GENERATION OF APPROXIMATE GAMMA SAMPLES BY PARTIAL REJECTION

S.H. Ong¹ Wen–Jau Lee² ¹Institute of Mathematical Sciences, University of Malaya, 50603 Kuala Lumpur, MALAYSIA E-mail : <u>ongsh@um.edu.my</u> ²Intel Technology, Bayan Lepas Free Industrial Zone, 11900 Penang, MALAYSIA E-mail : <u>wen.jau.lee@intel.com</u>

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1 Introduction

There are many known methods for the generation of random variates (Tadikamalla and Johnson, 1978) from the gamma distribution with probability density function (pdf)

 $f(x) = x^{\alpha-1}e^{-x} / \Gamma(\alpha), \quad \alpha > 0, \quad x > 0.$

Johnson et al (1995) provide a good reference to different types of gamma generators. Some of the leading algorithms are based on the rejection method such as those proposed by Ahrens and Dieter (1974), Wallace (1974), Fishman (1976), Marsaglia (1977), Atkinson (1977), Cheng (1977) and Tadikamalla (1978).

Recently Kundu and Gupta (2003) considered an approximate method of generating gamma random variables by using the generalized exponential distribution. This method is shown to have a high degree of closeness for the gamma shape parameter α in the range $1 < \alpha \le 2.5$. Tadikamalla and Ramberg (1975) have also proposed an approximate method based on the Burr distribution. A drawback of these methods is that nonlinear equations have to be solved to apply them. In this paper an approximate method, based on acceptance-rejection sampling, is proposed to generate gamma random samples which obviate the need to solve nonlinear equations. The proposed method is general and may be applied to distributions other than the gamma distribution.

The paper is organized as follows. In section 2 we consider the acceptance-rejection method and the closeness of the target and envelope distributions as measured by the Kullback-Leibler discrepancy measure, Kolmogorov-Smirnov and Minimum Hellinger Distances. Section 3 proposes the approximation of samples by partial-rejection approximation method and compares this with an approximation by no-rejection. In section 4 the proposed approximate method is illustrated with the generation of gamma samples based upon Cheng's (1977) gamma-log-logistic rejection algorithm. The last section gives the conclusion.

2 Acceptance-rejection algorithm and closeness of envelope and target distributions

The acceptance-rejection method or the envelope rejection method uses a proxy distribution with pdf g(x) to achieve computer sampling from the target distribution f(x). Central to this method is the evaluation of the inequality

u < f(x)/Mg(x) (2.1) where *u* is a random number from the uniform distribution over (0, 1) denoted $u \sim U(0,1)$ and *M* is a constant. If (2.1) holds, the *x* generated from g(x) is accepted as a realization from f(x). We will call this the *exact* acceptance-rejection condition. If the ratio T(x) = f(x)/Mg(x) on the right-hand side of (2.1) is difficult or time consuming to evaluate, the 'squeeze' technique (see Devroye, 1986) is often used, that is, easy to compute bounds $\ell_1(x)$ and $\ell_2(x)$ are found such that

$$\ell_1(x) \le f(x) / Mg(x) \le \ell_2(x).$$
(2.2)

The acceptance-rejection algorithm is then as follows:

Acceptance-Rejection Algorithm

- (1) Generate $u \sim U$.
- (2) Generate x from g(x).
- (3) If $u < \ell_1(x)$ go to (6).

(4) If $u > \ell_2(x)$ go to (1).

- (5) If u > f(x) / Mg(x) go to (1).
- (6) Accept x.

Remark. In step (3), the lower bound gives quick acceptance compared to the upper bound in step (4) which requires another check in step (5).

We now consider the closeness of the target and envelope distributions. As an illustration, we shall measure the closeness of the log-logistic distribution to the gamma distribution.

Kullback-Leibler discrepancy measure

The upper bounds derived below assumes that $f(x) \le M g(x)$, $M \ge 1$, has been determined for two *nonnegative* pdf's f(x) and g(x). The Kullback-Leibler discrepancy measure between f(x) and g(x) is given as

$$KL(f(x),g(x)) = \int_{0}^{\infty} \ln(f(x)/g(x))f(x) dx$$

 $D = \sup \left| F(x) - G(x) \right|$

where M is independent of x. Then

$$KL(f(x),g(x)) = \int_{0}^{\infty} \ln(f(x)/g(x))f(x)dx \le \int_{0}^{\infty} \ln(M)f(x)dx = \ln(M)$$
(2.3)

If M is close to 1, then $\ln M$ will be very close to 0 implying that f(x) is very close to g(x).

Kolmogorov-Smirnov Distance

The Kolmogorov-Smirnov (K-S) distance measure between distribution functions F(x) and G(x) is

where
$$F(x) = \int_{0}^{x} \frac{t^{\alpha - 1} \exp(-t)}{\Gamma(\alpha)} dt = \int_{0}^{x} f(t) dt$$
 and $G(x) = \int_{0}^{x} \frac{\mu \lambda t^{\lambda - 1}}{(\mu + t^{\lambda})^{2}} dt = \int_{0}^{x} g(t) dt$

Since $G(x) = \int_{0}^{x} g(t) dt \le 1$ we have

$$|F(x) - G(x)| \le \int_{0}^{x} |f(t) - g(t)| dt \le (M-1) \int_{0}^{x} g(t) dt \le (M-1).$$

Therefore, $D = \sup |F(x) - G(x)| \le (M-1).$ (2.4)

Minimum Hellinger distance

This is defined as $HD = \int_{0}^{\infty} \left(\sqrt{f(t)} - \sqrt{g(t)}\right)^{2} dt$. It follows that $HD = \int_{0}^{\infty} \left(\sqrt{f(t)} - \sqrt{g(t)}\right)^{2} dt \le \left(\sqrt{M} - 1\right)^{2} \int_{0}^{\infty} g(t) dt = \left(\sqrt{M} - 1\right)^{2}$ (2.5)

For the gamma pdf f(x) and log-logistic pdf g(x), with parameters as chosen in Cheng (1977), a numerical value for the upper bound may be obtained from the inequality. The upper bounds in (2.3), (2.4) and (2.5), with $M \approx 1.13$, are 0.122, 0.13 and 0.003969 respectively. These values show the closeness of the gamma to the log-logistic distribution. This closeness leads us to consider the generation of a log-logistic sample, with parameters as determined in Cheng's acceptance-rejection algorithm, without subjecting the generated variates to the exact acceptance-rejection condition (2.1) to approximate a gamma sample. However, the approximation, as judged by the K-S test, is found to be poor. This motivates us to propose a partial rejection method which is faster than the full rejection method of Cheng but provides a very good approximation to the gamma sample. This is discussed in the next section.

3 Generation of approximate gamma samples from log-logistic distribution

3.1 Partial-Rejection Approximation Method

In the rejection method, an acceptance-rejection condition is used to decide whether a generated value from the envelope distribution is accepted as value for the target. It is well-known that the accepted values are, in theory, exactly from the target distribution. In general the execution of the acceptance-rejection condition is slow due the computations of the functions in it. In order to speed up the generation, we have considered two methods of generating approximate samples S: (a) Generate from the envelope distribution and accept all generated values as the target sample, that is, without subjecting the generated values to the exact acceptance-rejection condition; (b) Generate from the envelope distribution by replacing the exact acceptance-rejection condition with an easily computed acceptance-rejection condition based on an lower/upper bound or preliminary test. We call method (a) the *no-rejection* approximation method and method (b) the *partial-rejection* approximation method. Note that in both approaches, an approximate sample S will contain rejected values from the envelope distribution. If the acceptance-rejection algorithm is very efficient then the proportion of rejected values in the approximate sample obtained by method (a) will be very small. The proportion of rejected values in the approximate sample obtained by partial rejection (method (b)) will be very small if the bound or preliminary test for the acceptance-rejection condition is tight. This can be seen as follows. With reference to (2.2), using the upper bound $\ell_2(x)$ in the place of T(x) = f(x)/Mg(x) in the acceptance-rejection condition (2.1) will result in accepting rejected values of x that satisfy $T(x) < u < \ell_2(x)$. Clearly, if $\ell_2(x)$ is tight, the proportion of rejected values that is accepted will be small. Note that the use of the lower bound $\ell_1(x)$ will mean accepting rejected values of x (those satisfy $\ell_1(x) < T(x) < u$) and also rejecting some values which should be accepted (those satisfying $\ell_1(x) < u < T(x)$). However this will be compensated by the increase in speed due to a much easily computed $\ell_1(x)$.

Mathematically, the approximate sample S for methods (a) and (b) arises from a mixture of two distributions with pdf given by

$$g(x) = pf_1(x) + (1-p)f_2(x), \quad 0
(3.1)$$

where $f_1(x)$ and $f_2(x)$ are the target and envelope pdf's respectively. The fraction (1-p) in (3.1) may be viewed as the fraction of contamination of the target sample by the envelope distribution. The proportion p is given by p = 1/M. If M is close to 1, the approximation is good. For p > 0.9, we have $1 \le M < 1.1$ while for p > 0.95, $1 \le M < 1.05$. If an approximate sample is deemed to be good when the fraction of contamination in the target sample is at most 0.1, then Method (a) will not give a good approximate sample if M > 1.1.

The perceived merit of methods (a) and (b) is that it will be faster to generate samples by avoiding the exact acceptance-rejection test or modifying it with an easily computed bound. We shall examine methods (a) and (b) and exemplify these methods with an established gamma acceptance-rejection algorithm.

3.2 Generation of approximate gamma samples

The comparison of the no-rejection and partial-rejection approximation methods will be based on Cheng's (1977) acceptance-rejection method for the gamma distribution with the log-logistic envelope. For the no-rejection method, with the parameters as determined in Cheng's acceptance-rejection algorithm, a sample S of log-logistic variates is generated without subjecting the variates to the test with the exact acceptance-rejection condition. Therefore, the sample S consists of gamma variates (accepted) and log-logistic variates (rejected). This sample is taken to be approximately from the gamma distribution. A good approximate gamma sample results if the fraction (1 - p) of rejected log-logistic variates is small (for example, 1 - p < 0.1). As discussed in the previous section this is dependent upon the acceptance-rejection constant M.

The partial-rejection method (b) is a refinement of no-rejection method (a) where only a portion of these rejected log-logistic variates is retained to form the required sample. Clearly, it is desirable to

retain only those rejected log-logistic variates which do not deviate much from the target gamma distribution. One possible approach is to use a quickly computed lower/upper bound for M in the place of the harder to compute M, or a preliminary test as in Cheng's gamma acceptance-rejection algorithm. We shall call this the screening inequality. Empirical studies show that if the bound is fairly tight only the rejected log-logistic variates that do not deviate much from the gamma distribution will be retained.

The K-S goodness-of-fit test is employed to determine if the approximate sample may reasonably be assumed to come from the gamma distribution.

4 Bound and preliminary test for gamma partial-rejection approximation

The screening inequality for the partial-rejection approximation method (b) is determined from Cheng's (1977, p. 73) gamma rejection algorithm (or Devroye, 1986, page 412):

For a pair of independent uniform random variables U_1 and U_2 , the inequality to reject the loglogistic random value X is given as

$$b + cV - X \ge \log U_1^2 U_2 \tag{4.1}$$

where $X = \alpha e^{V}$, $V = a \log \{U_1/(1-U_1)\}$, $a = (2\alpha - 1)^{-1/2}$, $b = \alpha - \log 4$, $c = \alpha + a^{-1}$, and α is the gamma shape parameter. Since $\log Z$ is a concave function of Z,

$$\theta Z - \log \theta - 1 \ge \log Z$$

By letting $Z = U_1^2 U_2$, it is found that $b + cV - X \ge \theta Z - \log \theta - 1$. This leads Cheng to propose a lower bound for the left-hand side of (4.1) given as

$$b + cV - X \ge 4.5Z - \log 4.5 - 1 \ge \log U_1^2 U_2 \tag{4.2}$$

with $\theta = 4.5$ for all α because the actual value of θ is not critical. A preliminary test of acceptance of a generated log-logistic variate is conducted by using $b + cV - X \ge 4.5Z - \log 4.5 - 1$. This avoids computing $\log U_1^2 U_2$ most of the time and helps to speed up the algorithm. Based on empirical evidence, this inequality is rather tight. The partial-rejection method is implemented with this preliminary test only.

A Microsoft (MS) Fortran (version 5.0) program is written to generate the log-logistic samples and gamma samples. The routine RANDOM() provided by MS Fortran is used to generated the uniform [0, 1) random numbers. These samples were submitted to Kirkman's (2006) online K-S two-sample test to obtain the *p*-values and K-S statistic D values. The K-S two-sample test program is developed with reference to the Numerical Recipes in Fortran 77 (1992) and was compiled using an Intel Fortran-for-Linux compiler.

The corresponding *p*-value and D for various (α, N) with 1000 replications are tabulated in Tables 1 through 5. These tables present the results for the control values (Gamma), which are gamma samples generated by Cheng's algorithm, Method (a) (No rejection) and Method (b) (Partial-rejection).

For the goodness-of-fit test, the null hypothesis is H_0 : Sample comes from the gamma distribution and the alternate hypothesis H_a : Samples is not from the gamma distribution. A large *p*-value means that the null hypothesis is very likely true. The very high *p*-values for the Gamma and Partial-rejection columns suggest that the partial-rejection sample may pass off as a gamma sample.

Table 1: α =1.25					
N	K-S Statistics	Gamma	Method (a) No rejection	Method (b) Partial-rejection	
	Average P-value	0.6812	0.8062	0.9217	
15	S.D. of P-value	0.2592	0.2628	0.1268	
15	Average K-S Stat.	0.2440	0.1914	0.1568	
	S.D. of K-S Stat.	0.0699	0.0929	0.0631	
25	Average P-value	0.7506	0.5981	0.8192	
	S.D. of P-value	0.2139	0.3098	0.1825	
	Average K-S Stat.	0.1798	0.2075	0.1592	

	S.D. of K-S Stat.	0.0449	0.0733	0.0473
	Average P-value	0.9242	0.4762	0.6690
40	S.D. of P-value	0.1455	0.3129	0.2323
40	Average K-S Stat.	0.1012	0.1905	0.1543
	S.D. of K-S Stat.	0.0340	0.0602	0.0384
	Average P-value	0.9241	0.3409	0.5799
50	S.D. of P-value	0.1415	0.3073	0.2519
50	Average K-S Stat.	0.0914	0.1988	0.1519
	S.D. of K-S Stat.	0.0312	0.0595	0.0368

		Table 2: α=	=5.5	
Ν	K-S Statistics	Gamma	Method (a)	Method (b)
			No rejection	Partial-rejection
	Average P-value	0.7171	0.9294	0.9894
15	S.D. of P-value	0.2310	0.1635	0.0467
15	Average K-S Stat.	0.2349	0.1062	0.0664
	S.D. of K-S Stat.	0.0610	0.0961	0.0647
	Average P-value	0.8292	0.8789	0.9873
25	S.D. of P-value	0.1630	0.1999	0.0478
25	Average K-S Stat.	0.1638	0.1176	0.0653
	S.D. of K-S Stat.	0.0349	0.0745	0.0470
	Average P-value	0.9810	0.8309	0.9842
40	S.D. of P-value	0.0620	0.2640	0.0615
40	Average K-S Stat.	0.0786	0.1041	0.0645
	S.D. of K-S Stat.	0.0249	0.0643	0.0330
	Average P-value	0.9722	0.7444	0.9781
7 0	S.D. of P-value	0.0742	0.3096	0.0764
50	Average K-S Stat.	0.0752	0.1138	0.0626
	S.D. of K-S Stat.	0.0243	0.0629	0.0305

	Table 3: $\alpha = 10.25$						
Ν	K-S Statistics	Gamma	Method (a) No rejection	Method (b) Partial-rejection			
	Average P-value	0.7203	0.9513	0.9883			
15	S.D. of P-value	0.2273	0.1325	0.0538			
13	Average K-S Stat.	0.2347	0.0914	0.0597			
	S.D. of K-S Stat.	0.0596	0.0896	0.0659			
	Average P-value	0.8373	0.9220	0.9887			
25	S.D. of P-value	0.1514	0.1517	0.0501			
25	Average K-S Stat.	0.1618	0.0990	0.0600			
	S.D. of K-S Stat.	0.0328	0.0693	0.0468			
	Average P-value	0.9860	0.8835	0.9844			
40	S.D. of P-value	0.0481	0.2132	0.0736			
40	Average K-S Stat.	0.0767	0.0868	0.0574			
	S.D. of K-S Stat.	0.0232	0.0596	0.0343			
	Average P-value	0.9768	0.8154	0.9767			
50	S.D. of P-value	0.0650	0.2668	0.0874			
30	Average K-S Stat.	0.0736	0.0964	0.0579			
	S.D. of K-S Stat.	0.0235	0.0588	0.0319			

Table 4: α =15.5							
Ν	K-S Statistics	Gamma	Method (a)	Method (b)			
			No rejection	Partial-rejection			
	Average P-value	0.7158	0.9590	0.9865			
15	S.D. of P-value	0.2301	0.1180	0.0596			
13	Average K-S Stat.	0.2355	0.0847	0.0600			
	S.D. of K-S Stat.	0.0599	0.0859	0.0665			
	Average P-value	0.8360	0.9377	0.9871			
25	S.D. of P-value	0.1548	0.1354	0.0570			
25	Average K-S Stat.	0.1618	0.0922	0.0607			
	S.D. of K-S Stat.	0.0335	0.0664	0.0481			
	Average P-value	0.9862	0.9013	0.9810			
40	S.D. of P-value	0.0475	0.1986	0.0808			
40	Average K-S Stat.	0.0757	0.0793	0.0566			
	S.D. of K-S Stat.	0.0233	0.0581	0.0363			
	Average P-value	0.9777	0.8479	0.9701			
50	S.D. of P-value	0.0664	0.2463	0.1025			
50	Average K-S Stat.	0.0735	0.0874	0.0577			
	S.D. of K-S Stat.	0.0232	0.0572	0.0349			

Ν	K-S Statistics	Gamma	Method (a)	Method (b)
			No rejection	Partial-rejection
	Average P-value	0.7164	0.9632	0.9847
15	S.D. of P-value	0.2293	0.1100	0.0638
15	Average K-S Stat.	0.2360	0.0811	0.0605
	S.D. of K-S Stat.	0.0590	0.0837	0.0679
	Average P-value	0.8366	0.9438	0.9850
25	S.D. of P-value	0.1538	0.1271	0.0588
	Average K-S Stat.	0.1616	0.0888	0.0615
	S.D. of K-S Stat.	0.0334	0.0650	0.0493
	Average P-value	0.9860	0.9151	0.9784
40	S.D. of P-value	0.0487	0.1787	0.0862
40	Average K-S Stat.	0.0756	0.0750	0.0559
	S.D. of K-S Stat.	0.0235	0.0559	0.0378
	Average P-value	0.9754	0.8667	0.9641
50	S.D. of P-value	0.0737	0.2278	0.1140
50	Average K-S Stat.	0.0735	0.0829	0.0582
	S.D. of K-S Stat.	0.0242	0.0552	0.0371

The samples in the "no rejection" and "partial-rejection" columns are subjected to the test by (4.1) to determine the number of "accept" and "reject". The numbers of "accept" and "reject" are presented in Tables 6 to 10. The last column of Tables 6 to 10 gives the overall percentage of the variates in the partial-rejection samples which should be rejected if the exact acceptance-rejection condition (4.1) is employed instead of the preliminary test. With 1000 replications for each N, the total number of variates equal 1000N for each combination of (α , N). This is given in bracket after the number of rejects for Method (b) in Table 6 only. The overall percentage of the rejected values in the approximate samples is seen to be less than 10 percent.

	Table 6: α =1.25						
N	Method (a)Method (b)No rejectionPartial-rejection				Percent of rejects		
	Accept	Reject	Accept	Reject	Partial-rejection		
15	10777	4223	13614	1386 (15000)	9.24%		
25	17913	7087	22712	2288 (25000)	9.15%		
40	29254	10746	36666	3334 (40000)	8.34%		
50	35302	14698	44981	5019 (50000)	10.04%		

	Table 7: α =5.5						
N		od (a) ection	Method (b) Partial-rejection		Percent of rejects Partial-rejection		
	Accept	Reject	Accept	Reject	Faitial-lejection		
15	12832	2168	14073	927	6.18%		
25	21190	3810	23519	1481	5.92%		
40	34375	5625	37811	2189	5.47%		
50	42066	7934	46709	3291	6.58%		

Table 8: α=10.25						
N	Meth No rej	Percent of rejects				
	Accept	Reject	Accept	Reject	Partial-rejection	
15	13028	1972	14187	813	5.42%	
25	21521	3479	23720	1280	5.12%	
40	34911	5089	38092	1908	4.77%	
50	42757	7243	47109	2891	5.78%	

	Table 9: α=15.5						
N	Method (a)Method (b)No rejectionPartial-rejection				Percent of rejects Partial-rejection		
	Accept	Reject	Accept	Reject	Partial-rejection		
15	13107	1893	14234	766	5.11%		
25	21656	3344	23808	1192	4.77%		
40	35117	4883	38219	1781	4.45%		
50	43024	6976	47302	2698	5.40%		

Table 10: α=20.5						
N	Method (a) Method (b) No rejection Partial-rejection				Percent of rejects Partial-rejection	
	Accept	Reject	Accept	Reject	Faitiai-rejection	
15	13141	1859	14261	739	4.93%	
25	21714	3286	23860	1140	4.56%	
40	35216	4784	38298	1702	4.26%	
50	43145	6855	47412	2588	5.18%	

5 Concluding remarks A partial-rejection approximation method is proposed to generate gamma random variables via Cheng's rejection method. The high *p*-values obtained from the K-S test showed that the level of

closeness between the approximate samples and the gamma samples is very good. The *p*-value obtained is consistently high and it improves with α indicating its wide range of applicability (α >1). The partial-rejection approximation method (Method (b)) has been compared to the no-rejection approximation method (Method (a)) where all the variates generated from the envelope distribution are not subjected to the acceptance-rejection condition. The no-rejection approximation method will give good approximate samples if the acceptance-rejection constant *M* is very close to 1 which is difficult to achieve in practice.

Clearly, the partial-rejection approximation method inherits the merits of the acceptance-rejection method with the additional advantage of speed. As remarked in the Introduction, the proposed method is general and may be applied, for instance, to generate negative binomial samples based on the acceptance-rejection algorithm of Ong and Lee (2008).

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