Generation and testing of pseudo-random numbers to be used in the stochastic simulation of econometric models

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GENERATION AND TESTING OF PSEUDO-RANDOM NUMBERS WITH ASSIGNED STATISTICAL PROPERTIES TO BE USED IN THE STOCHASTIC SIMULATION OF ECONOMETRIC MODELS

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PREFACE

The IBM Scientific Center of Pisa, the University of Pisa and the University of Siena have been carrying on a research on Stochastic Simulation of Econometric Models.

The first results have been summarized at the 2nd Meeting on "Teoria dei Sistemi ed Economia", Udine, October 1975, in the paper "Simulazione Stocastica ed Analisi di un Modello Aggregato dell'Economia Italiana" (Stochastic Simulation and Analysis of an Aggregated Model of the Italian Economy).

The following Technical Reports present in detail the methodological aspects and the complete results of the research:

P. Corsi,	"Eigenvalues and Multipliers of Alternative Estimates of an Aggregated Model of the Italian Economy", Technical Report CSP032/513-3542.
E. Cleur,	"Spectral Analysis of an Aggregated Model of the Italian Economy", Technical Report CSP033/513-3543.
G. Calzolari, T.A. Ciriani, P. Corsi,	"Generation and Testing of Pseudo-Random Numbers with Assigned Statistical Properties to be used in the Stochastic Simulation of Econometric Models", Technical Report CSP034/513-3544.
C. Bianchi et alii,	"Stochastic Simulation of an Aggregated Model of the Italian Economy: Methodological and Empirical Aspects", Technical Report CSP035/513-3545.

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1. INTRODUCTION

Purpose of this paper is the description of the tecniques used to generate pseudo-random numbers, to be added as disturbance terms to the stochastic structural equations of econometric models. These disturbance terms should have the same statistical properties as the residuals obtained, in each equation, during the estimation phase.

As the classical multiple regression scheme considers the residuals as random variables, object of these techniques is the generation of samples from a multivariate normal distribution with assigned parameters (mean, variance and covariance between equations).

The parameters are not exactly known, but only estimated. As currently done in these cases, the estimated values (resulting from an estimation algorithm such as OLS, 2SLS, 3SLS, FIML, LISE, etc.) are used instead of their expected values (or probability limits).

The generation procedure consists of three main steps:

1) Generation of pseudo-random numbers drawn from a population with uniform distribution in the interval (0,1).

2) Generation of pseudo-random numbers drawn from a population with univariate normal distribution, with zero mean and variance 1.

3) Generation of pseudo-random vectors drawn from a population with multivariate normal distribution with assigned parameters.

These three steps will be described in some detail, as far as implemented algorithms and performed statistical tests are concerned; no survey on the possible techniques of generation will be done, and the theoretical and philosophical problems of randomness of sequences will be left aside.

2. GENERATION OF PSEUDO-RANDOM NUMBERS WITH UNIFORM DISTRIBUTION

The most successful generators of uniformly distributed pseudo-random numbers known up to now [22, p. 9] follow the Linear Congruential scheme proposed by D.H. Lehmer [23, p. 141] .

A special case of this method, known as the Power Residue Method, has been adopted [17] .

For a good comprehension of the algorithm, a few concepts of Number Theory will be introduced here, not in the most general form, but adapted to the particular case here considered [34] .

2.1 Primitive roots of a prime modulus

Recalling that integer numbers are ... -2, -1, 0, 1, 2, ... a congruence is defined as follows:

if a, b, m are integers, a is said congruent to b modulo m

(1) $$a \equiv b \pmod{m}$$

if the integer a-b is a multiple of m.

For example $14 \equiv 4 \pmod{5}$ since $14-4 = 10$ is a multiple of 5.

If the modulus is a prime number (p = 2,3,5,7,11,13,17,.....) and a is an integer not a multiple of p, the following congruence holds:

(2) $$a^{p-1} \equiv 1 \pmod{p}$$

For example $2^{7-1} \equiv 1 \pmod{7}$ since $2^{7-1} - 1 = 63$ is a multiple of 7.
Also $3^{7-1} \equiv 1 \pmod{7}$ since $3^{7-1} - 1 = 728$ is a multiple of 7.

Eq. (2) is known as Fermat's theorem. The first demonstration of it was given by Euler in a more general form that, involving the multiplicative function $\varphi(m)$, extends eq. (2) to not prime moduli.

The demonstration of this theorem can be obtained by the elementary properties of the congruences and can be found in any introductory book of Number Theory [34, p. 37], [5, p. 13], [15 p. 63].

Referring to the last two examples, we notice a difference between the behaviour of the bases 2 and 3. Let the exponent run on the positive integers up to 7-1. We find that:

$$\left.\begin{array}{l} 2^1 \not\equiv 1 \\ 2^2 \not\equiv 1 \\ 2^3 \equiv 1 \\ 2^4 \not\equiv 1 \\ 2^5 \not\equiv 1 \\ 2^6 \equiv 1 \end{array}\right| \pmod 7, \quad \text{while} \quad \left|\begin{array}{r} 3^1 \not\equiv 1 \\ 3^2 \not\equiv 1 \\ 3^3 \not\equiv 1 \\ 3^4 \not\equiv 1 \\ 3^5 \not\equiv 1 \\ 3^6 \equiv 1 \end{array}\right| \pmod 7$$

The first column has a positive integer exponent less than 7-1 (3) that makes the power of 2 congruent to 1 modulo 7. In the second column no exponent makes it, untill 7-1; 3 is said "Primitive root modulo 7"; 2 is not a primitive root modulo 7.

In general a positive integer g is said "Primitive root modulo p" if [34, p. 76];

$$(3) \qquad g^n \not\equiv 1 \pmod p \qquad (n = 1,2, \ldots\ldots, p\text{-}3, p\text{-}2)$$

This definition leaves the problem of the existence of such primitive roots in general opened. This problem is solved by a theorem [34 p. 77] that states:

Each prime number has at least a primitive root.

As an immediate corollary it follows that, if g is a primitive root modulo p and h has no common factors to p-1, then also g^h is a primitive root modulo p. So each prime number has an infinity of primitive roots.

Given two integers a and m, it is called "minimum non negative residual of a modulo m" the integer u such that:

(4) $$a \equiv u \pmod{m} \qquad (0 \leq u < m)$$

It is clear that, given a modulus, two integers are congruent if, and only if, they have the same minimum non negative residual to that modulus.

We can now state a property of primitive roots used as the basis of the power residue method for random number generation.

Let p be a prime number and g one of its primitive roots. If n runs on all the integers between 1 and p-1, then the minimum non negative residual of g^n modulo p runs on all the integers between 1 and p-1.

A simple proof can be given ab absurdo:

Let be: $1 \leq h \leq p\text{-}1$
$1 \leq k \leq p\text{-}1$
$k < h$

If g^h and g^k have the same minimum non negative residual modulo p, then:

(5) $$g^h \equiv g^k \pmod{p}$$

From this follows, dividing by g^k, that is not multiple of p:

(6) $$g^{h-k} \equiv 1 \pmod{p}$$

As $1 \leq h\text{-}k < p\text{-}1$, from eq. (6) follows the absurdum that g cannot be a primitive root modulo p, and the proof is complete.

2.2 The Power Residue Method [17]

Using the same simbols as above, the Power Residue Method can be synthetized in the formula:

$$u_n \equiv g^n \pmod{p} \qquad 1 \leq u_n \leq p\text{-}1 \tag{7}$$

where u_n is the number generated at the *n-th* iteration.

As stated above this algorithm generates all the integer numbers between 1 and *p-1* without repetition, while the index n runs from 1 to p-1; the order of generation is, with some restrictions, so far from a trivial order that a generated sequence can be considered a sample of pseudo-random independent numbers drawn from a discrete uniform distribution.

Two main restrictions must be considered.

The first one concerns the length of the generated sequences, that always must have much less elements than p. We notice, in fact, that once a number has been generated, it cannot be generated any-more, unless the sequence is longer than p-1 (in that case the generation would be cyclical). So the generation looks like a sampling without replacement, while equiprobability of the uniform distribution would require a sampling with replacement. But it is known from the limit properties of the hypergeometric distribution that for large populations there is pratically no difference between sampling with or without replacement [11, p. 57].

So the first restriction is that the value of the prime modulus p must be larger than any possible length of sequences of practical use.

The second restriction deals with the primitive root g. If it is too small when compared to p, the generated sequences can be strongly autocorrelated.

This will be clear if we re-write the generator (eq. (7)) in the following way:

$$u_n \equiv g\, u_{n-1} \pmod{p} \qquad 1 \leq u_n \leq p\text{-}1 \tag{8}$$

putting in evidence the linkage between the value generated at the *n-th* iteration and the preceeding one, through the multiplier *g*.

If *g* is of the order of magnitude of few units, every time that a small value u_n is generated, it is followed by a rising sequence too long to be considered random. Problems of autocorrelation can rise also when the value of *g* is too close to *p*. Empirical considerations, supported by experimental simulations, suggest to choose a value of *g* of the same order of magnitude of $\sqrt{p}$, but not too close to it.

2.3 The adopted generator

The maximum integer number that can be represented in a word of the IBM System 370 (32 signed bits) is $2^{31} - 1 = 2147483647$, that is a prime number, and is large enough to be used as a modulus.

The research of a primitive root of such a prime is not quite elementary from a computational point of view. It has been done [24] and 7 was found to be such a root.

From the above considerations a multiplier that should give good results is $7^5 = 16807$; it is in fact of the order of magnitude of the square root of the modulus, and it is still a primitive root, since 5 and 2147483646 are relatively prime.

With these values of the modulus and the multiplier, the power residue generator is:

(9) $$u_n \equiv 16807\ u_{n-1} \pmod{2^{31} - 1} \qquad 1 \leq u_n \leq 2^{31} - 2$$

The generator was first used by Lewis, Goodman and Miller [24] , who performed on it several sophisticated statistical tests, finding satisfactory results.

As it will be explained in the next section, we do not need a discrete uniform distribution, but a continuous one in the open interval (0,1) of the real axis. We get a very good numerical approximation of it dividing the generated value u_n by the modulus:

(10) $$U_n = u_n \ / \ (2^{31} - 1)$$

3. GENERATION OF PSEUDO-RANDOM NUMBERS WITH NORMAL DISTRIBUTION

Most of the algorithms proposed in the literature [13] for the generation of pseudo-random numbers with normal distribution are based on asymptotic properties, so that they can be considered only approximations to normality, while on the other side they allow a considerable saving of computation time. Two methods can be considered theoretically exact, even if their numerical implementation involves some approximations. They are generally called:

— direct method, or polar method, or method of Box and Muller;

— inverse method.

For our purpose we have chosen these two methods even if they are much more expensive in terms of execution time.

3.1 The direct or polar method

This method was proposed by Box and Muller [4] in 1958. It states that if U_1 and U_2 are two values of independent random variables uniformly distributed in (0,1), then:

$$(11) \qquad \begin{cases} X_1 = (-2 \log U_1)^{1/2} \cos (2 \pi U_2) \\ X_2 = (-2 \log U_1)^{1/2} \sin (2 \pi U_2) \end{cases}$$

are two values of independent random variables normally distributed with mean 0 and variance 1.

The demonstration follows from the general method [20, p. 23] of computing the distribution function after a transformation of variables. Since in our transformation the Jacobian, with positive sign, is:

$J = \frac{2\pi}{U_1}$ and it is always > 0 in the open interval (0,1), then, calling $f(U_1, U_2)$ and $g(X_1, X_2)$ the joint density functions, we have:

$$g(X_1, X_2) = \frac{f(U_1, U_2)}{J}$$

Since U_1 and U_2 are independent uniform variables with density 1, we have

$$\frac{f(U_1, U_2)}{J} = \frac{1}{J} = \frac{U_1}{2\pi}$$

U_1 can be easily computed from eq. (11).

$$U_1 = e^{-\frac{X_1^2 + X_2^2}{2}}$$

So

$$g(X_1, X_2) = \frac{1}{\sqrt{2\pi}} e^{-\frac{X_1^2}{2}} \cdot \frac{1}{\sqrt{2\pi}} e^{-\frac{X_2^2}{2}} \tag{12}$$

that shows that X_1 and X_2 are independent normal variables with zero mean and variance 1.

3.2 The inverse method

As follows from the definition itself of density function [20, pag. 18-19] , any distribution can be easily transformed into the rectangular form. In fact if w is a random variable with density function $f(w)$, the transformation:

$$v = \int_{-\infty}^{w} f(t)\, dt$$

gives a random variable v with uniform distribution in the interval (0,1).
If X is a random variable with normal distribution, zero mean and variance 1, then

$$U = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{X} e^{-t^2/2}\, dt \tag{13}$$

is a variable with uniform distribution in the interval (0,1) (open interval if we exclude for X the values $\pm \infty$); viceversa, given a value for U, the corresponding value of X can be considered a value of a normal variable with the required parameters; this is what we call the inverse method. The problem is how to compute the corresponding value of X once a value for U in (0,1) is given.

Since an analytical method is not available, a numerical technique based on Chebyshev's orthogonal polinomials can be used. The algorithm we have used is [1, eq. 26-2-23], [16], [18]:

$$X = w - \sum_{i=0}^{2} a_i \, w^i \Big/ \sum_{i=0}^{3} b_i \, w^i \tag{14}$$

where a_i and b_i are assigned constants and $w = \sqrt{\log\left(\frac{1}{U^2}\right)}$ with $0 < U \leq 0.5$.

Even if the error of this approximation is very high, almost $5 \cdot 10^{-4}$, tests performed on it (see section 4) allow to consider this method quite equivalent to the direct method.

3.3 Shuffling technique

A problem arises when applying the Box-Muller transformation to numbers U_1 and U_2 coming from a power residue generator [30]. If U_1 and U_2 are consecutive numbers generated with the power residue generator, then from eq. (8) and (10) follows that:

$$u_2 = g \, u_1 - kp$$

where k is an integer. Dividing by p:

$$U_2 = g \, U_1 - k$$

With the Box-Muller transformation we have:

$$X_1 = (-2 \log U_1)^{\frac{1}{2}} \cos(2\pi U_2) = (-2 \log U_1)^{\frac{1}{2}} \cos(2\pi g U_1 - 2\pi K)$$

due to the periodicity of cosinum, we have:

$$X_1 = (-2 \log U_1)^{\frac{1}{2}} \cos(2\pi g U_1) \tag{15}$$

The same can be said for X_2.

The sin-cos transformation in some sense destroys the independence between U_1 and U_2. The distribution function of X_1 and X_2 cannot be elementarily computed as above. What is immediately clear from eq. (15) is that X_1 has not mean 0, while the variance not equal to 1 and the non normality of the distribution cannot be simply shown.

The same problem would arise even if, instead of consecutive numbers U_1 and U_2, we took the output numbers of the power residue generator in the order:

$$U_1 , U_{d+1}; U_2 , U_{d+2}; U_3 , U_{d+3}; \ldots\ldots$$

where d is a fixed distance. We would only find in eq. (15) g^d instead of g, and the method would be incorrect as before from a theoretical point of view.

Taking the values U_1 and U_2 in inverse order, some authors obtained good results, but from a theoretical point of view the method remains incorrect, since in eq. (15) we would find instead of g a number g', such that:

$$g.g' \equiv 1 \text{ (mod. } 2^{31} - 1) \quad [6]$$

We have adopted the solution proposed in [25] that consists of a shuffling of the output numbers of the power residue generator, before the application of the Box-Muller transformation. The first 128 ($= 2^7$) integer numbers generated (U_i) are consecutively stored into a vector, whose cells are addressed by numbers 0,1,2,...126, 127, (7 bits).

From this point each new number is stored into the cell addressed by its low order 7 bits, while the previous value occupying that cell is the output number. Even if this shuffling is strictly necessary only in the case of the Box and Muller method, we apply it also when using the inverse method. In this way the performances of the two methods can be compared, since they start from the same input values.

4. STATISTICAL TESTS

We have decided to concentrate statistical tests after the phase of the generation of pseudo-random numbers with univariate normal distribution.
Two ways can be followed at this point. The first involves applying the greatest possible number of different tests to the generator; if no one of them (or only few) reject the hypothesis on the distribution function, the generator can be defined good.
This way is almost always followed in the literature: a dozen of different tests of randomness [22] , [24] are applied to large samples of numbers, in order to test the asymptotic properties of the generator.

The second approach, the one adopted here, attempts to be more "finalized". Once the mode of use of the generator and the most important statistical properties to be observed are defined (among the infinite required by the perfect randomness), tests are concentrated on sequences roughly of the same length as those of practical use.

For the stochastic simulation of econometric models, in order to generate random numbers with multivariate normal distribution and assigned parameters it is necessary, for the univariate normal generator, to respect the following properties:

- Normal distribution
- Mean 0
- Variance 1
- Absence of serial correlation

Other properties, such as the distribution of the runs up and down, the sequences above and below the mean etc. do not look to be of the same importance.

Without going into deep details, that can be found, for example, in [21, p. 419 - 464], we give here a brief description of the performed tests.

4.1 The X^2 test

This classical test [21] , [22] introduced by K. Pearson in 1900, is based on the asymptotic properties of the multinomial distribution. After dividing the real axis into k intervals, we call P_i ($i = 1,2,... k$) the theoretical probability that a generated number fall into the *i-th* interval, according to the hypothized distribution function.

If N is the length of the sample, and n_i ($i = 1,2,... k$) is the number of values that actually fall into the *i-th* interval (so that $N = \sum_{i=1}^{k} n_i$), we compute:

$$X^2 = \sum_{i=1}^{k} \frac{(n_i - NP_i)^2}{NP_i} \tag{16}$$

X^2 is a random variable whose distribution function is asymptotically (as n_i increases for every i) a X^2 with k-1 degrees of freedom. The approximation error in using (16) as a X^2 variable is particularly small when P_i are all equal ($P_i = \frac{1}{k}$, $i = 1,2... k$), so that a value of few units for NP_i (for example ≥ 5 as suggested by many authors) is quite sufficient for a good approximation. We have followed this rule even if the choice of equiprobable intervals increases the cost of computation.

It is clear from eq. (16) that a high value of X^2 means a big difference between the observed and the theoretical numbers of values in the intervals. This suggests to reject the null hypothesis on the distribution when X^2 is high (upper-tail test). We have followed this rule according to [21, p. 422], even if other authors suggest a two-tailed test.

4.2 The Kolmogorov test

Given $F_o(X)$ the distribution function related to the null hypothesis H_o, if $S_n(X)$ is the empirical distribution function as it is estimated from a sample of n numbers, the following value is computed [21], [22]:

$$K_n = \sup_{-\infty < X < +\infty} \left| S_n(X) - F_o(X) \right| \tag{17}$$

The asymptotic distribution of K_n was obtained by Kolmogorov in 1933; when H_o holds, it is completely distribution free, and it should lead to a more accurate test than the χ^2 since it is based on the continuous distribution and does not require arbitrary divisions into intervals [22, p. 47].

A high value of K_n means great discordance between the hypothized and the sample distribution. This suggests to reject the hypothesis when K_n is high (upper-tail test). We have followed this rule, performing this test only on samples with at least 100 elements, when the asymptotic formula holds with good approximation [18].

4.3 The Z test on the mean

Once the distribution function (normal) and the value of the variance (1) have been tested and accepted, this simple test can be profitably employed to compare alternative hypotheses on the mean [9, p. 77].

It simply checks if the estimated mean lies inside or outside a confidence interval around the hypothized mean, whose amplitude depends on the confidence level and the sample length (for example $\pm \frac{1.96}{\sqrt{N}}$ if the confidence level is 95% and N is the sample length).

If only the null hypothesis is formulated, a two-tail test is usually performed; if also an alternative hypothesis is formulated, and this is the way followed by us, a one-tail test can be performed.

4.4 The test on the variance

Once the distribution function (normal) and the value of the mean (0) have been tested and accepted, this test can be employed to compare alternative hypotheses on the variance [9, p. 102].

After computing the sample variance, in the usual way as

(18) $$S^2 = \frac{\sum (X_i - \bar{X})^2}{N - 1}$$

if σ^2 is the true variance, the ratio $\frac{S^2}{\sigma^2}$ is a value of a random variable χ^2/df (chi square over degrees of freedom) where the number of degrees of freedom is N-1.

When comparing the null hypothesis on the variance with an alternative hypothesis, the rejection region is chosen on the right or on the left tail, according to the alternative value of σ^2 (that is if it is greater or less than the value of σ^2 of the null hypothesis).

4.5 The serial test

This simple test is used to check the absence of serial correlation in a sequence of random numbers (distribution free test) [17], [19], [22]. The sample is divided into a sequence of pairs, and the real axis is divided into K equiprobable intervals (according to the hypothesis on the distribution function). A (KxK) matrix is built, and its (i,j)-*th* cell is filled with the number of pairs in which a number of the *i-th* interval of the real axis is followed by a number of the *j-th* interval.

If serial correlation (of any order) exists, some cells of the matrix are expected to be filler than the others, so that a test should reject the hypothesis of uniform distribution of the elements of the matrix itself.

It must be noticed that this test is not a very powerful one, but is the only one performed by us to check the absence of serial correlation on the adopted generators. A more precise test, based on Bartlett's formulas, could be profitably performed [3].

4.6 Experimental results

The sequences of the pseudo-random numbers required for the stochastic simulation experiments are "medium" or "short". A pluriequational model, with a sample period of 20 years [31] , requires a sequence of 20 pseudo-random numbers for each replication. If, as usually happens, it is wished to perform 10 or 20 replications, it is clear that it is advisable to verify the statistical properties on "small" sequences with some tens of numbers and "medium" sequences with some hundreds of numbers.

The serial test presents some difficulties in the case of small samples, and was applied only to samples of medium length (500 and 1000, tab. 5). The other four tests were applied to small and medium samples, and an attempt was made to highlight not only the fit of the samples to the hypothesis on the population, but also the power of the tests to distinguish between alternative hypotheses on the distribution function (power of the test).

For each hypothesis a confidence level of 95% was assumed.

A certain number of samples of the same length was generated with the two methods (Inverse, tables x-1, Box-Muller, tables x-2, x from 1 to 4).

Keeping unchanged the hypothesis of normal distribution with variance 1, 18 different hypotheses were formulated with means $\neq 0$ (positive and negative) and the hypothesis of mean $= 0$. Each of these hypotheses was tested by means of χ^2 and Kolmogorov as many times as the generated samples.

On some occasions the test is satisfactorily concluded, and on others it is necessary to reject the hypothesis. Alongside each value of the mean, we indicate, in percentage form, the number of times that the hypothesis has been rejected. It is expected to observe a minimum in correspondence with the hypothesis "mean $= 0$", and it is expected that the value of this minimum will be about 5, and that it will converge towards 5 with the increase of the number of samples (NRUN on tables) irrespective of the length of each sample (ITIME in the tables). With the rise, instead, of the number of elements of each sample (ITIME) and irrespective of the number of samples, an ever-increasing selectivity is expected

(the same hypothesis of mean $\neq 0$ is rejected as many more times as ITIME is greater).

The Kolmogorov test, as explained above, was used only for samples of medium length (ITIME $\geq$ 100) (tables 1 and 2).

For the test we have kept to the empirical rule [21], [22] advising against ever having a theoretical frequency < 5 in any interval. In order later to have the maximum power of the test [21], albeit to the detriment of execution time, we chose on each occasion a breakdown into intervals (NINTRV is their number) of equal probability.

By means of a similar procedure we executed the test on the confidence interval of the estimated mean (Z test). In this case, any hypothesis of mean $\neq 0$ was subjected to the test against a precise alternative hypothesis, (mean $= 0$); the test, therefore, (one-tail test) proved to be particularly powerful.

Practically the same applies to the test on alternative variances. Taking as constant the normal distribution hypothesis with mean zero, 18 different hypotheses were formulated with variance $\neq 1$ and the hypothesis of variance $= 1$. In this case too each of these hypotheses was subjected to χ^2 test, to the Kolmogorov test and to the test of the confidence interval of the estimated variance. It should be noted that the latter test becomes less significant when the number of elements of the sample increases (we obtain a χ^2 with a high number of degrees of freedom), but this does not happen in the case, here described, of medium or small samples.

As a final comment on the structure of the tables, it should be said that every number shown summarises the results of a number of tests equal to NRUN. Thus, the table 1-1 alone summarises the results of 56,000 separate tests (6 tests on 19 hypotheses, with two repeated combinations, for a total of 112 tests repeated 500 times) on samples of length 200. The table 4-1 summarises the results of 375,000 separate tests on samples of 20 elements.

In every table NSEME is the number which starts the generator (U_0).

NSEME	1
NRUN	500
ITIME	200
NINTRV	20

Tab. 1 - 1

VAR = 1				MEAN = 0			
	χ^2	KOLMOG	Z TEST		χ^2	KOLMOG	VAR. TEST
MEAN	% OUT	% OUT	% OUT	VAR	% OUT	% OUT	% OUT
− 0.18	26.60	59.60	84.20	0.73	38.00	18.60	93.60
− 0.16	20.80	51.20	75.80	0.76	29.60	14.80	85.40
− 0.14	17.00	41.60	65.60	0.79	22.00	12.80	76.00
− 0.12	14.00	32.20	51.80	0.82	17.00	10.60	63.00
− 0.10	9.40	21.80	41.80	0.85	12.60	8.80	50.20
− 0.08	7.60	15.40	30.80	0.88	9.60	6.60	37.20
− 0.06	6.40	10.00	21.00	0.91	7.00	5.80	27.20
− 0.04	5.00	6.40	13.20	0.94	6.40	5.20	16.60
− 0.02	5.00	5.40	7.80	0.97	5.20	4.60	10.40
0.00	5.40	4.40	5.80	1.00	5.40	4.40	5.20
0.02	5.80	5.20	9.20	1.03	4.40	3.80	9.20
0.04	7.40	7.20	11.80	1.06	7.40	4.00	15.40
0.06	7.60	10.60	17.80	1.09	7.00	4.20	22.60
0.08	8.40	14.60	29.00	1.12	9.00	5.00	30.40
0.10	11.40	20.40	39.40	1.15	10.40	5.40	39.40
0.12	13.20	28.40	52.00	1.18	12.20	6.00	49.40
0.14	17.80	36.60	61.80	1.21	13.00	6.60	58.60
0.16	21.40	46.00	73.00	1.24	14.00	8.20	66.60
0.18	24.40	55.20	81.80	1.27	18.00	9.40	75.40

NSEME	1
NRUN	500
ITIME	200
NINTRV	20

Tab. 1 - 2

VAR = 1				MEAN = 0			
	χ^2	KOLMOG	Z TEST		χ^2	KOLMOG	VAR. TEST
MEAN	% OUT	% OUT	% OUT	VAR	% OUT	% OUT	% OUT
− 0.18	24.00	57.00	80.80	0.73	40.60	18.80	95.20
− 0.16	17.00	46.60	73.80	0.76	28.20	14.40	87.80
− 0.14	12.60	39.60	61.80	0.79	19.40	11.00	76.80
− 0.12	10.60	30.00	52.00	0.82	15.20	8.60	65.60
− 0.10	9.40	22.00	40.20	0.85	10.80	6.60	49.80
− 0.08	6.80	14.60	31.40	0.88	7.00	5.80	37.00
− 0.06	4.60	8.60	20.60	0.91	4.20	5.20	26.40
− 0.04	4.00	6.00	13.00	0.94	3.60	4.40	18.40
− 0.02	3.80	4.40	7.40	0.97	3.00	3.80	10.20
0.00	3.00	3.60	3.80	1.00	3.00	3.60	4.20
0.02	3.60	5.40	8.40	1.03	3.00	2.80	6.60
0.04	5.80	7.60	15.80	1.06	2.60	2.80	12.40
0.06	5.60	11.00	21.20	1.09	3.60	3.20	20.80
0.08	5.80	15.60	30.60	1.12	4.80	4.40	28.40
0.10	8.40	21.20	42.80	1.15	6.40	4.60	37.00
0.12	11.60	30.60	54.00	1.18	9.40	5.00	49.20
0.14	12.60	40.00	61.80	1.21	11.40	5.20	58.20
0.16	16.40	47.80	74.20	1.24	11.80	6.60	66.80
0.18	23.60	57.80	82.40	1.27	15.40	7.80	74.80

NSEME 1000000000
NRUN 1000
ITIME 100
NINTRV 10

Tab. 2 - 1

VAR = 1

MEAN	χ^2 % OUT	KOLMOG % OUT	Z TEST % OUT
− 0.18	18.50	34.50	56.10
− 0.16	15.10	27.20	48.70
− 0.14	12.40	21.70	42.50
− 0.12	9.40	16.70	32.70
− 0.10	7.90	13.80	25.80
− 0.08	6.50	10.90	20.20
− 0.06	5.90	8.00	14.40
− 0.04	4.90	6.70	10.90
− 0.02	4.60	5.70	7.60
0.00	6.00	5.60	5.20
0.02	6.10	5.40	7.70
0.04	6.60	6.20	10.50
0.06	8.20	8.40	15.30
0.08	8.50	10.50	21.40
0.10	10.90	14.00	28.10
0.12	11.10	18.30	34.30
0.14	13.60	23.50	41.40
0.16	16.20	28.40	48.10
0.18	19.00	33.50	54.30

MEAN = 0

VAR	χ^2 % OUT	KOLMOG % OUT	VAR. TEST % OUT
0.55	68.90	38.30	99.30
0.60	54.50	28.40	97.20
0.65	40.10	20.60	92.50
0.70	26.30	16.70	82.90
0.75	19.60	11.40	69.20
0.80	13.50	8.30	52.30
0.85	9.10	6.70	34.00
0.90	8.10	5.70	21.30
0.95	6.20	5.50	12.20
1.00	6.00	5.60	6.20
1.05	6.30	5.30	8.30
1.10	6.70	5.40	14.50
1.15	7.70	6.10	22.20
1.20	9.00	6.10	30.80
1.25	11.30	6.40	41.90
1.30	14.80	7.10	52.90
1.35	17.30	7.70	64.80
1.40	20.80	9.00	73.60
1.45	24.20	9.50	79.80

NSEME 1000000000
NRUN 1000
ITIME 100
NINTRV 10

Tab. 2 - 2

VAR = 1

MEAN	χ^2 % OUT	KOLMOG % OUT	Z TEST % OUT
− 0.18	16.20	31.00	52.90
− 0.16	13.30	26.20	45.30
− 0.14	12.10	20.30	37.40
− 0.12	9.90	15.90	30.30
− 0.10	8.30	12.00	25.60
− 0.08	6.90	9.40	18.90
− 0.06	6.70	7.00	14.00
− 0.04	5.80	5.90	10.00
− 0.02	5.10	3.60	7.70
0.00	4.90	3.40	4.70
0.02	4.10	3.30	6.30
0.04	4.70	4.60	10.00
0.06	4.50	6.40	14.40
0.08	6.50	8.50	19.50
0.10	7.40	11.40	26.40
0.12	8.90	14.80	33.60
0.14	11.10	19.10	42.10
0.16	13.80	25.10	50.40
0.18	17.80	30.90	58.40

MEAN = 0

VAR	χ^2 % OUT	KOLMOG % OUT	VAR. TEST % OUT
0.55	65.70	35.10	99.50
0.60	50.30	24.20	97.00
0.65	36.80	17.50	92.70
0.70	25.20	12.10	81.20
0.75	16.60	9.60	66.00
0.80	11.30	6.90	48.80
0.85	7.60	5.40	32.10
0.90	6.30	3.70	19.60
0.95	5.40	3.50	11.00
1.00	4.90	3.40	6.40
1.05	5.10	3.50	8.70
1.10	6.10	3.40	15.40
1.15	7.40	3.80	24.00
1.20	8.60	5.00	34.20
1.25	11.20	5.30	44.30
1.30	13.40	6.30	56.30
1.35	16.20	7.10	66.50
1.40	20.40	8.00	74.90
1.45	24.90	9.00	81.90

NSEME	1234567
NRUN	2000
ITIME	50
NINTRV	7

Tab. 3 - 1

VAR = 1			MEAN = 0		
	χ^2	Z TEST		χ^2	VAR. TEST
MEAN	% OUT	% OUT	VAR	% OUT	% OUT
− 0.36	38.80	82.10	0.46	52.85	98.25
− 0.32	30.85	72.80	0.52	39.35	94.00
− 0.28	23.80	62.90	0.58	28.05	87.50
− 0.24	16.70	51.45	0.64	19.85	75.05
− 0.20	12.25	39.65	0.70	13.35	59.00
− 0.16	9.70	29.15	0.76	9.65	42.80
− 0.12	7.55	20.30	0.82	6.75	28.90
− 0.08	5.60	13.20	0.88	5.30	16.90
− 0.04	4.65	7.90	0.94	4.60	8.35
0.00	4.80	4.20	1.00	4.80	4.40
0.04	4.70	8.70	1.06	4.65	7.85
0.08	5.80	13.90	1.12	5.40	12.00
0.12	7.75	21.30	1.18	6.20	16.90
0.16	8.85	30.30	1.24	7.20	23.75
0.20	13.15	41.60	1.30	8.60	31.70
0.24	17.95	52.75	1.36	9.65	40.10
0.28	23.40	64.60	1.42	11.35	48.40
0.32	31.65	74.55	1.48	14.50	56.20
0.36	40.15	82.40	1.54	17.45	64.35

NSEME	1234567
NRUN	2000
ITIME	50
NINTRV	7

Tab. 3 - 2

VAR = 1			MEAN = 0		
	χ^2	Z TEST		χ^2	VAR. TEST
MEAN	% OUT	% OUT	VAR	% OUT	% OUT
− 0.36	39.20	81.85	0.46	53.60	98.35
− 0.32	31.20	73.45	0.52	39.55	93.95
− 0.28	24.50	62.95	0.58	27.80	86.45
− 0.24	17.25	52.75	0.64	19.65	75.15
− 0.20	12.30	41.30	0.70	13.50	59.80
− 0.16	8.45	30.65	0.76	9.75	42.45
− 0.12	6.80	21.10	0.82	7.30	28.75
− 0.08	5.30	13.40	0.88	5.35	17.30
− 0.04	4.85	8.10	0.94	4.75	9.45
0.00	5.15	5.10	1.00	5.15	5.30
0.04	5.20	8.35	1.06	5.50	8.10
0.08	6.10	14.45	1.12	5.55	12.10
0.12	7.95	21.30	1.18	6.30	17.60
0.16	9.80	30.45	1.24	6.90	23.55
0.20	13.25	40.80	1.30	8.70	31.80
0.24	13.70	52.05	1.36	10.55	39.60
0.28	24.80	62.80	1.42	12.70	47.40
0.32	30.85	72.70	1.48	14.80	56.75
0.36	39.20	81.65	1.54	17.45	63.70

NSEME	65432
NRUN	5000
ITIME	20
NINTRV	3

Tab. 4 - 1

VAR = 1			MEAN = 0		
	χ^2	Z TEST		χ^2	VAR. TEST
MEAN	% OUT	% OUT	VAR	% OUT	% OUT
− 0.54	46.36	78.10	0.37	17.06	91.64
− 0.48	37.74	69.22	0.44	13.84	82.80
− 0.42	29.92	59.30	0.51	11.64	70.38
− 0.36	23.30	48.38	0.58	9.38	55.78
− 0.30	17.34	37.20	0.65	8.08	42.14
− 0.24	13.02	28.00	0.72	6.96	29.64
− 0.18	9.24	19.00	0.79	6.32	20.52
− 0.12	7.32	12.68	0.86	5.82	13.34
− 0.06	5.74	7.98	0.93	5.48	8.28
0.00	5.38	4.40	1.00	5.38	5.02
0.06	6.02	8.32	1.07	5.46	7.44
0.12	7.68	13.28	1.14	5.54	9.76
0.18	9.58	19.80	1.21	5.74	12.48
0.24	13.22	28.14	1.28	6.30	16.56
0.30	18.18	37.72	1.35	6.92	19.22
0.36	23.74	48.98	1.42	7.60	23.30
0.42	31.22	59.86	1.49	8.66	27.88
0.48	39.48	69.72	1.56	9.70	32.24
0.54	48.00	78.96	1.63	10.74	37.34

NSEME	65432
NRUN	5000
ITIME	20
NINTRV	3

Tab. 4 - 2

VAR = 1			MEAN = 0		
	χ^2	Z TEST		χ^2	VAR. TEST
MEAN	% OUT	% OUT	VAR	% OUT	% OUT
− 0.54	47.20	77.88	0.37	17.44	91.88
− 0.48	38.20	69.30	0.44	14.22	83.48
− 0.42	30.34	59.14	0.51	11.80	70.56
− 0.36	23.54	48.92	0.58	9.98	55.96
− 0.30	18.16	37.66	0.65	8.56	41.78
− 0.24	12.52	28.00	0.72	7.40	30.44
− 0.18	9.64	20.12	0.79	6.42	20.74
− 0.12	7.18	13.80	0.86	6.04	13.24
− 0.06	5.74	8.66	0.93	5.84	8.06
0.00	5.74	5.16	1.00	5.74	4.68
0.06	6.40	8.72	1.07	5.68	6.94
0.12	7.42	13.38	1.14	6.10	9.40
0.18	9.84	19.94	1.21	6.62	12.14
0.24	14.06	28.32	1.28	7.28	15.36
0.30	18.76	37.80	1.35	7.94	18.58
0.36	24.66	48.36	1.42	8.68	23.06
0.42	32.18	59.50	1.49	9.62	27.62
0.48	40.48	69.78	1.56	10.40	32.14
0.54	48.94	78.04	1.63	11.28	36.94

Tab. 5

SERIAL TEST

Inverse Method

NRUN = 100

NSEME	ITIME	% OUT
2000000000	500	6
2000000001	500	11
2000000002	500	3
2000000003	500	3
2000000004	500	5
2000000005	500	3

Direct Method

NRUN = 100

NSEME	ITIME	% OUT
1	1000	6
2	1000	4
1000000000	500	6
1000000001	500	4
1000000002	500	5
1000000003	500	5
1000000004	500	1
1000000005	500	7

4.7 Conclusions

The results experimentally obtained confirm that:

- Short or medium sequences of numbers generated with any one of the two methods (without preference for one or the other) may in fact be taken as drawn from a normal population with mean 0 and variance 1.

- The same sequences cannot be taken as drawn from a population with a mean "fairly" different from 0, or with a variance "fairly" different from 1 (where the term "fairly" indicates something that is a function of the length of the sequence).

- Once the hypothesis of the normality of the distribution has been accepted, the test of the confidence interval (of the estimated mean or variance) seems to be more powerful than χ^2 test and Kolmogorov test in rejecting hypotheses of mean $\neq 0$ or variance $\neq 1$.

- The Kolmogorov test seems to be more powerful than the χ^2 test in rejecting hypotheses of mean $\neq 0$.

- The χ^2 test seems instead to be more powerful than the Kolmogorov test in rejecting hypotheses of variance $\neq 1$ (for these sample sizes).

- Sequences of numbers of medium length generated with the two methods may be regarded as having no autocorrelation.

- In order to determine if, and how many times, they can instead be regarded as being affected by autocorrelation of a certain order with certain values of the coefficient $\rho \neq 0$, as well as for analysis of short sequences, a more accurate test (based, as said above, on the formulas of Bartlett [3])could be profitably performed.

5 GENERATION OF PSEUDO-RANDOM NUMBERS WITH ASSIGNED VARIANCE – COVARIANCE MATRIX

In this section two methods for the generation of pseudo-structural errors, to be used in the stochastic simulation of an econometric model are described.

The pseudo structural errors that are introduced during the solution in the behavioural equations of a model must have the same statistical properties (in terms of variance, of simultaneous covariance between equations and of serial correlation) embodied by the structure of the model [7] : in other words, these must come from the same multivariate distribution. Taking into account the fact that the structural errors are regarded as additive during the estimation phase, the pseudo-structural errors are added to the constant term of the behavioural equation during the solution stage. Added to this, they are normally generated in such a way that their variance-covariance matrix is asymptotically equal to the variance-covariance matrix relating to the sample period. Even if we shall disregard the problem of serial correlation within equation, this approach represents a more general procedure than the one described in [32] which uses a diagonal variance-covariance matrix, in such a way that the simultaneous covariances between the different equations are all equal to zero. Let us examine in detail two of the techniques proposed in the literature:

a – Nagar's algorithm [27]
b – McCarthy's algorithm [26]

Let U_{it} be the errors of the equation i at the various intervals t, we obtain the following relations:

$$E(U_{it_1} \; U_{jt_2}) = \begin{cases} \sigma_{ij} & \text{for } t_1 = t_2 \\ 0 & \text{for } t_1 \neq t_2 \end{cases} \tag{19}$$

$$\text{for } t_1, t_2 = 1,2,\ldots,T \quad \text{and} \quad i,j = 1,2,\ldots,M$$

where T is the length of the sample period and M is the number of structural equations.

Since,as we have mentioned in section 1, the pseudo-structural disturbances are generated in such a way as to follow the statistical properties which characterize the model, the previous hypothesis means considering in the model an error structure that is not serially correlated. Similar observations (with related formulas) are given in [26], [27] for the case of pseudo-structural disturbances correlated on time.

5.1 Nagar's algorithm

Nagar's algorithm makes it possible to obtain the desired matrix of pseudo-structural errors, by means of a linear transformation of an assigned matrix with independent random numbers normally distributed. It is wished to generate a matrix U with dimensions TxM:

$$U = \begin{bmatrix} U_{11} \cdots\cdots U_{1M} \\ \vdots \qquad\quad \vdots \\ U_{T1} \cdots\cdots U_{TM} \end{bmatrix} \tag{20}$$

so that the elements in the *m-th* column represent the pseudo-structural errors to be added to the *m-th* structural equation of the model at the various time intervals (1,2,....., T). The pseudo-structural disturbances U must have a zero mean and a specified variance-covariance matrix:

$$E(U) = 0 \qquad \frac{1}{T} E(U'U) = \sum = \begin{bmatrix} \sigma_{11} \cdots\cdots \sigma_{1M} \\ \vdots \qquad\quad \vdots \\ \sigma_{M1} \cdots\cdots \sigma_{MM} \end{bmatrix} \tag{21}$$

where σ_{ij} is the covariance between equation i and equation j.

During the experiments of stochastic simulation, we have available a matrix of dimensions TxM which contains independent pseudo-random numbers normally distributed with a zero mean and unitary variance:

$$X = \begin{bmatrix} X_{11} \cdots\cdots X_{1M} \\ \vdots \qquad\quad \vdots \\ X_{T1} \cdots\cdots X_{TM} \end{bmatrix} \tag{22}$$

Hence X satisfies the following conditions:

(23) $$E(X) = 0 \qquad \frac{1}{T} E(X'X) = I$$

where I is the identity matrix of dimensions MxM.

The step from X to U is obtained by means of a matrix of transformation A (of dimensions MxM) so that:

(24) $$U = XA$$

in such a way that, Σ having been specified previously, the following holds:

(25) $$\sum = \frac{1}{T} E(U'U) = \frac{1}{T} E(A'X'XA) = A' \frac{1}{T} E(X'X) A = A'A$$

having taken into account the fact that the elements of A' and A are deterministic and that $\frac{1}{T} E(X'X) = I$

As matrix Σ we utilize in pratice:

(26) $$\hat{\sum} = \frac{1}{T} \hat{U}' \hat{U}$$

(obtained from the estimation stage), $\hat{U}$ being the matrix of the structural residuals of dimensions TxM (1).

On the basis of eq. (25) and having established Σ, the matrix A is computed once for all at the beginning of the process of stochastic simulation. In practice, however, it must be born in mind that Σ is symmetrical, so that A is not univocally determinable, unless additional hypotheses are made (2); in the course of this work, we assumed A to be lower-triangular, as suggested in [27].

---

(1) From now on, no distinction will be made between Σ and $\hat{\Sigma}$, and the notation Σ will be used.

(2) The distinct elements of Σ are $\frac{M.(M+1)}{2}$, those of A are in general M^2.

The elements of A are determined by Σ making the corresponding elements of $A'A$ and Σ equal, starting from the element on the last line and on the last column and then working back to the first line (1), (2).

The present algorithm may be correctly utilized only if $T > M$. In fact, to avoid the generation of complex pseudo-structural errors U, the elements of the matrix A (in particular diagonal elements a_{ii}) must be real and this is guaranteed only if the matrix Σ is positive definite [27] .

The matrix $\Sigma = \frac{1}{T} \hat{U}' \hat{U}$ obtained from the structural residuals, if the number of observations T is less than the number of structural equations M , is, however, singular and hence is certainly not positive definite.

---

(1) The formulas for the calculation of the elements of A are the following [27] .

a) diagonal elements

$$(27) \qquad a_{ii} = \sqrt{\sigma_{ii} - \sum_{\mu=i+1}^{M} a_{\mu i}^2} \qquad i = 1, \ldots, M-1$$

$$(28) \qquad a_{MM} = \sqrt{\sigma_{MM}}$$

b) non diagonal elements of A

$$(29) \quad i < j \qquad a_{ij} = 0 \qquad \text{by definition}$$

$$(30) \quad i > j \qquad a_{ij} = \left(\sigma_{ij} - \sum_{\mu=i+1}^{M} a_{\mu i} \; a_{\mu j} \right) / \; a_{ii} \qquad i = 1, \ldots, M-1$$

$$(31) \qquad a_{Mj} = \frac{\sigma_{Mj}}{a_{MM}} \qquad j = 1, \ldots, M-1$$

(2) This procedure is in all respects equivalent to the one described in Naylor [28] , [29] for the generation of a normal multivariate distribution. The only difference, which determines the diversity of the relative formulas (see [29, p. 98]) lies in the fact that the transformation matrix A is in Naylor used to pre-multiply the X.

In the model used as a sample [31] , with $M=5$ and $T=20$, Nagar's algorithm can be correctly applied. With regard to the practical implementation of the algorithm, since in our case we proceed by carrying out all the replications for a year before going on to the next year, the U matrix was "generated and utilized" from the standpoint of the rows; each row of the matrix represents, for each period, the pseudo-structural errors to be added to the M equations of the model. In fact, as we are hypothesizing serial independence for U_{it}, row dimension is non-essential. Furthermore, the utilized algorithm ensures that the normal pseudo-random numbers generated are independent one from the other. Hence, once a specific year has been established, a row vector u_i of length M is generated at each replication, utilizing not the whole matrix but only one of its row vectors X_i of length M. When there are no remaining replications for that given year, we move on to the subsequent year, which is equivalent to generating, for each replication, a new row vector of X and then of U, and so on.

5.2 McCarthy's algorithm

In recent years, most stochastic simulation applications of econometric models, [8], [10], [12], [14], [33], have been based on another algorithm (McCarthy's) which is not subject to the limit ($T > M$) of Nagar's algorithm, which is simpler computation wise and which exploits the structural residuals directly.

In this case too, let us take an X matrix of independent random numbers normally distributed with a zero mean and a unitary variance of dimensions qxT (where q is the number of periods (years) for which we wish to obtain the U matrix of pseudo-structural errors and T is the dimension of the sample) and an $\hat{U}$ matrix, of dimensions TxM (M being the number of structural equations in the model), of structural residuals of the sample period.

The pseudo-structural disturbances to be added to the model are given, for each period and for each replication, by a row of the matrix, of dimensions qxM:

$$U = \frac{1}{\sqrt{T}} X \hat{U} \tag{32}$$

It can be shown [26] that for models estimated by consistent methods, the covariance matrix of U will be asymptotically equal to the true covariance matrix of the system.

From the standpoint of practical implementation, a row vector u_j of length M is also generated in this case at each replication; the difference as compared with Nager is that the row vector of X which is utilized each time is of length T.

As mentioned earlier, the limit of applicability of Nagar's technique does not exist for this algorithm but, naturally, the statistical properties of the pseudo-structural errors generated depend on the number of observations available for the estimation of the model.

The feature common to both algorithms is that both are based on appropriate changes in the residuals of the sample period which are obtained from the estimated model. As mentioned, in McCarthy's algorithm these residuals are utilized directly and constitute the weights for a combination of normal independent random variables.

In Nagar's algorithm, on the other hand, the residuals are utilized indirectly, that is to say they go to make up the Σ matrix, which in turn is used to determine the A matrix and then, finally, the U matrix.

5.3 Descriptive statistics and tests on the generation of the multivariate normal distribution: a Monte Carlo study

As stated previously, for both Nagar's and McCarthy's algorithms the pseudo-structural errors are obtained via a linear transformation of normal independent random numbers produced by a generator.

Hence, the pseudo-structural errors should have the properties hypothesized in [26], [27] which should not have to undergo statistical tests.

However, considering the complexity of the transformation algorithms, it cannot be ruled out a-priori that an error in the generator which proved acceptable from the tests undergone by the generator may be amplified to the extent of invalidating the properties of the pseudo-structural errors.

We used as sample the variance-covariance matrix of the structural form of the model presented in [31] , estimated with the method of ordinary least squares.

5.3.1 Mean

An initial analysis consisted in computing the mean of u (where u indicates the vector $1xM$ generated for each replication and for each period) over the subsequent replications, for the purpose of verifying empirically the property $E(u^*) = 0$, where 0 is a vector of zeroes measuring $1xM$. Table 6 shows some results relating to the two described algorithms, in correspondence with number of replications (1) equal to 1000, 5000, 10000, 50000 and 100000.

The results relating to the two algorithms were obtained by starting from the same initial value in the generation of random numbers. Given the difference in the methods, the random numbers used overall are not however the same, since, starting from the same value, the McCarthy method utilizes T extractions of random numbers at each replication instead of M extractions as in Nagar's method.

Regarding the utilized numbers, in the test with 5 000 replications we use the 1000 numbers relating to the previous test, in the one with 10 000 replications we use the 5000 previous numbers, and so on.

---

(1) By replication is meant an individual experiment of stochastic simulation made by attributing to each structural equation of the model a random disturbance belonging to a multivariate distribution assigned a priori.

Tab. 6

Value of $\bar{u}^*$ on the variation of the number of replications.

McCarthy

	NREP = 1000	NREP = 5000	NREP = 10000	NREP = 50000	NREP = 100000
$\bar{u}_1^*$	6.110	2.938	2.766	−.374	−.633
$\bar{u}_2^*$	6.594	1.514	1.016	−.160	−.019
$\bar{u}_3^*$	5.861	6.874	−2.268	−.816	−.119
$\bar{u}_4^*$	6.238	3.542	2.019	0.346	0.213
$\bar{u}_5^*$	0.032	−.031	−.019	0.0071	0.011

Nagar

	NREP = 1000	NREP = 5000	NREP = 10000	NREP = 50000	NREP = 100000
$\bar{u}_1^*$	8.014	−.481	−3.1440	0.217	−.768
$\bar{u}_2^*$	1.963	0.213	0.2110	0.407	−.171
$\bar{u}_3^*$	−2.070	1.016	−.0571	−1.122	−.062
$\bar{u}_4^*$	5.052	−.225	−.8510	−.136	−.164
$\bar{u}_5^*$	−0.132	−.033	−.0004	−.005	.002

On an initial examination, a certain convergence of the individual elements of the vector $\bar{u}^*$ towards 0 can be noted even though it is not reached numerically with even 100 000 replications. The hypothesis $E(\bar{u}^*)=0$ can however be subjected to Z test, by fixing a 95% confidence interval for the hypothesis. The hypothesis is not rejected if the computed value $\bar{u}_i^*$ falls in the interval

$$\pm\ 1.96\ \sqrt{\frac{\sigma_{ii}}{NREP}}$$

where σ_{ii} is the value of the theoretical variance relating to the *i-th* equation, that is to say:

$\sigma_{11} = 247.451$
$\sigma_{22} = 101.727$
$\sigma_{33} = 167.008$
$\sigma_{44} = 138.223$
$\sigma_{55} = 1.804$

The values of: $1.96\ \sqrt{\frac{\sigma_{ii}}{NREP}}$

are given in the following table:

NREP = 1000	NREP = 5000	NREP = 10000	NREP = 50000	NREP = 100000
15.3372	6.85898	4.85003	2.16900	1.53372
6.3051	2.81973	1.99835	0.89167	0.63051
10.3515	4.62923	3.27336	1.46380	1.03513
8.5671	3.83134	2.70017	1.21158	0.85617
0.1119	0.04999	0.03535	0.01581	0.01118

Comparing tables 6 and 7, it can be seen that the hypothesis is refused only 3 times, namely twice in McCarthy in correspondence with $\bar{u}_2^*$ (1000 replications) and with $\bar{u}_3^*$ (5000 replications), and once in Nagar in correspondence with $\bar{u}_5^*$ (1000 replications).

Tab. 8

Values of Σ and Σ^* on the variation of the number of replications (McCarthy).

	Σ	Σ^* (NREP = 1000)	Σ^* (NREP = 5000)	Σ^* (NREP = 10000)	Σ^* (NREP = 50000)	Σ^* (NREP = 100000)
(1,1)	61231.87	64750.97	60822.27	61504.77	61415.43	61189.60
(1,2)	115.94	721.56	607.37	130.59	419.69	199.30
(1,3)	−9370.23	−8375.02	−9335.52	−9584.55	−9273.34	−9156.83
(1,4)	16777.79	17523.72	15966.35	16808.95	16896.83	16896.34
(1,5)	−129.51	−139.02	−126.77	−124.60	−131.81	−129.05
(2,1)	115.94	721.56	607.37	130.59	419.69	199.30
(2,2)	10348.36	10735.74	10592.01	10323.94	10314.41	10347.07
(2,3)	388.71	180.95	275.93	299.34	464.13	375.71
(2,4)	−2370.93	−1959.77	−2296.93	−2374.25	−2300.87	−2347.48
(2,5)	−82.50	−83.90	−83.24	−80.75	−81.72	−82.27
(3,1)	−9370.23	−8375.02	−9335.52	−9584.55	−9273.34	−9156.83
(3,2)	300.71	180.95	275.93	299.34	464.13	375.71
(3,3)	27891.74	25651.58	27805.52	27721.06	27825.73	27747.06
(3,4)	−3594.15	−3008.98	−3702.35	−3769.39	−3646.64	−3658.75
(3,5)	141.27	132.36	144.31	143.80	140.65	140.60
(4,1)	16777.79	17523.73	15966.35	16808.95	16896.83	16896.34
(4,2)	−2370.93	−1959.77	−2296.93	−2374.25	−2300.87	−2347.48
(4,3)	−3594.15	−3008.98	−3702.35	−3769.39	−3646.64	−3658.75
(4,4)	19105.53	19628.72	18469.12	19043.21	19206.00	19190.92
(4,5)	10.24	4.32	7.91	8.08	9.26	9.46
(5,1)	−129.51	−139.02	−126.77	−124.60	−131.81	−129.05
(5,2)	−82.50	−83.90	−83.24	−80.75	−81.72	−82.27
(5,3)	141.27	132.36	144.31	143.80	140.65	140.60
(5,4)	10.24	4.32	7.91	8.08	9.26	9.46
(5,5)	3.25	3.30	3.26	3.21	3.25	3.25

Tab. 9

Values of Σ and Σ^* on the variation of the number of replications (Nagar).

	Σ	Σ^* (NREP = 1000)	Σ^* (NREP = 5000)	Σ^* (NREP = 10000)	Σ^* (NREP = 50000)	Σ^* (NREP = 100000)
(1,1)	61231.87	59294.39	60275.21	61396.77	61223.46	61505.58
(1,2)	115.94	−1257.58	−430.46	−172.13	58.25	178.39
(1,3)	−9370.23	−9674.38	−9400.28	−9157.08	−9201.24	−9309.74
(1,4)	16777.79	15211.04	16507.12	17072.89	16829.73	16856.87
(1,5)	−129.51	−124.81	−117.69	−121.11	−127.50	−128.29
(2,1)	115.94	−1257.58	−430.46	−172.13	58.25	178.39
(2,2)	10348.36	11292.49	10609.46	10440.12	10297.76	10306.23
(2,3)	388.71	322.97	382.84	310.54	274.13	298.70
(2,4)	−2370.93	−3553.77	−2623.30	−2494.99	−2365.68	−2345.17
(2,5)	−82.50	−86.79	−82.78	−82.89	−81.49	−82.52
(3,1)	−9370.23	−9674.38	−9400.28	−9157.08	−9201.24	−9309.74
(3,2)	388.71	322.97	382.84	310.54	273.13	298.70
(3,3)	27891.74	27277.49	28235.19	27960.10	28005.10	27988.57
(3,4)	−3594.15	−3132.73	−3631.83	−3706.44	−3600.87	−3614.10
(3,5)	141.27	145.74	142.88	142.25	142.48	141.61
(4,1)	16777.79	15211.04	16507.12	17072.89	16829.73	16856.87
(4,2)	−2370.93	−3553.77	−2623.30	−2494.99	−2365.68	−2345.17
(4,3)	−3594.15	−3132.73	−3631.83	−3706.44	−3600.87	−3614.10
(4,4)	19105.53	18387.54	18740.23	18977.61	190911.62	19042.69
(4,5)	10.24	18.47	10.11	8.12	9.04	9.34
(5,1)	−129.51	−124.81	−117.69	−121.11	−127.50	−128.29
(5,2)	−82.50	−86.79	−82.78	−82.89	−81.49	−82.52
(5,3)	141.27	145.74	142.88	142.25	142.48	141.61
(5,4)	10.24	18.47	10.11	8.12	9.04	9.34
(5,5)	3.25	3.41	3.25	3.23	3.22	3.24

The case $\bar{u}_5^*$ (10000 replications) of McCarthy is exactly at the limit, if we consider the inevitable rounding off errors.

The results therefore well concord with the confidence level of the test (95%), given that they refer to 50 events (25 for Nagar and 25 for McCarthy).

5.3.2 Variance-covariance matrix

If we collect the vectors $\bar{u}^*$, we can compute a variance-covariance matrix Σ^*

In the described hypotheses we have:

(33) $$E(\Sigma^*) = \frac{1}{T}\hat{U}'\hat{U} = \Sigma$$

A qualitative check of this property can be made by means of tables 8 and 9 (for McCarthy's and Nagar's methods respectively). In these, 6 columns are compared, representing the Σ and Σ^* relating to 1000, 5000, 10000, 50000 and 100000 replications respectively.

An element of the various matrixes is given on each line, starting from the element σ_{11}, σ_{12}, up to σ_{55}.

The symmetrical elements are computed twice to ensure that the results are numerically correct, and both are shown for completeness reasons.

A more exact idea of the validity of the results could be obtained only by performing an appropriate test. However, as this is a test on variance, as always happens when there are large numbers of samples, it does not prove very significant, given the low selectivity of χ^2 with many degrees of freedom. We will therefore confine ourselves to noting the clear concordance of the simulated values with the theoretical ones.

A more exact test, which can be carried out simultaneously on the variances and covariances (more precisely, on the simulated correlation coefficients, the theoretical correlation coefficients being known) is the one described in [2], based on "Fisher's *Z*".

It can be seen that even for a fairly small number of replications, the

$$\Sigma^* \simeq \Sigma$$

is satisfactorily verified, as numerical values, element by element, and in particular for the diagonal elements (variances), whereas there is some sign discordance for the covariances in Nagar's method.

In particular, for the covariance between equations 1 and 2 (elements σ_{12} and σ_{21}) the sign is reproduced correctly only if we start from 50000 replications. Even in this event, however, the asymptotic properties show up, given that compared with $\sigma_{12} = 115.94$, σ^*_{12} goes from -1257.6 to -430.4, to -172.1, to 58.25 and finally to 178.39.

In addition to this σ^*_{12}, in correspondence with McCarthy's algorithm is also rather unstable as the number of replications varies.

This instability is attributable to the fact that the theoretical variances of equations 1 and 2 are very high, whereas the covariance between them is very low: hence, if we take into account the structure of the covariance, it is not unreasonable in the case of small samples to expect the sign of the simulated covariance to be different from the theoretical one.

5.4 Conclusions

The results exprimentally obtained confirm that:

- in spite of the complexity of the transformation algorithms, there seems not to be an amplification of the errors;
- as far as the mean and the variance of the generated pseudo-structural errors are concerned, there seems not to be a clear cut prevalence of one algorithm on the other;
- in spite of the narrower applicability, the Nagar algorithm is faster than the McCarthy's, expecially when the number of behavioural equations is much less that the sample period length.

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