GHK in General

The GHK simulator in general is appropriate for the following class of problems:

$$\mathbf{x} \sim N(\mu, \Sigma)$$

$$P\left[\mathbf{x} \in D\right] = P\left[x_k \in (a_k, b_k), \quad k = 1, \ldots, K\right]$$

$$P = \int_{a_1}^{b_1} \cdots \int_{a_K}^{b_K} f(x_1, \ldots, x_K) dx_1 \ldots dx_K$$

Re-express the joint probability:

$$\begin{aligned} P\left[\mathbf{x} \in D\right] &= P\left[x_k \in (a_k, b_k), \quad k = 1, \ldots, K\right] \\ &= P\left[x_1 \in (a_1, b_1)\right] \times P\left[x_k \in (a_k, b_k), \forall k = 2, \ldots, K \mid x_1 \in (a_1, b_1)\right] \\ &= P\left[x_1 \in (a_1, b_1)\right] \times P\left[x_2 \in (a_2, b_2) \mid x_1 \in (a_1, b_1)\right] \times P\left[x_3 \in (a_3, b_3) \mid x_k \in (a_k, b_k), k = 1, 2\right] \times \\ &\cdots \times P\left[x_K \in (a_K, b_K) \mid x_k \in (a_k, b_k), k = 1, \ldots, K-1\right] \\ &= \prod_{k=1}^{K} P\left[x_k \in (a_k, b_k) \mid x_j \in (a_j, b_j) \; \forall j < k\right] \end{aligned}$$

Note that each entry in the product is a univariate, truncated conditional normal probability of the form:

$$P_{k|<k} = P\left[x_k \in (a_k, b_k) \mid x_j \in (a_j, b_j) \; \forall j < k\right]$$

Distribution expressions:

$$x_k \mid x_1, \ldots, x_{k-1} = x_k \mid x_{<k} \sim N(\mu_{k|<k}, \Sigma_{k|<k})$$

$$\mu_{k|<k} = \mu_k + \Sigma_{k,<k} \Sigma^{-1}_{<k,<k} \left(x_{<k} - \mu_{<k}\right)$$

$$\Sigma_{k|<k} = \Sigma_{kk} - \Sigma_{k,<k} \Sigma^{-1}_{<k,<k} \Sigma_{<k,k}$$

Recall that a draw from a univariate truncated normal distribution with mean μ and standard deviation σ can be taken via the inversion method:

$$\varepsilon = F^{-1}(\bar{u}), \quad \bar{u} = (1-u)F(a) + uF(b), \quad u \sim UNIF(0,1)$$

where

$$F(a) = \Phi\left[\frac{a-\mu}{\sigma}\right], \quad F(b) = \Phi\left[\frac{b-\mu}{\sigma}\right]$$

STEPS IN THE SIMULATOR

1) Set k=1 and compute

$$p_1^r = p_1 = P\left[x_1 \in (a_1, b_1)\right] = \Phi\left[\frac{b_1 - \mu_1}{\Sigma_{11}}\right] - \left[\frac{a_1 - \mu_1}{\Sigma_{11}}\right]$$

2) Draw x_1^r from the truncated normal distribution with mean mean μ_1 and variance Σ_{11}

3) Increment k by 1 and compute

$$p_{k|<k}^r = P\left[x_k \in (a_k, b_k) \mid x_{<k}^r\right] = \Phi\left[\frac{b_k - \mu_{k|<k}(x_{<k}^r)}{\Sigma_{k|<k}}\right] - \Phi\left[\frac{a_k - \mu_{k|<k}(x_{<k}^r)}{\Sigma_{k|<k}}\right]$$

4) If k<K draw $x_{k|<k}^r$ from the truncated univariate conditional normal distribution with mean $\mu_{k|<k}(x_{<k}^r)$ and variance $\Sigma_{k|<k}$ and return to step 3. Else continue to step 5.

5) Compute

$$p^r = \prod_{k=1}^{K} p_{k|<k}^r$$

6) Repeat steps 1 through 5 for r=1,…,R and compute

$$p_R^{GHK} = \frac{1}{R}\sum_{r=1}^{R} p^r$$

1 GHK simulator: get draws from truncated multivariate normal distribution

You want draws from

$$\begin{pmatrix} x_1 \\ x_2 \\ \vdots \\ x_n \end{pmatrix} \sim TN\left(\vec{\mu}, \Sigma; \vec{a}, \vec{b}\right) \equiv N\left(\vec{\mu}, \Sigma\right) \text{ s.t. } \vec{a} < \vec{x} < \vec{b} \tag{1}$$

where the difficulty is that Σ is not necessarily diagonal (i.e., elements of $\vec{x}$ are correlated).

Let $(u_1, \ldots, u_n)'$ denote an n-vector of independent multivariate standard normal random variables. Let $\Sigma^{1/2}$ denote the (lower-triangular) Cholesky factorization of Σ, with elements

$$\begin{bmatrix} s_{11} & 0 & \cdots & 0 & 0 \\ s_{21} & s_{22} & \cdots & 0 & 0 \\ \vdots & \vdots & s_{ii} & 0 & 0 \\ s_{n1} & s_{n2} & \cdots & s_{nn-1} & s_{nn} \end{bmatrix}.$$

Then we can rewrite (1) as:

$$\vec{x} = \vec{\mu} + \Sigma^{1/2}\vec{u} \sim N\left(\vec{\mu}, \Sigma\right) \ s.t.$$

$$\begin{pmatrix} \frac{a_1-\mu_1}{s_{11}} \\ \frac{a_2-\mu_2-s_{21}u_1}{s_{22}} \\ \vdots \\ \frac{a_n-\mu_n-\sum_{i-1}^{n-1} s_{ni}u_i}{s_{nn}} \end{pmatrix} < \begin{pmatrix} u_1 \\ u_2 \\ \vdots \\ u_n \end{pmatrix} < \begin{pmatrix} \frac{b_1-\mu_1}{s_{11}} \\ \frac{b_2-\mu_2-s_{21}u_1}{s_{22}} \\ \vdots \\ \frac{b_n-\mu_n-\sum_{i-1}^{n-1} s_{ni}u_i}{s_{nn}} \end{pmatrix} \tag{2}$$

The above suggests that the answer is to draw $(u_1, \ldots, u_n)$ **recursively**. First draw u_1^s from $N\left(0, 1; \frac{a_1-\mu_1}{s_{11}}, \frac{b_1-\mu_1}{s_{11}}\right)$, then u_2^s from $N\left(0, 1; \frac{a_2-\mu_2-s_{21}u_1^s}{s_{22}}, \frac{b_2-\mu_2-s_{21}u_1^s}{s_{22}}\right)$, and so on.

Finally we can transform $(u_1^s, \ldots, u_n^s)$ to the desired $(x_1^s, \ldots, x_n^s)$ via the transformation

$$\vec{x}^s = \vec{\mu} + \Sigma^{1/2}\vec{u}^s.$$

Remark 1: It is easy to draw an n-dimensional vector $\vec{u}$ of independent truncated standard normal random variables with rectangular truncation conditions: $\vec{c} < \vec{u} < \vec{d}$. You draw a vector of independent uniform variables $\vec{\tilde{u}} \sim \mathcal{U}[\Phi(\vec{c}), \Phi(\vec{d})]$[1] and then transform $u_i = \Phi^{-1}(\tilde{u}_i)$.

Remark 2: Principle of importance sampling:

$$\int_{\mathcal{F}} sf(s)ds = \int_{\mathcal{G}} s\frac{f(s)}{g(s)}g(s)ds.$$

That is, sampling s from $f(s)$ distribution equivalent to sampling $s * w(s)$ from $g(s)$ distribution,. with importance sampling weight $w(s) \equiv \frac{f(s)}{g(s)}$. ($f$ and g should have the same support.)

The GHK simulator is an importance sampler. The importance sampling density is the multivariate normal density $N(\vec{\mu}, \Sigma)$ truncated to the region characterized in Eqs. (2). This is a recursively characterized truncation trgion, in that the range of, say, x_3 depends on the draw of x_1 and x_2. This is different than the multivariate normal density $N(\vec{\mu}, \Sigma)$ truncated to the region $(\vec{a} \leq \vec{x} \leq \vec{b})$.[2]

For the GHK simulator, the importance sampling weight attached to each draw $\vec{x}^s$ is given by:

$$w(\vec{x}^s) \equiv \left[\Phi\left(\frac{b_1 - \mu_1}{s_{11}}\right) - \Phi\left(\frac{a_1 - \mu_1}{s_{11}}\right)\right] \prod_{i=2}^{m} \left[\Phi\left(\frac{b_i - \mu_i - \sum_{j=1}^{i-1} s_{ij}u_j^s}{s_{ii}}\right) - \Phi\left(\frac{a_i - \mu_i - \sum_{j=}^{i-}\right.\right.$$

Hence, the GHK simulator for $\int_{\vec{a}\leq\vec{x}\leq\vec{b}} \vec{x}f(\vec{x})d\vec{x}$, where $f(\vec{x})$ denote the $N(\vec{\mu}, \Sigma)$ density, is $\frac{1}{S}\sum_{s=1}^{S} \vec{x}^s w(x^s)$.

Remark 3: w^s (even just for one draw: cf. (Gourieroux and Monfort 1996, pg. 99)) is an unbiased estimator of the truncation probability Prob $\left(\vec{a} < \vec{x} < \vec{b}\right)$. But in general, we can get a more precise estimate by averaging over w^s:

$$T_{\vec{a},\vec{b}} \equiv \text{Prob}\left(\vec{a} < \vec{x} < \vec{b}\right) \approx \frac{1}{S}\sum_{s} w^s$$

for (say) S simulation draws.

[1] Just draw $\hat{u}$ from $\mathcal{U}[0, 1]$ and transform $\tilde{u} = \Phi(c) + (\Phi(d) - \Phi(c))\hat{u}$.

[2] See (Hajivassiliou and Ruud 1994), pg. 2005.

2 Monte Carlo Integration using the GHK Simulator

Clearly, if we can get draws from truncated multivariate distributions using the GHK simulator, we can use these draws to calculate integrals of functions of $\vec{x}$. There are two important cases here, which it is crucial not to confuse.

2.1 Integrating over untruncated distribution $\mathbf{F}(\vec{\mathbf{x}})$, but $\vec{\mathbf{a}} < \vec{\mathbf{x}} < \vec{\mathbf{b}}$ defines region of integration

If we want to calculate

$$\int_{\vec{a}<\vec{x}<\vec{b}} g(\vec{x}) f(\vec{x}) d\vec{x}$$

where f denotes the $N(\vec{\mu}, \Sigma)$ density, we can use the GHK draws to derive a Monte-Carlo estimate:

$$E_{\vec{a}<\vec{x}<\vec{b}} g(\vec{x}) \approx \frac{1}{S} \sum_s g(\vec{x}^s) * w^s.$$

The most widely-cited example of this is the likelihood function for the multinomial probit model (cf. (McFadden 1989)):

Multinomial probit with K choices, and utility from choice k $U_k = X\beta_k + \epsilon_k$. Probability that choice k is chosen is probability that $\nu_i \equiv \epsilon_i - \epsilon_k < X\beta_i - X\beta_k$, for all $i \neq k$. For each parameter vector β, use GHK to draw S (K-1)-dimensional vectors $\vec{\nu}^s$ subject to $\vec{\nu} < (\vec{x\beta})$. Likelihood function is

$$\begin{aligned} \text{Prob}(k) &= \int_{\vec{\nu}} \mathbf{1}\left(\vec{\nu} < (\vec{x\beta})\right) f(\vec{\nu}) d\vec{\nu} \\ &= \int_{\vec{\nu}<(\vec{x\beta})} f(\vec{\nu}) d\vec{\nu} \\ &\approx \frac{1}{S} \sum_s w^s. \end{aligned}$$

2.2 Integrating over truncated (conditional) distribution $\mathbf{F}(\vec{\mathbf{x}}|\vec{\mathbf{a}} < \vec{\mathbf{x}} < \vec{\mathbf{b}})$.

The most common case of this is calculating conditional expectations (note that the multinomial probit choice probability is *not* a conditional probability!)[3].

[3]This is a crucial point. The conditional probability of choice k conditional on choice k is trivially 1!

If we want to calculate

$$E_{\vec{a}<\vec{x}<\vec{b}}g(\vec{x}) = \int_{\vec{a}<\vec{x}<\vec{b}} g(\vec{x})f(\vec{x}|\vec{a}<\vec{x}<\vec{b})d\vec{x} = \frac{\int_{\vec{a}<\vec{x}<\vec{b}} g(\vec{x})f(\vec{x})d\vec{x}}{Prob(\vec{a}<\vec{x}<\vec{b})}.$$

As before, we can use the GHK draws to derive a Monte-Carlo estimate:

$$E_{\vec{a}<\vec{x}<\vec{b}}g(\vec{x}) \approx \frac{1}{T_{\vec{a},\vec{b}}}\frac{1}{S}\sum_s g(\vec{x}^s) * w^s.$$

The crucial difference between this case and the previous one is that we integrate over a conditional distribution by essentially integrating over the unconditional distribution over the restricted support, but then we need to divide through by the probability of the conditioning event (i.e., the truncation probability).

An example of this comes from structural common-value auction models, where:

$$v(x,x) \equiv \mathcal{E}\left(v|x_1 = x, \min_{j\neq 1} x_j = x\right) =$$

$$\underbrace{\int\cdots\int}_{x_k\geq x,\ \forall k=3,\ldots,n} \mathcal{E}\left(v|x_1,\ldots,x_n\right)\ dF\left(x_3,\ldots,x_n|x_1=x,x_2=x,x_k\geq x,k=3,\ldots,n;\theta\right) =$$

$$\frac{1}{T_x}\underbrace{\int\cdots\int}_{x_k\geq x,\ \forall k=3,\ldots,n} \mathcal{E}\left(v|x_1,\ldots,x_n\right)\ dF\left(x_3,\ldots,x_n|x_1=x,x_2=x;\theta\right) \tag{3}$$

where F here denotes the conditional distribution of the signals $x_3,\ldots,x_n$, conditional on $x_1 = x_2 = x$, and T_x denotes the probability that $(x_k \geq x, k = 3,\ldots,n|x_1 = x, x_2 = x;\theta)$.

If we assume that $\vec{x} \equiv (x_1,\ldots,x_n)'$ are jointly log-normal, it turns out we can use the GHK simulator to get draws of $\tilde{x} \equiv \log\vec{x}$ from a multivariate normal distribution subject to the truncation conditions $\tilde{x}_1 = \tilde{x}, \tilde{x}_2 = \tilde{x}, \tilde{x}_j \geq \tilde{x}, \forall j = 3,\ldots,n$. Let $\mathcal{A}(x)$ denote the truncation region, for each given x.

Then we approximate:

$$v(x,x) \approx \frac{1}{T_{\mathcal{A}(x)}}\frac{1}{S}\sum_s \mathcal{E}\left(v|\tilde{x}^s\right) * w^s$$

where $T_{\mathcal{A}(x)}$ is approximated by $\frac{1}{S}\sum_s w^s$.

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A MATLAB® Implementation of a Halton Sequence-Based GHK Simulator for Multinomial Probit Models*

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April 2005

*I would like to thank Kurt Schmidheiny for acknowledging my request for his MATLAB® Econometrics Toolbox and Kenneth Train for his online course in UC Berkeley. Nonetheless, all errors are mine.

1 Introduction

The popularity of logit-based models is due to the availability of closed-form expressions for their choice probabilities. Unfortunately, Logit-based models have important limitations particularly the inability to handle random taste variation, general forms of substitution patterns, and repeated choice situations with serially correlated errors (Train, 2003). To remedy these deficiencies, the Multinomial Probit (MNP) model is often used. However closed-form choice probabilities for MNP are not readily available. Numerical integration methods can be utilized to solve these integrals. However, most numerical integration methods are only feasible and practical to use when the dimension of integration is small enough (< 5) because of limitations in computing power. Therefore simulation methods can be employed to address this computational limitation. This is the prime motivation for studying simulation-based methods applied to MNP and other Discrete Choice models with analytically intractable choice probabilities.

In using simulation to estimate the choice probabilities of a high-dimensional MNP model, the first step is to find an appropriate algorithm to use that would provide an estimate with minimal variance relative to the true value of the integral. In general, when estimating an integral, variance reduction techniques such as Antithetic Monte Carlo and Importance Sampling are used to introduce some negative correlation or other "nice" properties among the pseudo-random draws for the simulation. Crude or Non-weighted Monte Carlo techniques that rely solely on pseudo-random generators often perform poorly due to their low equidistribution property (Sandor and Andras, 2004) and high discrepancy (Brandimarte, 2002). With this in mind, different simulators have been used in the MNP context. Among these different methods, the GHK (Geweke, 1989, 1991; Hajivassiliou and McFadden, 1998; Keane, 1990, 1994) simulator is the most widely utilized (Train, 2003) and has been studied and observed to perform better than other simulators (Geweke *et al*., 1994; Borch-Supan and Hajivassiliou, 1993; Hajivassilious *et al*., 1996).

Aside from Monte Carlo based variance reduction techniques, Quasi-Monte Carlo methods can be employed to improve estimation. The main idea behind this is that since the generation of pseudo-random numbers is actually deterministic, the researcher can manipulate and devise alternative deterministic sequences of numbers that display better equidistirbution and low discrepancy properties. Sandor and Train (2002) observe that (*t, m, s*)-nets and Halton draws perform better than independent draws in an application to maximum simulated likelihood estimation of a mixed logit model. More recently, Sandor and Andras (2004) show that quasi-Monte Carlo samples and samples based on orthogonal arrays have better performance in general, compared to Crude Monte Carlo and Antithetic Monte Carlo samples when used with GHK simulators[1]

[1] However, the authors do not examine the "quality" of these GHK simulators by applying it in a MNP model and examining whether estimates using GHK simulators with different samples differ significantly. Thus this paper focuses on the *practicality* of using simulators based on a particular Quasi-Monte Carlo method.

This paper provides a simple and practical incorporation of a quasi-Monte Carlo sample into Kurt Schmidheiny's MNP routine in MATLAB® (based on the toolbox used in Schmidheiny [2003]).[2] The quasi-Monte Carlo sample used is the Halton sequence which is the simplest. Specifically, a randomized Halton sequence is incorporated in the GHK simulator of the toolbox. Though more sophisticated and effective randomization techniques for Halton sequences are available (Tuffin, 1996; Wang and Hickernell, 2000), a simple randomization procedure suggested by Train (2003) is used. Lastly, comparisons between a pseudo-random generator based GHK simulator and a randomized Halton sequence-based GHK simulator is carried out using the travel choice data studied in Greene (2003) and Greene and Hensher (1997). Both GHK simulators provide similar estimates even with only few simulation runs. This shows that firstly, the GHK simulator itself performs well enough even with few simulation runs (given that the number of observations is sufficiently large), and secondly, only marginal improvements, if any, can be achieved with a (crude) randomized Halton sequence-based GHK simulator that tend to expend more estimation time.

The next section provides a brief background on how the GHK simulator is constructed in general settings. In Section 3, a non-technical discussion of Halton sequences is given. Section 4 briefly discusses the data used followed by the main results of our experiment. The last section concludes.

2 GHK Simulator

The GHK Simulator is based on Importance Sampling with a recursively truncated multivariate normal as its Importance pdf. The basic idea is to directly approximate a rectangular probability (Gourieroux and Monfort, 1996). As mentioned, the GHK simulator is the most popular simulator for MNP (Train, 2003) and has been observed to perform better than other simulators (Geweke *et al*., 1994; Borch-Supan and Hajivassiliou, 1993; Hajivassilious *et al*., 1996).

Consider a general model with J alternatives. The utility of person n from choosing alternative j is given by

$$U_{nj} = V_{nj} + \varepsilon_{nj} \qquad (1)$$

for $j = 1,\ldots, J$. After applying the normalization (for identification) method suggested by Train (2003) and expressing (1) as differences against alternative i, we have the following:

[2] The main issue is the estimation of choice probabilities using simulation. Issues regarding the full estimation of the MNP model using simulation (whether and how to implement Maximum Simulated Likelihood Estimation or Method of Simulated Moments) are not dealt with in this short paper.

$$\tilde{U}_{nji} = \tilde{V}_{nji} + \tilde{\varepsilon}_{nji} \quad (1')$$

where $\tilde{\varepsilon}_{ni} = (\tilde{\varepsilon}_{n1i},...,\tilde{\varepsilon}_{nJi})' \sim N(0, \tilde{\Omega}_i)$ and is *(J-1) x 1*. The probability that person *n* chooses alternative *i* will then be given as

$$P_{ni} = \Pr(\tilde{V}_{nji} + \tilde{\varepsilon}_{nji} < 0 \ \forall \ j \neq i) \quad (2).$$

Note that via Choleski decomposition, $\tilde{\Omega}_i = L_i L_i'$ where[3]

$$L_i = \begin{pmatrix} c_{11} & 0 & \cdots & 0 \\ c_{21} & c_{22} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ c_{J1} & c_{J2} & \cdots & c_{JJ} \end{pmatrix}$$

and consequently (1') can be reinterpreted as

$$\tilde{U}_{ni} = \tilde{V}_{ni} + L_i \eta_n \quad (1'')$$

where $\tilde{U}_{ni} = (\tilde{U}_{n1i},...,\tilde{U}_{nJi})'$, $\tilde{V}_{ni} = (\tilde{V}_{n1i},...,\tilde{V}_{nJi})'$ and $\eta_n = (\eta_{n1},...,\eta_{nJ})'$. Note also that $\eta_{nj} \sim N(0,1)$. The above transformation allows us to proceed with simulations using independent draws.

Using Bayes' Rule recursively, the choice probability for alternative *i* can then be rewritten conveniently as

$$\begin{aligned} P_{ni} = & \Pr(\eta_1 < \frac{-\tilde{V}_{n1i}}{c_{11}}) \\ & \times \Pr(\eta_2 < \frac{-(\tilde{V}_{n2i} + c_{21}\eta_1)}{c_{22}} \mid \eta_1 < \frac{-\tilde{V}_{n1i}}{c_{11}}) \\ & \times \Pr(\eta_3 < \frac{-(\tilde{V}_{n3i} + c_{31}\eta_1 + c_{32}\eta_2)}{c_{33}} \mid \eta_2 < \frac{-(\tilde{V}_{n2i} + c_{21}\eta_1)}{c_{22}} \cap \eta_1 < \frac{-\tilde{V}_{n1i}}{c_{11}}) \\ & \times \cdots \end{aligned} \quad (2').$$

The GHK simulator is then calculated as follows (Train, 2003):

1. Calculate $\Pr(\eta_1 < \frac{-\tilde{V}_{n1i}}{c_{11}}) = \Phi(\frac{-\tilde{V}_{n1i}}{c_{11}})$.
2. Draw a value η_1, denoted as η_1^r from a truncated standard normal truncated at $\frac{-\tilde{V}_{n1i}}{c_{11}}$.[4]

[3] L_i is *(J-1) x (J-1)*.

[4] Refer to Train (2003) on how to obtain a draw from a truncated standard normal distribution. It is important to note that in drawing from a truncated standard normal, *U(0,1)* draws are used.

3. Calculate $\Pr(\eta_2 < \frac{-(\tilde{V}_{n2i} + c_{21}\eta_1)}{c_{22}} | \eta_1 = \eta_1^r) = \Phi(\frac{-(\tilde{V}_{n2i} + c_{21}\eta_1^r)}{c_{22}})$.
4. Draw a value η_2, denoted as η_2^r from a truncated standard normal truncated at $\frac{-(\tilde{V}_{n2i} + c_{21}\eta_1^r)}{c_{22}}$.
5. Calculate
$$\Pr(\eta_3 < \frac{-(\tilde{V}_{n3i} + c_{31}\eta_1 + c_{32}\eta_2)}{c_{33}} | \eta_1 = \eta_1^r \cap \eta_2 = \eta_2^r) = \Phi(\frac{-(\tilde{V}_{n3i} + c_{31}\eta_1^r + c_{32}\eta_2^r)}{c_{33}})$$
6. Repeat steps 1-5 for all alternatives except *i*.
7. The simulated probability for the *rth* draw of $\eta_1, \ldots \eta_J$ is given as
$$\breve{P}_{ni}^r = \Phi(\frac{-\tilde{V}_{n1i}}{c_{11}}) \times \Phi(\frac{-(\tilde{V}_{n2i} + c_{21}\eta_1^r)}{c_{22}} \times \Phi(\frac{-(\tilde{V}_{n3i} + c_{31}\eta_{1\,1}^r + c_{32}\eta_2^r)}{c_{33}}) \times \cdots$$
8. Repeat steps 1-7 for *r = 1,…, R* where *R* is the number of replications for the GHK simulator.
9. Finally, the simulated choice probability is $\breve{P}_{ni} = \frac{1}{R}\sum_{r=1}^{R} \breve{P}_{ni}^r$.

This algorithm is implemented in Schmidheiny's MATLAB® toolbox.

3 Halton Sequence

This section provides a non-technical introduction to Halton Sequences. For a more technical treatment, consult the references cited in Sandor and Andras (2004). Consider a one-dimensional Halton sequence in base 2. Divide the unit line into equal partitions corresponding to the base chosen (*i.e.* cut in half). The first element of the sequence is 2^{-1}. Add 2^{-2} to 0 and 0.5 to get the second and third elements of the sequence respectively. Our sequence now is {0.5, 0.25, 0.75}. Add 2^{-3} to zero and each element of the sequence in proper order. Our sequence is now {0.5, 0.25, 0.75, 0.125, 0.625, 0.375, 0.875}. Repeat the process until one has the desired number of elements.

The main rationale for choosing a Halton sequence over a simple pseudo-random generator is that we want our draws to mimic a uniform distribution as much as possible. A possible way to do this is to introduce some negative correlation between successive draws so that each side of the distribution is represented almost equiproportionally. This is the same working idea for using antithetic Monte Carlo techniques. With the Halton sequence, each successive draw jumps from one side of the distribution to the other.

One measure of performance for pseudo-random or deterministic samples that approximate the continuous uniform distribution is Discrepancy. Mathematically, Discrepancy is defined as

$$D(\mathbf{x}^1, ..., \mathbf{x}^n) = \sup_{\mathbf{x} \in I^m} | S_n(G_{\mathbf{X}}) - n x_1 \cdots x_m |$$

where I^m is an m-dimensional hypercube, G_X is a subspace of I^m, and $S_n(G_X)$ is a function that counts the number of sample points contained in each subspace. Lower discrepancy means that our sample points are more dispersed in I^m which is our desired characteristic.

Consider a comparison of the pseudo-random generator of MATLAB® (rand()) and a (randomized) Halton sequence in a two-dimensional space:[5]

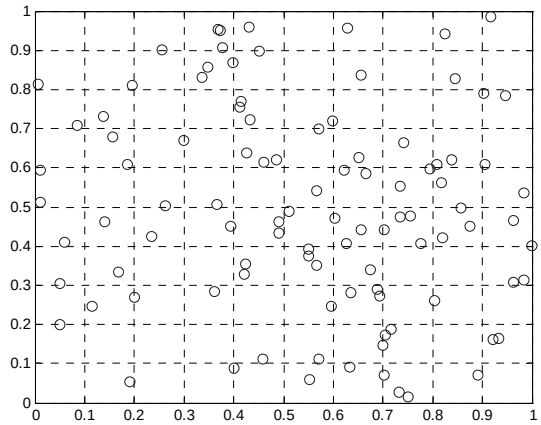

Figure 1a: Pseudo-Random Generator

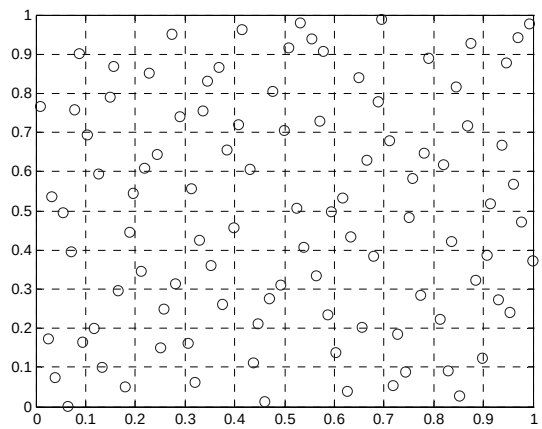

Figure 1b: (Randomized) Halton Sequence

By visual inspection, Figure 1a has higher discrepancy compared to Figure 1b. In other words, the Halton sequence is more dispersed across the region compared to the simple pseudo-random generator and therefore we expect that the former will perform better than the latter in estimation via simulation.

4 Data and Results

Schmidheiny's MATLAB® toolbox contains the data set and applies the MNP routine using the data set as a demo. The data set originally comes from Greene and Hensher (1997) and is closely studied in

[5] The two-dimensional randomized Halton sequence is of base 2 and 3. See the appendix for the MATLAB® code.

Greene (2003). The data set contains 840 observations on 4 travel modes for 210 individuals. The 4 modes consist of `Air`, `Train`, `Bus` or `Car`. The choice attributes in the model are `gc` (generalized cost measure), `ttime` (terminal waiting time), `hinc` (household income), and `hinc2air` (household income interacted with air dummy). Estimation is performed using maximum simulated likelihood. The MSLE results are given below:

Table 1: MSLE Results

	A	B	C	D	E
Constants					
`Air`	0.490338	0.393034	0.237583	0.907016	0.791799
	(0.665986)	(0.609776)	(0.699832)	(0.603322)	(0.688239)
`Train`	1.073865***	0.920257***	0.984482***	1.161474***	1.157948***
	(0.327818)	(0.316232)	(0.358488)	(0.266942)	(0.303521)
`Bus`	0.901261***	0.775379***	0.827658***	0.967196***	0.980992***
	(0.298812)	(0.277521)	(0.320735)	(0.253812)	(0.294183)
Slope Coefficients					
`gc`	-0.008676***	-0.008022***	-0.008299***	-0.009196***	-0.008777***
	(0.001937)	(0.001861)	(0.002240)	(0.001676)	(0.001723)
`ttime`	-0.020413**	-0.017641**	-0.017224**	-0.023799***	-0.023548***
	(0.007984)	(0.007142)	(0.008391)	(0.007210)	(0.007904)
`hinc2air`	0.013081**	0.010907*	0.014265**	0.008765	0.010879*
	(0.006459)	(0.006444)	(0.006303)	(0.005848)	(0.006398)
# of Observations (Individuals)	210	210	210	210	210
Type of draws	**`rand()`**	**`rand()`**	**Halton**	**`rand()`**	**Halton**
# of GHK Replications	1000	10	10	2	2
Substitution Pattern	Unrestricted, Normalized	Unrestricted, Normalized	Unrestricted, Normalized	Unrestricted, Normalized	Unrestricted, Normalized
Computational Time (in minutes)	59.79	4.82	11.31	4.57	6.75

Significance Levels: 1% (***), 5% (**), 10% (*)
Note: Normalization algortihm for unrestricted substitution pattern is based on Train (2003) and is implemented in Schmidheiny's toolbox

Models A, B and D are based on the pseudo-random generator `rand()` and Model A is used as the benchmark model. Models C and E utilize draws from randomized Halton sequences of *k-1 x r* dimension where *k* is the number of alternatives (corresponds to the number of bases used) and *r* is the number of replications (corresponds to the number of elements in each base). With a few minor exceptions, all of the models have similar estimation results which can mean two things. First, the (ordinary) GHK simulator is robust enough to handle extremely small replications and exhibits the same performance as a Halton sequence-based GHK simulator. Second, our experiment is not entirely conclusive from a *theoretical* point of view since there seems to be some divergence in terms of our objective and the measure of performance used in the analysis and comparison of the two samples. Specifically, our objective is to see how well the different samples actually estimate the choice probabilities but the yardstick of performance is based on estimated coefficients for the choice attributes. We are actually looking at how well these samples yield an estimate via MSLE which is affected by the number of observations used in the study and not simply on the number of replications. With a large enough sampled population, the estimate will be rather precise even if the number of replications is small (Train, 2003). Nonetheless from a *practical* point of view, if the researcher has a sufficiently large number of observations and the only issue is the number of replications to be used, then an ordinary GHK simulator performs as well as a Halton-sequence based GHK simulator[6], as mentioned previously.

5 Conclusion

As we have seen in the previous section, a GHK simulator performs as well as a Halton sequence-based GHK simulator, assuming the researcher has enough observations. Though a randomized Halton sequence is easy to incorporate in any programming routine for MNP models (see the Appendix), a considerable amount of computing time is expended during estimation and thus may not be worth it (again, given that we have a sufficiently large number of observations). Nevertheless, other quasi-Monte Carlo samples and samples based on orthogonal arrays can be incorporated. How these samples actually perform in practical applications still remains to be studied.

[6] Given that the number of observations is sufficiently large, using a Halton sequence-based GHK simulator has only marginal improvements with respect to the estimates but takes considerably more time to perform the estimation. Therefore, on these grounds and as explained above, an ordinary GHK simulator would be most likely preferred in practical applications.

Appendix

The randomized Halton sequence generator can be easily incorporated into the GHK simulator by replacing the function that calls `rand()` with a function that gives us a randomized Halton sequence of size *k-1 x r*.[7] The MATLAB® code for generating randomized Halton sequences is as follows:

```
function r = RandHaltVec(m,n)
% Returns a matrix of random Halton draws of size m x n (n draws
from m bases)
r = [];
vP = GeneratePrime(m);
for i = 1:m
    r(i,:) = RandomHalton(n,vP(i));
end

function r = RandomHalton(m,b)
% Randomizes Halton draws with base b and m elements
Halton_nonR = GetHalton(m,b);
u = rand(1,1);
% The following ensures that our randomized Halton element is within
% (0,1):
for i = 1: m
    if Halton_nonR(i) + u < 1;
        rt(i) = Halton_nonR(i) + u;
    else
        rt(i) = Halton_nonR(i) + u - 1;
    end
end
r =rt';
```

where `GetHalton(m,b)` is a function that provides a Halton sequence in base *b* and with size *m x 1* (Brandimarte, 2002). The function `RandomHalton(m,b)`is based on a randomizing procedure suggested by Kenneth Train in his online course in UC Berkeley[8].

[7] This occurs when we draw a sample point from a truncated standard normal.
[8] http://elsa.berkeley.edu/~train/distant.html

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`triprobit` and the *GHK* simulator: a short note

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1 The trivariate probit

Consider three binary variables y_1, y_2 and y_3, the trivariate probit model supposes that:

$$\begin{aligned} y_1 &= \begin{cases} 1 & \text{if } X\beta + \varepsilon_1 > 0 \\ 0 & \text{otherwise} \end{cases} \\ y_2 &= \begin{cases} 1 & \text{if } Z\gamma + \varepsilon_2 > 0 \\ 0 & \text{otherwise} \end{cases} \\ y_3 &= \begin{cases} 1 & \text{if } W\theta + \varepsilon_3 > 0 \\ 0 & \text{otherwise} \end{cases} \end{aligned} \tag{1}$$

with

$$\begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \end{pmatrix} \rightarrow N(0, \Sigma) \tag{2}$$

For identification reasons, the variances of the epsilons must equal 1.

Evaluation of the likelihood function requires the computation of trivariate normal integrals. For example, the probability of observing $(y_1 = 0, y_2 = 0, y_3 = 0)$ is:

$$\Pr[y_1 = 0, y_2 = 0, y_3 = 0] = \int_{-\infty}^{-X\beta} \int_{-\infty}^{-Z\gamma} \int_{-\infty}^{-W\theta} \phi_3(\varepsilon_1, \varepsilon_2, \varepsilon_3, \rho_{12}\rho_{13}\rho_{23}) \, \mathrm{d}\varepsilon_3 \mathrm{d}\varepsilon_2 \mathrm{d}\varepsilon_1 \tag{3}$$

where $\phi_3(.)$ is the trivariate normal p.d.f., and ρ_{ij} is the correlation coefficient between ε_i and ε_j.

While Stata provides commands to compute univariate and bivariate normal CDF (`norm()` and `binorm()`), no command is available for the trivariate case (as a matter of fact, numerical approximations perform poorly in computing high order integrals).

The `triprobit` command uses the *GHK* (Geweke-Hajivassiliou-Keane) smooth recursive simulator to approximate these integrals

2 The *GHK* simulator

Let us illustrate the *GHK* simulator in the trivariate case (generalization to higher orders is straightforward)

We wish to evaluate

$$\Pr(\varepsilon_1 < b_1, \varepsilon_2 < b_2, \varepsilon_3 < b_3) \tag{4}$$

where $(\varepsilon_1, \varepsilon_2, \varepsilon_3)$ are normal random variables with covariance structure given in (2)

Equation (4) can be rewritten as a product of conditional probabilities:

$$\Pr(\varepsilon_1 < b_1) \Pr(\varepsilon_2 < b_2 | \varepsilon_1 < b_1) \Pr(\varepsilon_3 < b_3 | \varepsilon_1 < b_1, \varepsilon_2 < b_2) \tag{5}$$

Let L be the lower triangular Cholesky decomposition of Σ, such that: $LL' = \Sigma$:

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I am very much indebted to Wolfgang Schwerdt who has provided numerous advices

$$L = \begin{pmatrix} l_{11} & 0 & 0 \\ l_{21} & l_{22} & 0 \\ l_{31} & l_{32} & l_{33} \end{pmatrix}$$

We get:

$$\begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \end{pmatrix} = \begin{pmatrix} l_{11} & 0 & 0 \\ l_{21} & l_{22} & 0 \\ l_{31} & l_{32} & l_{33} \end{pmatrix} \begin{pmatrix} \nu_1 \\ \nu_2 \\ \nu_3 \end{pmatrix} \tag{6}$$

where the ν_i are *independent* standard normal random variables.

By (6), we get:

$$\begin{aligned} \varepsilon_1 &= l_{11}\nu_1 \\ \varepsilon_2 &= l_{21}\nu_1 + l_{22}\nu_2 \\ \varepsilon_3 &= l_{31}\nu_1 + l_{32}\nu_2 + l_{33}\nu_3 \end{aligned}$$

Thus:

$$\Pr(\varepsilon_1 < b_1) = \Pr(\nu_1 < b_1 / l_{11}) \tag{7}$$

and

$$\Pr(\varepsilon_2 < b_2 | \varepsilon_1 < b_1) = \Pr(\nu_2 < (b_2 - l_{21}\nu_1) / l_{22} \mid \nu_1 < b_1 / l_{11}) \tag{8}$$

and

$$\begin{aligned} &\Pr(\varepsilon_3 < b_3 | \varepsilon_1 < b_1, \varepsilon_2 < b_2) = \\ &\Pr(\nu_3 < (b_3 - l_{31}\nu_1 - l_{32}\nu_2) / l_{33} \mid \nu_1 < b_1 / l_{11}, \nu_2 < (b_2 - l_{21}\nu_1) / l_{22}) \end{aligned} \tag{9}$$

Since (ν_1, ν_2, ν_3) are independent random variables, equation (4) can be expressed as a product of univariate CDF, but conditional on unobservables (the ν).

Suppose now that we draw a random variable ν_1^* from a truncated standard normal density with upper truncation point of b_1 / l_{11}, and another one, ν_2^*, from a standard normal density with upper truncation point of $(b_2 - l_{21}\nu_1^*) / l_{22}$. These two random variables respect the conditioning events of equations (8) and (9).

Equation (5) is then rewritten as:

$$\Pr(\nu_1 < b_1 / l_{11}) \Pr(\nu_2 < (b_2 - l_{21}\nu_1^*) / l_{22}) \Pr(\nu_3 < (b_3 - l_{31}\nu_1^* - l_{32}\nu_2^*) / l_{33}) \tag{10}$$

The *GHK* simulator of (4) is the arithmetic mean of the probabilities given by (10) for D random draws of ν_1^* and ν_2^*:

$$\widetilde{\Pr}_{GHK} = \frac{1}{D} \sum_{d=1}^{D} \left\{ \Phi[b_1 / l_{11}] \, \Phi\left[\left(b_2 - l_{21}\nu_1^{*d}\right) / l_{22} \right] \Phi\left[\left(b_3 - l_{31}\nu_1^{*d} - l_{32}\nu_2^{*d}\right) / l_{33} \right] \right\} \tag{11}$$

where ν_1^{*d} and ν_2^{*d} are the d-th draw of ν_1^* and ν_2^*, and where $\Phi(.)$ is the univariate normal CDF.

The simulated probability (11) is then plugged into the likelihood function, and standard maximisation techniques are used.

3 An example on artificial data

```
set obs 5000
local rho12=0.3
local rho13=-0.3
local rho23=0.3
drawnorm eps1 eps2 eps3 ,corr(1    , `rho12' , `rho13' \ /*
                        */ `rho12' ,   1   , `rho23' \ /*
                        */ `rho13' , `rho23' ,  1    )
```

```
drawnorm x1 x2 x3 x4 x5 x6 x7 x8 x9
gen y3=(1+x6+x7+x8+x9+eps3>0)
gen y2=(1+x4+x5+x6+eps2>0)
gen y1=(1+y2+y3+x1+x2+x3+eps1>0) /*note that y2 and y3 are endogenous*/
triprobit ( y1= y2 y3 x1 x2 x3)(y2= x4 x5 x6)(y3 = x6 x7 x8 x9)

trivariate probit, GHK simulator, 25 draws

Comparison log likelihood = -3876.3152

initial:       log likelihood = -3876.3152
<output omited>
Iteration 5:   log likelihood = -3838.0791

                                                Number of obs   =       5000
                                                Wald chi2(12)   =    3576.34
Log likelihood = -3838.0791                     Prob > chi2     =     0.0000

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
y1           |
          y2 |   .9232884   .0927705     9.95   0.000     .7414615    1.105115
          y3 |   .9222976   .0765911    12.04   0.000     .7721818    1.072413
          x1 |   1.065994   .0470546    22.65   0.000     .9737688    1.158219
          x2 |    .991229   .0449885    22.03   0.000     .9030532    1.079405
          x3 |   1.037427   .0453475    22.88   0.000     .9485477    1.126307
       _cons |   1.085532   .0735326    14.76   0.000     .9414105    1.229653
-------------+----------------------------------------------------------------
y2           |
          x4 |   1.000869   .0338369    29.58   0.000     .9345499    1.067188
          x5 |    .963295   .0340263    28.31   0.000     .8966047    1.029985
          x6 |   1.066905   .0352755    30.24   0.000     .9977661    1.136044
       _cons |    1.01315   .0314987    32.16   0.000     .9514141    1.074887
-------------+----------------------------------------------------------------
y3           |
          x6 |   1.023065   .0353343    28.95   0.000     .9538105    1.092319
          x7 |   1.023166   .0351069    29.14   0.000     .9543577    1.091974
          x8 |    1.03172   .0347611    29.68   0.000     .9635901    1.099851
          x9 |   1.017668   .0348807    29.18   0.000     .9493033    1.086033
       _cons |   1.015376   .0326298    31.12   0.000      .951423    1.079329
-------------+----------------------------------------------------------------
athrho12     |
       _cons |   .1457736   .0471507     3.09   0.002       .05336    .2381872
-------------+----------------------------------------------------------------
athrho13     |
       _cons |   -.278662   .0546056    -5.10   0.000     -.385687   -.1716371
-------------+----------------------------------------------------------------
athrho23     |
       _cons |   .2598698   .0348018     7.47   0.000     .1916596      .32808
------------------------------------------------------------------------------
------------------------------------------------------------------------------
rho12=  .14474975  Std. Err.=  .04616273  z=  3.1356413  Pr>|z|=  .00171479
rho13= -.27166631  Std. Err.=  .05057554  z= -5.3714955  Pr>|z|=  7.809e-08
rho23=  .25417374  Std. Err.=  .03255343  z=  7.8078952  Pr>|z|=  5.773e-15
------------------------------------------------------------------------------
LR test of rho12=rho13=rho23=0: chi2(3) =  76.472099  Prob > chi2 =  1.752e-16
```