

# Rejection method for generating Nakagami- $m$ independent deviates

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The Nakagami- $m$  distribution has gained considerable research interest in the area of wireless communications thanks to its good fit to empirical fading data. A simple scheme for the generation of independent Nakagami- $m$  random variables (RVs) is presented and compared with the existing methods available in the literature.

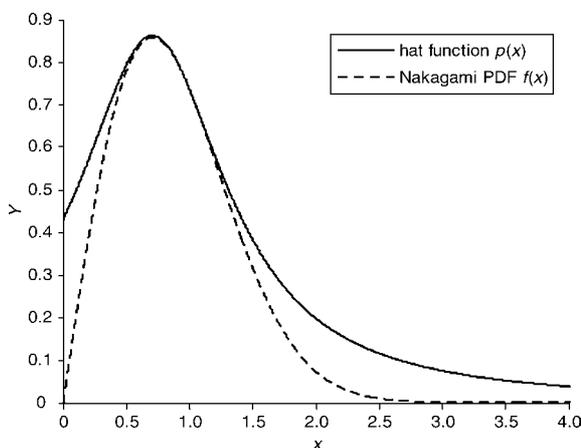
**Introduction:** It is well established that the Nakagami- $m$  distribution [1] yields a satisfactory fit with measured fading data over a wide range of frequency bands [2]. The Nakagami- $m$  probability density function (PDF) of the signal's envelope  $r$  is given by the formula

$$f(x) = \frac{2}{\Gamma(m)} \left(\frac{m}{\Omega}\right)^m x^{2m-1} e^{-mx^2/\Omega} \quad (1)$$

$x \geq 0, \quad m \geq 0.5, \quad \Omega \geq 0$

where  $\Gamma(\cdot)$  expresses the gamma function,  $m = E^2(x^2)/\text{var}(x^2)$  is the shape parameter, determining the severity of fading, and  $\Omega = E(x^2)$ . The generation of independent Nakagami- $m$  RVs can provide an insight into the characterisation of practical diverse systems operating in slowly varying Nakagami- $m$  fading environments. Surprisingly, to the best of the authors' knowledge, few results have been reported dealing with the computer simulation of independent Nakagami- $m$  fading [3–5]. The so called 'brute method' [3], which considers the square root of a sum of squares of  $n$  zero-mean identically distributed Gaussian random variables, leads to a Nakagami distribution with  $m = n/2$ ; however, this scheme is limited to integer and half-integer values of  $m$ . The authors in [4] showed that the product of a square-root beta process and a complex Gaussian process holds an accurate model but similarly is valid only for values of  $m < 1$ . The inverse method proposed in [5] is sufficiently accurate for arbitrary values of  $m$  but requires the computation of a different set of coefficients for each  $m$  value.

In this Letter, we present a novel technique for generating independent Nakagami- $m$  samples based on the rejection method [6]. A similar approach has been recently addressed in [7] but lacks a uniform approach for the whole range of  $m$  values. In particular, the authors suggest the use of either the folded-Gaussian ( $0.5 \leq m \leq 1.0$ ) or the Gaussian ( $m \geq 1.0$ ) PDFs as hat functions, resulting in the achieved efficiency being strongly dependent on the corresponding interval (65.75 and 66.67% respectively), with the option to select different constants (which are determined empirically) to improve efficiency for particular ranges of  $m$  (see Tables 1 and 2 in [7]). This was achieved by applying the rejection scheme only in the confined region  $0 \leq x \leq 4\Omega$ . In light of this fact, a simple uniform technique, without any constraints on the range of random values, is proposed herein, which alleviates the deficiencies of the aforementioned schemes and yields an excellent accuracy.



**Fig. 1** Rejection method for generating random Nakagami- $m$  deviates using inverse polynomial function

**Rejection method:** The rejection method relies on the selection of a comparison function (usually referred to as the hat function)  $p(x)$  that has finite area and satisfies the inequality  $p(x) \geq f(x)$ , where  $f(x)$  is the original PDF. We propose the use of a second-order inverse polynomial function which can be expressed as

$$p(x) = \frac{A\sqrt{\Omega}}{\Omega - B\sqrt{\Omega}x + x^2} \geq f(x) \quad (2)$$

An illustrative graph of the two functions under investigation is shown in Fig. 1. Taking into account that the maxima of (1) and (2) should coincide, it is trivial to show that  $B = 2\sqrt{(2m-1)/2m}$ . The scaling factor,  $A$ , is set such that the curves intersect at a single point,  $x = x_{\max}$ , without crossing. Thus

$$A = \frac{\Omega - B\sqrt{\Omega}x_{\max} + x_{\max}^2}{\sqrt{\Omega}} f(x_{\max}) \quad (3)$$

Solving  $x \rightarrow x_{\max} \quad d/dx(p(x) - f(x)) = 0$  gives one real positive solution at  $x_{\max} = \sqrt{\Omega}$ , which, when substituted into (3), yields

$$A = (2 - B) \frac{2m^m}{\Gamma(m)} e^{-m} \quad (4)$$

To generate independent samples from (2) we employ the widely known inverse method [6]; firstly, the indefinite integral  $\int p(x)dx$  of (2) is computed, leading to the closed-form function

$$t = \frac{2A \tan^{-1} \left( \frac{2x}{\sqrt{\Omega}} - B \right)}{\sqrt{4 - B^2}} \quad (5)$$

A random sample of  $x$  is generated via the inverse function of (5)

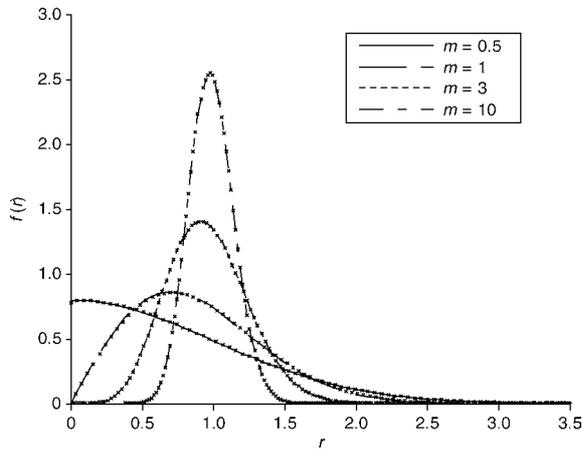
$$x = \frac{\sqrt{\Omega}}{2} \left( \sqrt{4 - B^2} \tan \left( \frac{t\sqrt{4 - B^2}}{2A} \right) + B \right) \quad (6)$$

where  $t$  is a RV distributed uniformly in the range

$$\left[ \frac{2A \tan^{-1} \left( \frac{-B}{\sqrt{4 - B^2}} \right)}{\sqrt{4 - B^2}}, \frac{A\pi}{\sqrt{4 - B^2}} \right]$$

It is worth noting that the above limits express, respectively, the minimum and maximum of (5) and define also the efficiency of the rejection method; in fact, their difference represents the area below  $p(x)$ . The generated sample  $x$  is accepted or rejected as a deviate based on the difference between (1) and (2). A detailed description of this well known algorithm can be found in [6].

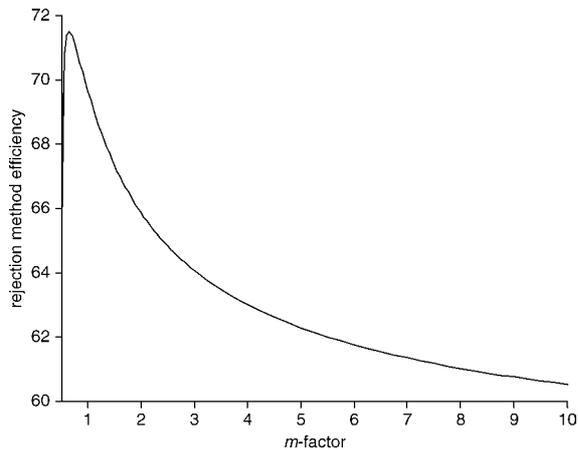
**Performance evaluation:** By generating  $2^{20}$  random  $x$  samples using (6) we were able to study the algorithm's performance in depth. Fig. 2 shows the theoretical and simulated Nakagami- $m$  PDFs for  $\Omega = 1$ ; it can be clearly seen that the achieved accuracy is noticeably high for all values of  $m$ , validating the choice of the rejection scheme as a powerful and straightforward technique for generating random deviates. A further study revealed that the maximum-likelihood (ML) estimators for the two shape parameters of the Nakagami PDF ( $\Omega$  and  $m$ ) give excellent agreement with theoretical values.



**Fig. 2** Theoretical and simulated Nakagami- $m$  PDFs for arbitrary values of  $m$  ( $\Omega = 1$ )

— theoretical curve  
 x simulated curve

*Efficiency:* It can be easily inferred that the method's efficiency is directly related to the  $m$  value. For high values of  $m$ , the tails of (1) decay slower than those of (2) and therefore the achieved efficiency decreases. In any case though, the efficiency in the common range of interest ( $0.5 \leq m \leq 2.5$ ) lies above 65% (see Fig. 3).



**Fig. 3** Efficiency of rejection method against  $m$  factor

*Conclusions:* The generation of independent Nakagami- $m$  deviates has been addressed by means of the rejection scheme based on an inverse polynomial function. It has been shown that the method can be easily applied for all values of the  $m$  parameter, yielding a high accuracy along with a satisfactory efficiency.

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