Fast Perfect Simulation of Vervaat Perpetuities

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Abstract

This work presents a faster method of simulating exactly from a distribution known as a Vervaat perpetuity. A parameter of the Vervaat perpetuity is \( \beta \in (0, \infty) \). An earlier method for simulating from this distribution ran in time \( O((2.23\beta)^{\beta}) \). This earlier method utilized dominated coupling from the past that bounded a stochastic process for perpetuities from above. By extending to non-Markovian update functions, it is possible to create a new method that bounds the perpetuities from both above and below. This new approach is shown to run in \( O(\beta \ln(\beta)) \) time.

Keywords  exact simulation; dominated coupling from the past

MSC[2010]  68Q25, 65C05

1 Introduction

A perpetuity is defined as follows.

Definition 1. A perpetual

\[ Y = W_1 + W_1W_2 + W_1W_2W_3 + \cdots , \]

where the \( \{W_i\} \) are an independent, identically distributed (iid) sequence of random variables.
Suppose that each $W_i$ has the same distribution as $W$ (write $W_i \sim W$). Then it also holds that $Y \sim W(1 + Y')$ for $Y$ and $W$ independent. As pointed out in [4], this distributional identity also characterizes perpetuities.

Throughout this work it will be assumed that $W \geq 0$ (with probability 1) and $\mathbb{E}[W] < 1$. These two assumptions give that $Y$ is nonnegative and finite with probability 1. In fact, the Monotone convergence theorem gives that

$$
\mathbb{E}[Y] = \frac{\mathbb{E}[W]}{1 - \mathbb{E}[W]}. \tag{2}
$$

### 1.1 Vervaat perpetuities

The running time of the classic **Quickselect** algorithm of Hoare [5] for finding order statistics of an unsorted set of elements approaches a perpetuity. If one pivot is chosen, then asymptotically the running time approaches a perpetuity known as the Dickman distribution. Write $U \sim \text{Unif}([0, 1])$ to mean that $U$ has the uniform distribution over $[0, 1]$.

**Definition 2.** The **Dickman distribution** is a perpetuity where $W \sim \text{Unif}([0, 1])$.

No closed form for this distribution is known. The Dickman distribution also arises in largest prime factors, and in longest cycles in permutations. See [6] for more details. The Dickman distribution is a special case of the family of Vervaat perpetuities.

**Definition 3.** A **Vervaat perpetuity** is a perpetuity where $W_i \sim U^{1/\beta}$ for some $\beta \in (0, \infty)$ for $U \sim \text{Unif}([0, 1])$.

(Note that some authors define the Dickman distribution as $1 + Y$ for $Y$ a Vervaat perpetuity with $\beta = 1$.) The first to simulate from the Dickman distribution was Fill, then Devroye [2] followed with a substantially different method based on envelope refinement of acceptance/rejection. In [1] Fill and the second author improved upon Fill’s method for the problem and applied it to general Vervaat perpetuities. Returning to the Dickman distribution, Devroye and Fawzi [3] improved the algorithm to the point where only 2.32 uniforms were needed on average to generate one Dickman random variable. Blanchet and Sigman [1] applied dominated coupling from the past to more general perpetuities, but only showed that there method had finite expected running time [1].

Returning to the Vervaat class, in the case of large $\beta$ the running time in [1] takes $O((2.23\beta)^3)$ steps on average. This is fine for the Dickman distribution where $\beta = 1$, but very bad for general Vervaat perpetuities.
The goal of this work is to develop a faster method for simulating random variates from the Vervaat perpetuity distribution, particularly when \( \beta \gg 1 \).

**Theorem 1.** The algorithm for generating Vervaat perpetuities from Section 2 uses \( T \) uniform random variates, where

\[
\mathbb{E}[T] \leq O(\beta \ln(\beta)).
\]

This work is organized as follows. Section 2 gives the algorithm and proves correctness. Section 3 then proves the running time bound.

## 2 The method

The method used here is a variant of coupling from the past (cftp). In [4], monotone dominated cftp was employed to draw samples from (1). We begin by presenting the intuition behind Propp and Wilson’s monotone cftp [9].

### 2.1 Monotone cftp

Recall that a Markov chain is a stochastic process such that the next state depends only on the current state, and not on the past history of the process. That means that the next state of the process can be determined from the current state and some independent randomness using a deterministic function called an update function.

**Definition 4.** For a Markov chain \( \{X_t\} \) with state space \( \Omega \), \( \phi : \Omega \times [0, 1] \to \Omega \) is an *update function* if for \( U \sim \text{Unif}([0, 1]) \), \( [X_{t+1}]|X_t = x_t \sim \phi(x_t, U) \).

In general update functions can employ much more general randomness than a single uniform, such as multiple uniforms or even an iid sequence of uniforms. For notational simplicity this description supposes that the randomness comes from a single uniform, but everything said here applies to the more general case.

Now suppose that \( \preceq \) is a partial order on the state space \( \Omega \) (so \( a \preceq a \), \( a \preceq b \) and \( b \preceq a \) implies \( a = b \), and \( a \preceq b \) and \( b \preceq c \) implies \( a \preceq c \).)

**Definition 5.** An update function is *monotonic* for \( (\preceq, \Omega) \) if

\[
(\forall x, y \in \Omega)(\forall u \in [0, 1])(x \preceq y \Rightarrow \phi(x, u) \preceq \phi(y, u)).
\]
Let π be a distribution over the state space of the Markov chain. Then say π is stationary if \(X_t \sim \pi\) implies \(X_{t+1} \sim \pi\) as well. For example, for the Markov chain defined by \(X_{t+1} = U_{t+1}^{1/\beta}(1 + X_t)\) where \(U_1, U_2, \ldots\) are iid \(\text{Unif}([0, 1])\), the stationary distribution of the chain is the Vervaat perpetuity. Markov chain Monte Carlo takes advantage of the fact that under limited assumptions, for any fixed \(x_0\), the distribution of \(X_t\) approaches \(\pi\) as \(t\) goes to infinity.

When applicable, cftp allows the user to directly simulate from \(\pi\), the stationary distribution of the Markov chain. The intuition is to view the Markov chain as running for times starting from the far past, so for times \(\{\ldots, -3, -2, -1, 0\}\). In other words, it has already been running for an infinite amount of time up to time \(t = 0\). Having run for an infinite number of steps, the idea is that \(X_0\) comes exactly from the stationary distribution of the Markov chain.

More precisely, fix a time \(t < 0\). Suppose that \(M\) is the largest state in the state space, and \(m\) the smallest, so that \(m \leq x \leq M\) for all \(x \in \Omega\). Let \(m_t = m\) and \(M_t = M\). For \(r\) from \(t + 1\) up to \(0\), let \(M_r = \phi(M_{r-1}, U_r)\) and \(m_r = \phi(m_{r-1}, U_r)\).

Since \(m_t \leq X_t \leq M_t\), a simple induction gives that \(m_r \leq X_r \leq M_r\) for all \(r\) up to \(0\). In particular, if \(m_0 = M_0\) then \(X_0\) also equals that common value, and the algorithm terminates with \(X_0 \sim \pi\).

If \(m_0 \neq M_0\), then recursively call the algorithm to obtain \(X_t\). Then use \(U_{t+1}, \ldots, U_0\) to update \(X_t\) forward to \(X_0\), and output \(X_0\). Either way, the algorithm will output \(X_0 \sim \pi\).

### 2.2 Dominated cftp

The basic monotone cftp method cannot be used here because the state space is \([0, \infty)\). So no state \(M\) is an upper bound on \(\Omega\). Kendall and Møller \([7, 8]\) solved this issue by introducing dominating coupling from the past (dcftp), also known as coupling into and from the past.

In their approach, a second update function \(\phi_D\) is needed which dominates the original update function in the sense that

\[
(\forall x, w \in \Omega)(\forall u \in [0, 1])(x \preceq w \Rightarrow \phi(x, u) \preceq \phi_D(w, u)).
\]

Call the Markov chain created by update function \(\phi_D\) the *dominating chain*. The chain must have the following properties.

- The dominating chain must have a stationary distribution \(\pi_D\)
- It must be possible to draw from \(\pi_D\).
• It must be possible to run the dominating chain $D_t$ backwards from stationarity, that is, to draw $D_{t-1}$ given $D_t \sim \pi$.

• It must be possible to impute the forward $U_t$ values. That is, using the relationship $D_t = \phi_D(D_{t-1}, U_t)$, it must be possible to simulate from $[U_t|D_t, D_{t-1}]$.

With such a dominating chain in place, dcftp runs as follows. Assume $t < 0$ is a parameter given to the program, and that $m$ is a minimum state of the chain, so $(\forall x \in \Omega)(m \preceq x)$.

1. Draw $D_0$ from $\pi_D$. Set $t_{old}$ to 0.
2. For $i$ from $t_{old} - 1$ down to $t$, draw $D_i$ given $D_{i+1}$.
3. For $i$ from $t + 1$ to $t_{old}$, draw $U_i$ to be uniform over $[0, 1]$ conditioned on $\phi_D(D_{i-1}, U_i) = D_i$.
4. Set $M_t$ to $D_t$, and $m_t$ to $m$.
5. For $i$ from $t + 1$ to 0, let $m_i$ be $\phi(m_{i-1}, U_i)$ and $M_i$ be $\phi(M_{i-1}, U_i)$
6. If $M_0 = m_0$, then output this common value and quit. Else, set $t_{old}$ to $t$, $t$ to $2t$, and return to line 2.

Note that by setting $t$ to $2t$ in the last line, the value of $t$ quickly grows to the size needed to have a good chance that $m_0 = M_0$. Setting $t$ to $t + 1$ minimizes the number of random draws that are generated, but if $\phi$ takes a long time to calculate, this approach can result in a much longer computational time.

2.3 The earlier method

The monotone dominated cftp method of [4] operated as follows. First, the update function used the following fact about uniforms raised to powers.

**Lemma 1.** Let $x \geq 0$, and $W = U^{1/\beta}$ where $U \sim \text{Unif}(0, 1))$. Then

$[(1 + x)W | (1 + x)W \leq 1] \sim W$.

**Proof.** Suppose $\beta = 1$. Then $(1 + x)W \sim \text{Unif}([0, 1 + x])$. Conditioning on $(1 + x)W \leq 1$ is the same as conditioning on $W \leq 1/(1 + x)$. A uniform conditioned on lying in a smaller space is uniform over that smaller space, so
\[ [W|(1 + x)W \leq 1] \sim \text{Unif}([0, 1/(1 + x)]) \] which makes \([(1 + x)W|(1 + x)W \leq 1] \sim \text{Unif}([0, 1]) \sim W.

Now for \( \beta \neq 1 \). Note \(((1 + x)W)^{\beta} \sim U \cdot (1 + x)^{\beta}\). If \((1 + x)W \leq 1\), then \(((1 + x)W)^{\beta} \leq 1\). From the \( \beta = 1 \) case, conditioned on \( U(1 + x)^{\beta} \leq 1\), we have \( U \cdot (1 + x)^{\beta} \sim \text{Unif}([0, 1]) \). So

\[ [U \cdot (1 + x)^{\beta}|W(1 + x) \leq 1] \sim U. \]

Raising both sides to the \( 1/\beta \) power then gives the result.

This gives rise to the following update function. Draw two uniforms. The first uniform \( U(1) \) determines if \( U(1) \) is used to set the next state to \( U(2)^{1/\beta} \). Otherwise \( U(1)^{1/\beta}(1 + x) > 1\), and the next state should be \( U(1)^{1/\beta}(1 + x) \).

Let \( \mathbb{1}(\cdot) \) denote the usual indicator function that evaluates to 1 if the Boolean argument is true, and is 0 otherwise. With this notation, let \( S(x, u) = \mathbb{1}(u < 1/(1 + x)^{\beta}) \), and then the update function becomes

\[
\phi(x, u(1), u(2)) = S(x, u(1))u(2)^{1/\beta} + [1 - S(x, u(1))]u(1)^{1/\beta}(1 + x).
\] (3)

The key property of this update function, is that if \( u(1) < 1/(1 + x)^{\beta} \), then the value of \( \phi(x, u(1), u(2)) \) no longer depends on \( x \)! No matter what \( x \) is at that point, \( \phi(x, u(1), u(2)) = u(2)^{1/\beta} \). So this couples together the process, bringing our bounds on \( x \), which used to form an interval, to the same value. The chance that this coupling occurs is simply the chance that \( u(1) < 1/(1 + x)^{\beta} \), which is \( 1/(1 + x)^{\beta} \).

Now when \( \beta \) is large, \( x \) has to be small before this coupling will occur with reasonable probability. For \( U \sim \text{Unif}([0, 1]) \), \( \mathbb{E}[U^{1/\beta}] = \beta/(1 + \beta) \). Then equation (2) gives that the expected value of a draw from the perpetuity is \( \beta \), and \( \mathbb{P}(U^{1/\beta}(1 + \beta) \leq 1) = (1 + \beta)^{-\beta} \). On average, this event takes \( (1 + \beta)^{\beta} \) steps to occur. This is what leads to the poor running time for large \( \beta \).

The dominating function for the method is an asymmetric simple random walk on the shifted integers \( \{x_0 - 1, x_0, x_0 + 1, \ldots\} \). For \( \beta \in (0, \infty) \), let

\[
x_0 = \frac{1 + (2/3)^{1/\beta}}{1 - (2/3)^{1/\beta}}
\]

and

\[
\phiD(x, u(1), u(2)) = x + \mathbb{1}(u(1) > 2/3) - \mathbb{1}(u(1) \leq 2/3, x \geq x_0)
\]

[Note that this is a slight change from the \( x_0 \) of [1] that simplifies the algorithm slightly.]
Since the difference between adjacent states of this chain is \{-1, 0, 1\}, this chain is time reversible, which means that from the stationary distribution a simulation forward in time has the same distribution as a simulation backwards in time. Therefore the only question is in evaluating the forward \(U_t\) conditioned on \(D_t\) and \(D_{t-1}\). This is easy: conditioned on \(D_t = D_{t-1} + 1\), \(U_t \sim \text{Unif}(2/3, 1]\). Conditioned on \(D_t \leq D_{t-1}\), \(U_t \sim \text{Unif}(0, 2/3]\).

**Lemma 2.** For all \(x \in [0, y]\), \(y \geq x_0 - 1\), \(u(1) \in [0, 1]\), and \(u(2) \in [0, 1]\),

\[
\phi(x, u(1), u(2)) \leq \phi_D(y, u(1), u(2)).
\]

**Proof.** Suppose \(u(1) > 2/3\) so \(D_t = D_{t-1} + 1\). Then for all \(x\) and \(u(2)\), it is always true that \(\phi(x, u(1), u(2)) \leq 1 + x\), hence the result holds.

Next suppose that \(u(1) \leq 2/3\). By the monotonicity of \(\phi\), \(\phi(x, u(1), u(2)) \leq \phi(y, u(1), u(2))\), so it suffices to show that \(\phi(y, u(1), u(2)) \leq \phi_D(y, u(1), u(2))\), or equivalently, that

\[
u(1)^{1/\beta}(1 + y) \leq y - 1.
\]

The value of \(x_0\) was chosen so that this inequality is equivalent to \(y \geq x_0\), so the result holds.

The last case to consider is when \(y = x_0 - 1\). Then \(\phi_D(y, u(1), u(2)) = y\). Again, \(x_0\) is large enough that \((2/3)^{1/\beta}(1 + y) \leq y\) when \(y = x_0 - 1\), so the result holds for this last case as well. \(\square\)

### 2.4 The new method

The new method takes advantage of a simple fact: dominated coupling from the past works even if the update function for the underlying chain is changing from time step to time step. The Markov chain itself is time homogeneous: the distribution of \(X_t\) given \(X_{t-1} = x\) is unchanging with \(t\). However, the update function used to move the chain can be changing from step to step as long as each update function is still an update function for the original chain, and the dominating chain is still dominating at each step. That is, it is important to have a family of update functions \(\phi_t\) such that:

\[
(\forall t)(\forall x \in \Omega)(U \sim \text{Unif}(0, 1]) \rightarrow \phi_t(x, U) \sim [X_{t+1}|X_t = x]
\]

and

\[
(\forall t)(\forall x \preceq w)(\forall u \in [0, 1]](\phi_t(x, u) \preceq \phi_D(w, u))
\]

To take advantage of this flexibility, we need to generalize Lemma 1.
Lemma 3. For any $x > 0$ and $a \geq 1$,

$$[W(1 + x)|W(1 + x) \leq a] \sim aU^{1/\beta}$$

Proof. Let $U_1 \sim \text{Unif}([0,1])$ and $W = U_1^{1/\beta}$. Then $W(1 + x) \leq a \Rightarrow U_1 \in [0,(a/(1+x)^\beta)]$. Let $U_2 \sim \text{Unif}([0,(a/(1+x)^\beta)])$. Then $[W(1 + x)|W(1 + x) \leq a] \sim U_2^{1/\beta}(1 + x)$. For $U_3 \sim \text{Unif}([0,1])$, $U_3(a/(1 + x))^\beta \sim U_2$. So

$$[W(1 + x)|W(1 + x) \leq a] \sim (U_3(1/(1 + x))^\beta(1 + x) = aU_3,$$

which completes the proof. \qed

Now suppose it is known that $m_t \leq x_t \leq M_t$. Then the update function at time $t$ depends on $m_t$. That is,

$$\phi_t(x, u(1), u(2)) = \phi(x, u(1), u(2), m_t)$$

$$= r \cdot (1 + m_t)u(2)^{1/\beta} + (1 - r) \cdot (1 + x)u(1)^{1/\beta}$$

where

$$r = r(x, u(1), m_t) = 1 \left( u(1) \leq \left( \frac{1 + m_t}{1 + x} \right)^\beta \right).$$

When $m_t = 0$, this is the same as the previous update function. However, when $m_t > 0$ this can give a much improved chance of coupling occurring. Note that the dominating chain for this new method is the same as the old. This gives the following procedure for simulating from Vervaat perpetuities. Write $X \sim \text{Geo}(p)$ if $P(X = i) = p(1-p)^{i}$ for $i \in \{0, 1, \ldots\}$. Unless specifically mentioned, all random variable draws are taken to be independent.

1. Inputs are $\beta$ (the parameter of the Vervaat family), $\ell$ (the initial number of steps to run), and an optional input $D_0$ (the value of the dominating chain at time 0).

2. Initialize by setting $x_0 \leftarrow (1 + (2/3)^{1/\beta})/(1 - (2/3)^{1/\beta})$.

3. If $D_0$ is given as an input to the algorithm, use it, otherwise, let $D_0 \leftarrow x_0 - 1 + G$, where $G \sim \text{Geo}(1/2)$.

4. Generate $D_{-1}, D_{-2}, \ldots, D_{-\ell}$ using a reversible asymmetric simple random walk with partially reflecting boundary at $x_0 - 1$. That is, for $t$ from $-1$ down to $-\ell$, draw $A \sim \text{Unif}([0,1])$, then let

$$D_{t-1} \leftarrow D_t + 1(A > 2/3) - 1(A \leq 2/3, D_t \geq x_0).$$
5. Set $m_{-\ell}$ equal to 0 and $M_{-\ell}$ equal to $D_{-\ell}$. For $t$ from $-\ell + 1$ up to 0, draw $U_t(1)$ as $\text{Unif}([0, 2/3])$ if $D_t \leq D_{t-1}$, or as $\text{Unif}((2/3, 1])$ if $D_t > D_{t-1}$. In either case, draw $U_t(2) \sim \text{Unif}([0, 1])$.

6. For $t$ from $-\ell + 1$ to 0, let
   
   $$\begin{align*}
   m_t &\leftarrow \phi(m_{t-1}, U_t(1), U_t(2), m_{t-1}), \\
   M_t &\leftarrow \phi(M_{t-1}, U_t(1), U_t(2), m_{t-1}).
   \end{align*}$$

7. If $m_0 = M_0$, output this common value as the result and quit. Otherwise, perform the following steps. First, call the algorithm recursively, with input for the dominating chain of $D_{-\ell}$, and time steps $2\ell$ ($\beta$ remains the same). Call the outcome of the recursive call $Y_{-\ell}$. Next, set $m_{-\ell} \leftarrow 0$ and $M_{-\ell} \leftarrow D_{-\ell}$. Then for $t$ from $-\ell + 1$ to 0, let $m_t \leftarrow \phi(m_{t-1}, U_t(1), U_t(2), m_{t-1}), M_t \leftarrow \phi(M_{t-1}, U_t(1), U_t(2), m_{t-1})$, and $Y_t \leftarrow \phi(Y_{t-1}, U_t(1), U_t(2), m_{t-1})$. Finally, output $Y_0$ and quit.

This procedure is implemented in R in the appendix.

The new algorithm differs in two key ways from dominated cftp of the previous section. First, it maintains both an upper and a lower bound on the process, thereby speeding coalescence. Second, since the algorithm is being called recursively, the values of the lower and upper process are reset when the recursive call ends.

So for example, suppose initially $t = 10$. Then the process is run over 10 steps, from time $t = -10$ up to $t = 0$. In the recursive call, twice as many steps are used, so in this example 20 steps. This can be viewed as generating the value of the process from time $t = -30$ up to $t = -10$. If coalescence occurs at or before time $t = -10$, when the process reaches time $-10$, $m_{-10}$ is still reset to 0, and $M_{-10}$ is reset to the value of the dominating process before the state is run forward up to time 0. This ensures that every step is updated according to the same update function, using the same random choices.

3 The run time

Now consider the average number of steps taken by the algorithm. This is proportional to the largest value of $\ell$ input to the algorithm, and so to understand the running time it is necessary to under how large $\ell$ grows on average.

**Lemma 4.** For $D_0 = x_0 - 1 + G$, and $\ell \geq \ln(4\delta^{-2}\beta(x_0 + 1))(1 + \beta) + 1$ for $\delta > 0$, the chance that the algorithm returns $Y$ at the first step is at least $1 - \delta$. 

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Figure 1: Density of Vervaat perpetuity with $\beta = 10$ estimated from 10,000 samples. This $\beta$ would have required something like $(22.3)^{10}$ steps for a single sample using the old method. With the new method, on the order of $10 \ln(10) \approx 23$ steps per sample were required, and 10,000 samples were generated in 144 seconds using R on a Windows 10 machine with an Intel Core i7-6600U CPU at 2.60GHz.

**Proof.** The expected value of $D_0$ is $x_0 + 1$. Let $m \leq M$ and consider $m' = \phi(m, U_1(1), U_2(2), m)$, $M' = \phi(M, U_1(1), U_2(2), m)$. Then

$$E[M' - m'|m, M] = E[U_1^{1/\beta}(1 + M)|M] - E[U_1^{1/\beta}(1 + m)|m] = \frac{\beta}{\beta + 1}(M - m).$$

At the beginning of line 6, $M - m = D_{-\ell} - 0$. Now let $M_{-1}$ and $m_{-1}$ be the values of $M$ and $m$ at the end of $\ell - 1$ steps in line 6. Then a simple induction gives

$$E[M_{-1} - m_{-1}|D_{-\ell}] = \left(\frac{\beta}{\beta + 1}\right)^{\ell-1} D_{-\ell}.$$

Taking the expected value of both sides and $\beta/(\beta + 1) \leq \exp(-1/(\beta + 1))$ gives

$$E[M_{-1} - m_{-1}] \leq (x_0 + 1) \exp(-\ell/(\beta + 1)).$$

Then

$$(\forall a > 0)(P(M_{-1} - m_{-1} \geq a) \leq a^{-1}(x_0 + 1) \exp[-(\ell - 1)/(\beta + 1)]).$$
by Markov’s inequality.

When $U_0(1) \leq ((1 + m)/(1 + M))^\beta$, then $m_0 = M_0$ at the final step, so the next goal is to show that $((1 + m)/(1 + M))^\beta$ is close to 1. Suppose $((1 + m)/(1 + M)) \geq 1 - (1/2)\delta/\beta$. It is easy to show that for $\beta \geq 1$,

$$\left(1 - \frac{\delta}{2\beta}\right)^\beta \geq 1 - \frac{\delta}{2},$$

Since $(1 + m)/(1 + M) = 1 - (M - m)/(1 + m)$ and $m \geq 0$, this means

$$\mathbb{P}(m_0 = M_0 | M - m \leq (1/2)\delta/\beta) \geq 1 - \delta/2.$$  \hspace{1cm} (4)

Suppose $\ell \geq \ln(4\delta^{-2}\beta(x_0 + 1))(\beta + 1) + 1$. Then the chance that $M - m > (1/2)\delta/\beta$ is at most $2\beta\delta^{-1}(x_0 + 1)\exp(-\ln(4\delta^{-2}\beta(x_0 + 1))) = \delta/2$, which together with (4) completes the proof. \hfill \Box

For $\beta \geq 1$, it holds that $\ln(x_0 + 1) \leq \ln(6\beta)$. Suppose that

$$\ell = (\beta + 1)[2\ln(\delta^{-1}) + \ln(4) + \ln(\beta) + \ln(6\beta)] + 1.$$

Then it holds that

$$2\ell \geq (\beta + 1)[2\ln(\delta^{-2}) + \ln(24) + 2\ln(\beta)] + 1.$$

That is to say, if $\ell$ gives a chance of failure to recurse of $\delta$, then $2\ell$ steps gives a chance of failure to recurse of at most $\delta^2$. Hence if the initial $\ell$ satisfies the inequality with $\delta = 1/5$, then $2\ell$ satisfies the inequality with $\delta = (1/5)^2 = 1/25$, and so forth.

**Lemma 5.** Let $T$ be the sum of all the values of $\ell$ in the inputs to all the calls to the algorithm. Then

$$\mathbb{E}[T] \leq (5/3)((\beta + 1)[2\ln(\beta) + \ln(600)] + 1).$$

**Proof.** Let $\ell_i = 2^i$, where $i$ is the depth of the recursion. Then if $R$ is the greatest level of recursion called (and recursion level 0 refers to the initial call to the algorithm), then

$$\mathbb{E}[T] = \sum_{i=0}^{\infty} 2^i \cdot \mathbb{P}(i \leq R).$$

Let $n = (\beta + 1)[2\ln(5) + \ln(24) + 2\ln(\beta)] + 1$. Then for $i < \log_2(n)$, $\mathbb{P}(i \leq R) \leq 1$. The sum of $2^i$ for these terms is at most $n$.

From the previous discussion $\mathbb{P}(\lceil \log_2(n) \rceil \leq R) = 1/5$, $\mathbb{P}(\lceil \log_2(n) \rceil + 1 \leq R) \leq 1/25$, and so on. The sum of these $2^i \mathbb{P}(i \leq R)$ terms is $2n/5 + 4n/25 + \cdots = (2/3)n$. Therefore $\mathbb{E}[T] \leq (5/3)n$, which completes the proof of the bound of the mean. \hfill \Box
Theorem 1 follows immediately. The variance can be bounded in a similar fashion.

Lemma 6. For $T$ as before,

$$E[T^2] \leq \frac{38}{3}(\beta + 1)[2\ln(\beta) + \ln(600)] + 1)^2.$$ 

Proof. Start with $n$ and $R$ as in the previous proof, then

$$T^2 = \sum_{i=0}^{\infty} \sum_{j=0}^{i} 2^i 2^j 1(i \leq R)1(j \leq R) \leq \sum_{i=0}^{\infty} 2^{2i+1} 1(i \leq R).$$

Now the sum of the expectations of the individual terms is $2(4/3)n^2$ for $i < \log_2(n)$, and $2[(4/5)n^2 + (16/25)n^2 + \cdots] = 10n^2$ for the rest of the terms, giving the result.

4 Acknowledgments

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A Code

The following code implements the Vervaat perpetuity algorithm of Section 2 for R version 3.0.2 (2013-09-25).

```r
vervaat <- function(beta = 1, steps = 1, d = -1) {
  # Written by Kirkwood Cloud and Mark Huber 20 August, 2015
  # Line 2
  x0 <- (1+(2/3)^((1/beta)))/(1-(2/3)^((1/beta)))
  # Line 3
  if (d == -1) d <- x0 - 1 + rgeom(1, prob=1/2)
  # Line 4
  d <- c(rep(0,steps),d); a <- runif(steps)
  for (t in steps:1) d[t] <- d[t+1]+(a[t]>2/3)-(a[t]<=2/3)*(d[t+1]>=x0)
  # Line 5
  m <- 0; M <- d[1]; u1 <- rep(0,steps); u2 <- runif(steps)
  for (t in 2:(steps+1)) {
    up <- d[t]>d[t-1]; u1[t - 1] <- runif(1, min=2/3*up, max=2/3+1/3*up)
    u1[t] <- u1[t-1] + up * a[t]
    u2[t] <- u2[t-1] * (1-up)
    d[t] <- d[t]+u1[t]*up + (1-u1[t])*u2[t]
  }
  return(d)
}
```
for (t in 2:(steps+1)) {
  m <- (1+m)*u2[t-1]^(1/beta)
  a <- u1[t-1]^(1/beta); s <- (a < ((1+m)/(1+M))); M <- s*m+(1-s)*a*(1+M)
}

if (m == M) return(m) else {
  y <- vervaat(beta,2*steps,d[1]); m <- 0; M <- d[1]
  for (t in 2:(steps+1)) {
    r <- (u1[t-1] < ((1+m)/(1+y))^(1/beta))
    m <- (1+m)*u2[t-1]^(1/beta); y <- r*m+(1-r)*u1[t-1]^(1/beta)*(1+y)
  }
  return(y)
}

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