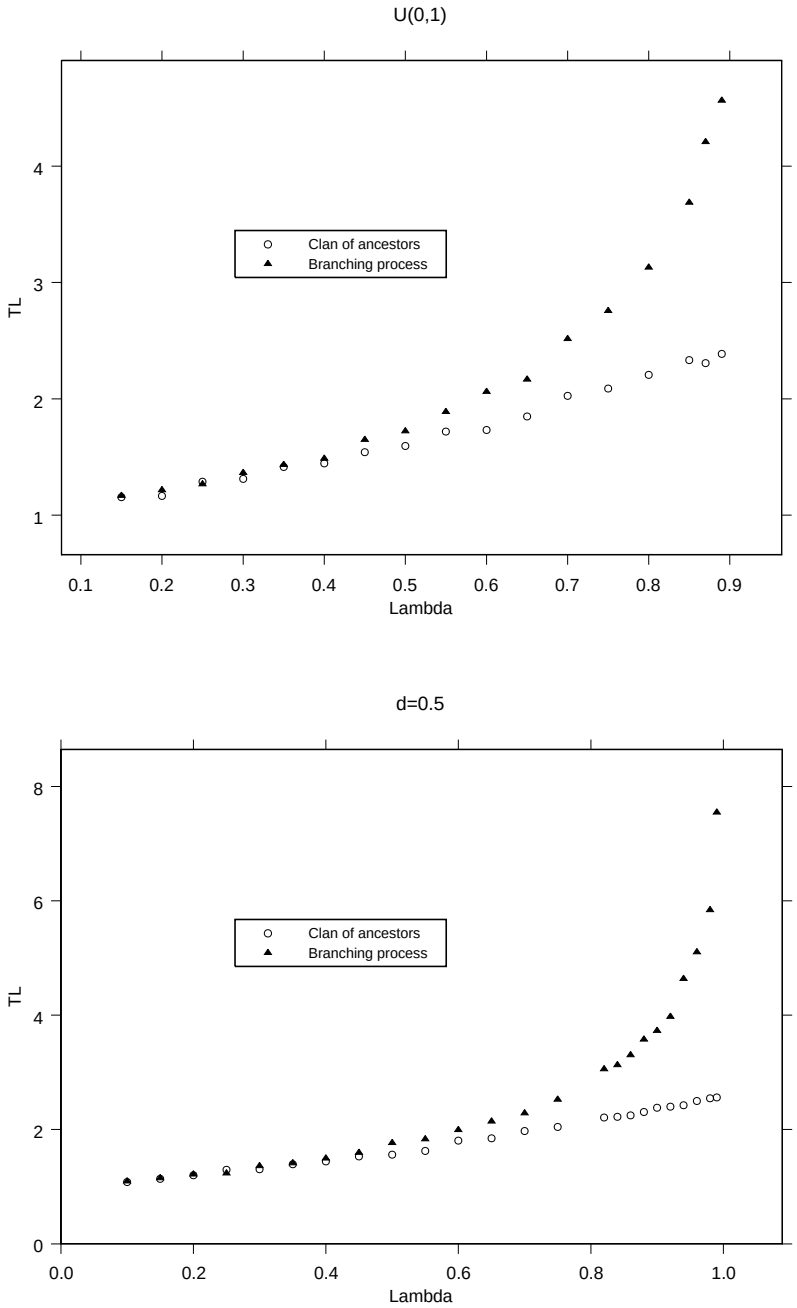
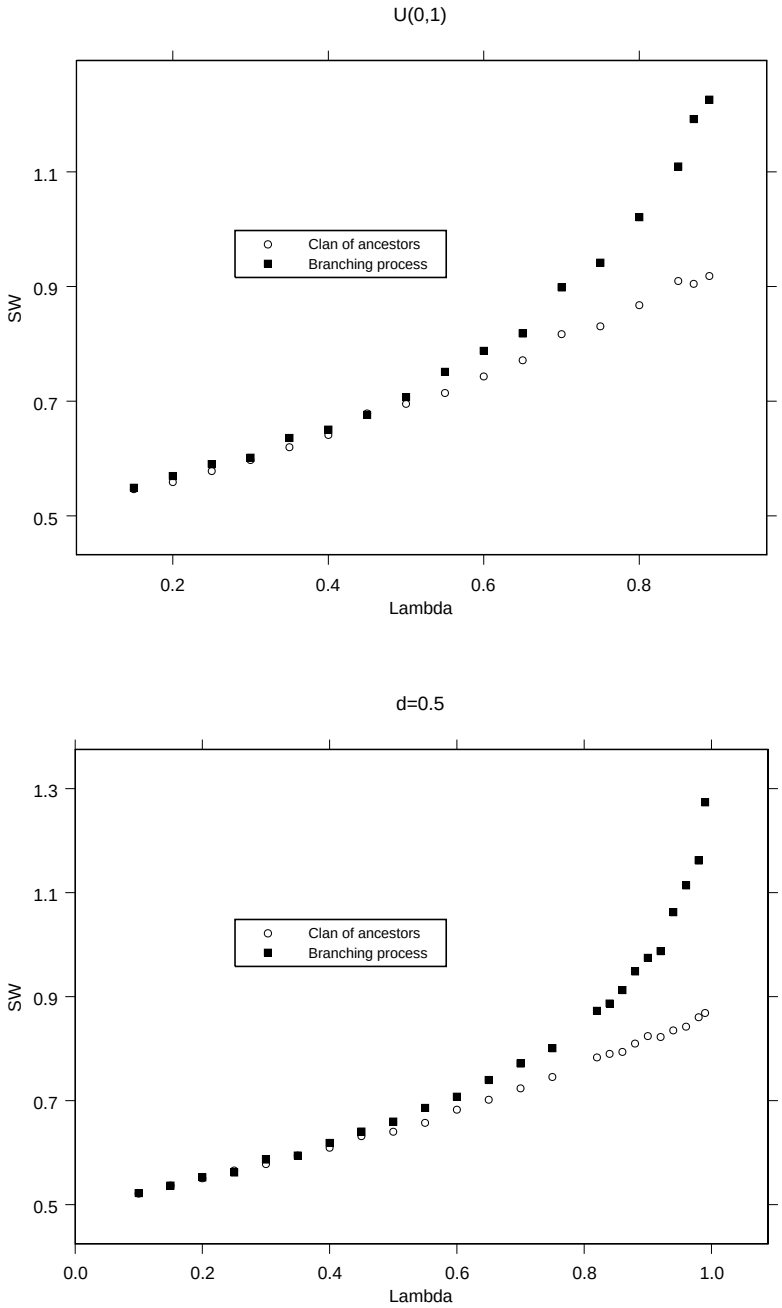


Figure 9.11: Expected space width ($\mathbb{E}(SW)$) for the branching process and the clan of ancestors. a) $U(0,1)$ b) $d = 0.5$



case of rectangles in $\mathbb{R}^2$. Just by the simulation results we can have an idea of these distributions through the histograms (Figures 9.12, 9.13 and 9.14).

Figure 9.12: Histogram for $TL$ for 1,000 simulations for $U(0,1)$ and $\lambda = 1$

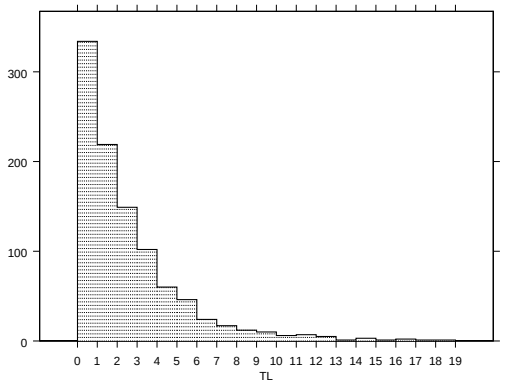



Figure 9.13: Histogram for $SW$ for 1,000 simulations for $U(0,1)$ and $\lambda = 1$

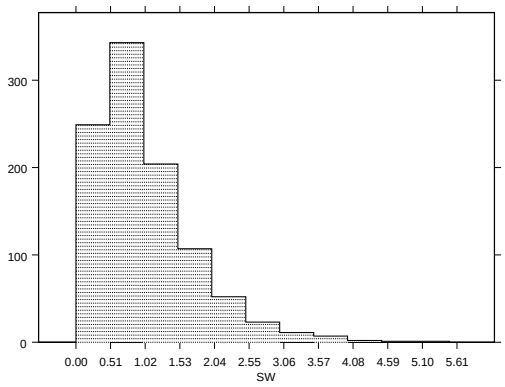
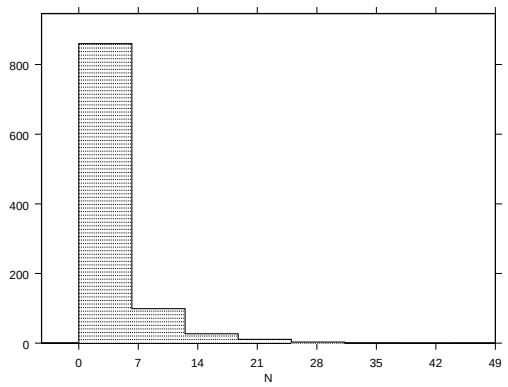


Figure 9.14: Histogram for $N$ for 1,000 simulations for $U(0,1)$ and $\lambda = 1$




## 9.1 Estimation of the critical value using simulations

The purpose of this section is to study the behavior of the clan of ancestors as $\lambda$ increases above $\lambda_c^*$. From Figures 9.9, 9.10 and 9.11 we can see that the critical value obtained through the domination by a branching process underestimates the true value of the finiteness of the clan of ancestors. The idea behind these results is to generate samples for increasing values of $\lambda$ and to study the total number of rectangles. Our conjecture is that, close to the true critical value $\lambda_c$ the total number of rectangles should grow exponentially fast. Thus finding an assintote for $\mathbb{E}(N)$ would give us an estimate of $\lambda_c$. This is true for the branching process, comparing the value of $\mathbb{E}(N)$ as $\lambda$ approaches $\lambda_c^*$ in Figure 9.9 we can see visually a vertical assintote at $\lambda_c^*$.

From now on, for all distributions, we sampled 1,000 observations of the clan of ancestors and computed $\bar{N}$ (the sample mean) for each value of $\lambda$. Figure 9.15 present the results for fixed length calls, $d = 0.5$.

At first sight we see that there is an assintote close to 2.8. To be more precise, we tried to find a root for the equation $1/log(\bar{N}) = 0$ ( see Figure 9.16). We used a degree 19 polynomial to approximate $1/log(\bar{N})$ and found a root in $\lambda = 2.8231$.

Several simulations were performed for several values of $d$ just to get a more precise estimate for $\lambda_c$ since due to the invariance of the Poisson process for fixed call length there is a linear relationship among the critical values for all $d$, see Table 9.1 and Figure 9.17.

Figure 9.15: Expected number of rectangles in the clan of ancestors ($\mathbb{E}(N)$) for $d = 0.5$

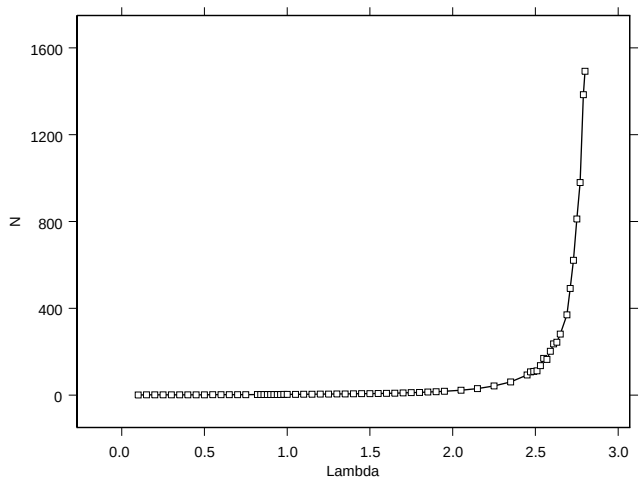



Figure 9.16: $1/log(\bar{N})$ for $d = 0.5$

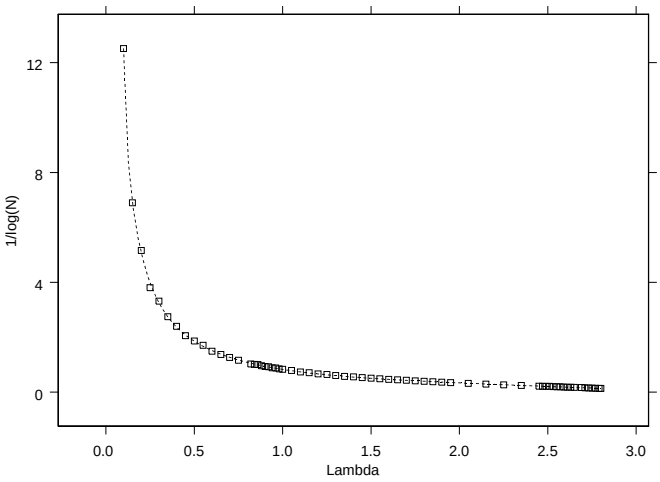


Table 9.1: Critical value of $\lambda_c$ obtained through simulation for several call lengths

| d | 0.3 | 0.5 | 0.7 | 1.0 | 1.2 | 1.4 | 1.6 | 1.8 | 2.0 | 2.5 | 3.0 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| $\lambda_c$ | 4.6688 | 2.8231 | 2.0641 | 1.4193 | 1.1905 | 1.0254 | 0.9120 | 0.8084 | 0.7312 | 0.5682 | 0.4537 |
| d | 3.5 | 4.0 | 4.5 | 5.0 | | | | | | | |
| $\lambda_c$ | 0.3931 | 0.3530 | 0.3103 | 0.2833 | | | | | | | |

Figure 9.17: Critical value of $\lambda_c$ obtained through simulation for several call lengths

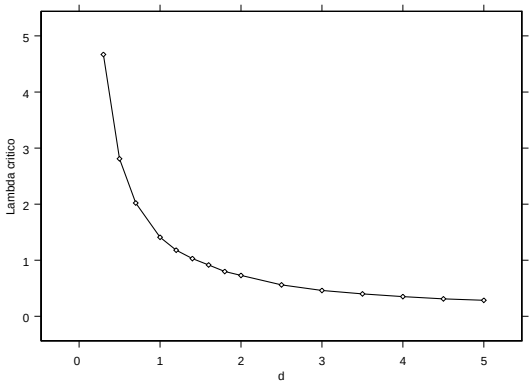


Table 9.2: Critical value of $\lambda_c$ obtained through simulation for distributions $U(0,1)$ and Beta$(\alpha, \beta)$

| Distribution | $\lambda_c$ | $\lambda_c/\lambda_c^*$ |
|---|---|---|
| U(0,1) | 2.6135 | 2.8157 |
| Beta(2,1) | 2.0888 | 2.8695 |
| Beta(2,2) | 2.6746 | 2.8022 |
| Beta(3,1) | 1.8597 | 2.8353 |
| Beta(3,2) | 2.3079 | 2.8444 |
| Beta(1,2) | 3.7981 | 2.8166 |

Comparing the values of $\lambda_c^* = \frac{1}{2d}$ and $\lambda_c$ we can see clearly a linear tendency and we can adjust a regression model with no intercept using weighted least squares to get

$$\lambda_c = 2.8246 \cdot \frac{1}{2d}. \tag{9.3}$$

The question now is to perform the same comparison using different random distributions for $\pi$. We simulated clan of ancestors for several Beta distributions and compared $\lambda_c^*$ and $\lambda_c$. Table 9.2 presents these results along with the ratio $\lambda_c/\lambda_c^*$. We can see that $\lambda_c \approx 2.82\lambda_c^*$. Adjusting a least square model without any intercept:

$$\lambda_c = 2.8243 \cdot \lambda_c^*. \tag{9.4}$$

# 10 A better theoretical bound for $\lambda_c$

Consider two incompatible rectangles $R$ and $R'$ such that $R$ is an ancestor of $R'$. Let $R$ be of type $u$ and $R'$ of type $w$, $R = [x, x+u] \times [t_i + s_1, t_i]$ and $R' = [0, w] \times [t_{i-1} + s_2, t_{i-1}]$. Indexes $i$ and $i-1$ should be associated to the generation number of ancestors of some initial rectangle alive at time 0. Life spans $s_1, s_2$ are exponentially distributed with mean 1, as usual. Now consider the areas $A = [x - v, x + u] \times [0, t_i]$ and $A' = [-v, w] \times [0, t_{i-1}]$. In these areas the parents of type $v$

are generated for $R$ and $R'$ respectively. Here lies a difference between the branching process and the ancestors clan since in the branching case the rate of reproduction is not influenced by other rectangles which is not the case for the ancestors process. By constructivistic approach, following the backward step of the perfect simulation scheme, Section 8.1, one can see that in the area $A \cap A'$ we do not generate new points ( once we generated all possible ancestors of $R'$) in order to keep the driving process $\lambda$-homogeneous. As for the branching process, new points are generated in the entire area $A$, and the Poisson process rate is therefore duplicated in $A \cap A'$. Our goal is to estimate the number of such rectangles that should be excluded from the branching process in order to get better sub-criticality condition for the ancestors process. Observe that we exclude rectangles just from the areas of type $A \cap A'$, considering "parent-child" relation which is still far away of obtaining the ancestors process where exists dependence even among "children".

Recall the rectangles $R$ and $R'$ and consider the area $D = A \cap A'$

$$D = A(x) \times [0, t_{i-1}], \text{ where} \tag{10.1}$$

$$A(x) = [\max(x - v, -v), \min(x + u, w)]. \tag{10.2}$$

Define $d^i(u, v)$ as the number of ancestors of type $v$ of a rectangle $R$, type $u$, which is in the $i$-th generation, that are also ancestors of the "child" of $R$, say $R'$. Then

$$d^i(u, v) = d_1^i(u, v) + d_2^i(u, v) \tag{10.3}$$

where $d_1^i(u, v)$,$d_2^i(u, v)$ is the number of such ancestors that died before and after time $t = 0$, respectively. Now, we have

$$P(d_1^i(u, v) = k | w, t_i, t_{i-1}) = e^{-p_1 \lambda |D|} \frac{(-p_1 \lambda |D|)^k}{k!} \tag{10.4}$$

and

$$P(d_2^i(u, v) = k | w, t_i, t_{i-1}) = e^{-p_2 \lambda |A(x)|} \frac{(-p_2 \lambda |A(x)|)^k}{k!} \tag{10.5}$$

where $p_1$ is the probability that a rectangle who died in the area $D$ is really an ancestral of $R$ of type $v$, and analogously for $p_2$

$$p_1 = \pi(v) P(Y + S > t_i) \tag{10.6}$$

$$= \pi(v) e^{-t_i} (e^{t_{i-1}} - 1)/t_{i-1} \tag{10.7}$$

and

$$p_2 = \pi(v)P(S > t_i) \tag{10.8}$$

$$= \pi(v)e^{-t_i} \tag{10.9}$$

where $Y \sim U(0, t_{i-1})$ and $S \sim \exp(1)$ are independent random variables.

Since $d_1^i(u,v)$ and $d_2^i(u,v)$ are independent $d^i(u,v)$ is Poisson distributed with mean

$$\pi(v)(p_1\lambda|D| + p_2\lambda|A(x)|) = \pi(v)\lambda|A(x)|e^{-(t_i - t_{i-1})}. \tag{10.10}$$

In order to find the distribution of $t_i - t_{i-1}$, $i \geq 1$, notice that $t_i > t_{i-1}$ and we are given the parent relation, so for $Y \sim U(0, t_{i-1})$ and $S \sim \exp(1)$ independent, $t_i = Y + S$. Then, for $t \geq 0$

$$P(t_i - t_{i-1} \leq t) = P(Y + S - t_{i-1} \leq t | Y + S > t_{i-1}) = \frac{P(t_{i-1} < Y + S \leq t_{i-1} + t)}{P(Y + S > t_{i-1})} \tag{10.11}$$

$$= \frac{\frac{1}{t_{i-1}}(e^{t_{i-1}} - 1)(e^{-t_{i-1}} - e^{-t_{i-1}-t})}{\frac{1}{t_{i-1}}(1 - e^{-t_{i-1}})} = 1 - e^{-t} \tag{10.12}$$

that gives exactly distribution $\exp(1)$. Therefore $\mathbb{E}(e^{-(t_i - t_{i-1})}) = 1/2$.

Furthermore

$$|A(x)| = \min(x + u, w) - \max(x - v, -v) \tag{10.13}$$

and given $w$, $x$ is distributed uniformly in $(-u, w)$ so it is easy to get

$$\mathbb{E}(|A(x)||w) = v + \frac{uw}{u + w}. \tag{10.14}$$

Defining a function $\theta(y) = \int \frac{u}{y+u}\,\pi(du)$, for $y \geq 0$ we have that

$$\mathbb{E}(|A(x)|) = v + u\theta(u). \tag{10.15}$$

Therefore

$$\delta(u,v) = \mathbb{E}(d^i(u,v)) = \frac{1}{2}\lambda\pi(v)(v + u\theta(u)). \tag{10.16}$$

## 10.1 Sub-criticality:

We are interested in sub-criticality conditions for the branching process after the exclusions described above. Therefore, our aim is to establish conditions for the convergence of the series

$$\sum_{n\geq 1}\sum_{v} m_*^{(n)}(u,v) \tag{10.17}$$

where

$$\begin{aligned} m_*^{(1)}(u,v) &= m(u,v) \\ \text{and} & \\ m_*^{(n)}(u,v) &= \sum_{w} m_*^{(n-1)}(u,w)m_*(w,v), \quad \text{for } n>1. \end{aligned}$$

Independently of the generation number the mean of excluded offsprings of type $v$, of an $u$-individual is $\delta(u,v)$, so the mean of "not-excluded" offsprings is

$$\begin{aligned} m_*(u,v) &= m(u,v)-\delta(u,v) && (10.18)\\ &= \lambda\pi(v)(u+v-1/2(v+u\theta(u))) \\ &= \lambda\pi(v)(h(u)+\frac{v}{2}) && (10.19) \end{aligned}$$

where

$$h(u) = u(1-\frac{\theta(u)}{2}). \tag{10.20}$$

We may perform the same technique used in Section 5 to simplify this series:

$$\begin{aligned} \sum_v m_*^{(n)}(u,v) &= \sum_v\sum_{v_1}\cdots\sum_{v_{n-1}} m(u,v_1)m_*(v_1,v_2)\cdots m_*(v_{n-1},v) && (10.21)\\ &= \lambda^n \sum_v\sum_{v_1}\cdots\sum_{v_{n-1}} \pi(v_1)(u+v_1)\pi(v_2)(h(v_1)+\frac{v_2}{2})\cdots\pi(v)(h(v_{n-1})+\frac{v}{2}) \end{aligned}$$

Observe that

$$\sum_v \pi(v)(h(v_{n-1})+\frac{v}{2}) = h(v_{n-1})+\frac{\rho_1}{2} = f_1^* + g_1^* h(v_{n-1}) \tag{10.22}$$

where $f_1^* = \frac{\rho_1}{2}$ and $g_1^* = 1$, and define inductively

$$\sum_{v_{n-i+1}} \pi(v_{n-i+1})(h(v_{n-i})+\frac{v_{n-i+1}}{2})(f_{i-1}^* + g_{i-1}^* h(v_{n-i+1})) = f_i^* + g_i^* h(v_{n-i}). \tag{10.23}$$

Let

$$a = \int u\, h(u)\, \pi(du) \tag{10.24}$$

$$b = \int h(u)\, \pi(du) \tag{10.25}$$

then we have

$$\begin{bmatrix} f^*_{j+1} \\ g^*_{j+1} \end{bmatrix} = \begin{bmatrix} \rho/2 & a/2 \\ 1 & b \end{bmatrix} \cdot \begin{bmatrix} f^*_j \\ g^*_j \end{bmatrix} = \begin{bmatrix} \rho/2 & a/2 \\ 1 & b \end{bmatrix}^{j-1} \cdot \begin{bmatrix} \rho/2 \\ 1 \end{bmatrix} \tag{10.26}$$

and consequently

$$\sum_v m^{(n)}_*(u,v) = \lambda^n \sum_{v_1} \pi(v_1)(u+v_1)(g^*_{n-1}v_1 + f^*_{n-1}) = \tag{10.27}$$

$$= \lambda^n (u(g^*_{n-1}\rho_1 + f^*_{n-1}) + \rho_2 g^*_{n-1} + \rho_1 f^*_{n-1}). \tag{10.28}$$

In order to find $f^*_n, g^*_n$ we exponentiate $T^* = \begin{bmatrix} \rho_1/2 & a/2 \\ 1 & b \end{bmatrix}$. For this operation suffices the eigenvalues of $T^*$, $\varepsilon_1$ and $\varepsilon_2$ given by

$$\varepsilon_{1,2} = \frac{\rho_1/2 + b \pm \sqrt{(\rho_1/2 - b)^2 + 2a}}{2}. \tag{10.29}$$

and two corresponding normalized eigenvectors

$$\frac{1}{\sqrt{1+(\varepsilon_1 - b)^2}} \begin{bmatrix} \varepsilon_1 - b \\ 1 \end{bmatrix}, \quad \frac{1}{\sqrt{1+(\varepsilon_2 - b)^2}} \begin{bmatrix} \varepsilon_2 - b \\ 1 \end{bmatrix}. \tag{10.30}$$

From (10.26) it follows

$$f^*_n = \frac{1}{\varepsilon_1 - \varepsilon_2}(\varepsilon_1^n(\varepsilon_1 - b) + \varepsilon_2^n(b - \varepsilon_2)) \tag{10.31}$$

$$g^*_n = \frac{1}{\varepsilon_1 - \varepsilon_2}(\varepsilon_1^n - \varepsilon_2^n). \tag{10.32}$$

Using the fact that $|\varepsilon_2/\varepsilon_1| \leq 1$ in (10.28) and the Cauchy-Hadamard formula, we obtain that the radius of convergence of the series (10.17) is

$$R^* = \frac{1}{\varepsilon_1} = \frac{2}{\rho_1/2 + b + \sqrt{(\rho_1/2 - b)^2 + 2a}}. \tag{10.33}$$

Therefore, as long as $\lambda < R^*$ the ancestors process is sub-critical. Although this condition is obtained for countably many types it can be extended to an uncountable case in the same manner we did in Section 5.

This bound (10.33) can be expressed more simply. For this, let

$$\begin{aligned} b_1 &= \int u^2\, \phi(u)\, \pi(du) \\ a_1 &= \int u^3\, \phi(u)\, \pi(du) \\ \phi(y) &= \int \frac{1}{y+u}\, \pi(du). \end{aligned}$$

Then

$$\theta(a) = 1 - a\phi(a) \tag{10.34}$$

$$b = (\rho_1 + b_1)/2 \tag{10.35}$$

$$a = (\rho_2 + a_1)/2 \tag{10.36}$$

and

$$R^* = \frac{2}{\rho_1 + b_1/2 + \sqrt{\rho_2 + a_1 + b_1^2/4}}. \tag{10.37}$$

So, sub-criticality is guaranteed as long as

$$\lambda < \frac{2}{\rho_1 + b_1/2 + \sqrt{\rho_2 + a_1 + b_1^2/4}}. \tag{10.38}$$

*Remark: for $\pi$ being density of U(0,1) the condition is $\lambda < 1.4302$*

Observe that $0 \le \theta(y) \le 1$ for $y \ge 0$ implies $b_1 \le \rho_1$ and $a_1 \le \rho_2$ while the Jensen's inequality assures $b_1 \ge \rho_1/2$ and $a_1 \ge \rho_1^2/2$. Consequently

$$R^* \le \frac{8}{5\rho_1 + \sqrt{16\rho_2 + 9\rho_1^2}} \le \frac{4}{5\rho_1} \tag{10.39}$$

$$R^* \ge \frac{4}{3\rho_1 + \sqrt{\rho_1^2 + 8\rho_2}} \ge \frac{4}{3(\rho_1 + \sqrt{\rho_2})} = 4/3\lambda_c^*. \tag{10.40}$$

The last inequality proves that a better bound for the critical value is obtained.

# 11 Conclusion

This is one of the first works where the clan of ancestors algorithm was implemented. Berthelsen and Møller (2001) compared it to the dominated CFTP introduced by Kendall and Møller (2000). Based on simulation results, they show that the dominated CFTP is better than the algorithm based on the clan of ancestors in the particular case of a Strauss process

$$\mu_\Lambda(dN) = \frac{1}{Z_\Lambda} e^{\beta_1 N(\Lambda) + \beta_2 S(N,\Lambda)} \, \mu^0_\Lambda(dN) \tag{11.1}$$

defined on a unit square with $e_1^\beta = 100$ and $e_2^\beta = 0$ (the so-called hard-core process), 0.5 and 1 (a Poisson processes with rate 100). This is obviously the case from the description of the processes since the backward construction of BFA stops when the dominated Poisson process regenerates and usually the coupling of CFTP is achieved before it in the finite case. However, it should be noticed that the algorithm based on the clan of ancestors was designed for sampling the infinite-volume process viewed in a finite window. This seems to be a much more interesting and challenging problem which has been studied in this work for the specific case of one-dimensional loss networks with bounded calls. No comparison was made to other perfect simulation schemes.

Moreover, we can see that the simulation of the invariant measure can bring information about unknown variables related to the clan of ancestors. The bound described in Section 10 was found by a better understanding of the simulation procedure.

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