Advanced Statistical Computing Project

Hierarchical-block conditioning approximations for high-dimensional multivariate normal probabilities

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1 Introduction

The computation of multivariate normal probability appears various fields. For instance, the inferences based on the central limit theorem, which holds when the sample size is large enough, is widely used in the social sciences and engineering as well as in the natural sciences. Recently, the dimensionality of data and models has been grown significantly, and in this respect, so does a need for the methodology to efficiently calculate high-dimensional multivariate normal probability.

Cao, Genton, Keyes, and Turkiyyah (2019) proposes new approaches to approximate high-dimensional multivariate normal probability

$$\Phi_n(\mathbf{a}, \mathbf{b}; 0, \mathbf{\Sigma}) = \int_a^b \frac{1}{\sqrt{(2\pi)^n \mathbf{\Sigma}|}} \exp\left(-\frac{1}{2}\mathbf{x}^T \mathbf{\Sigma}^{-1}\mathbf{x}\right) d\mathbf{x}, \tag{1}$$

using the hierarchical matrix $\mathcal{H}$ (Hackbusch, 2015) for the covariance matrix $\mathbf{\Sigma}$. The methods are based on two state-of-arts methods, among others, are the bivariate conditioning method (Trinh & Genz, 2015) and the hierarchical *Quasi-Monte Carlo* method (Genton, Keyes, & Turkiyyah, 2018). Specifically, Cao et al. (2019) generalize the bivariate conditioning method to a d-dimension and combine it with the hierarchical representation of the covariance matrix.

2 Multidimensional Conditioning Approximations

2.1 Quasi Monte Carlo Method

Error bound of $O(N^{-1/2})$ for monte carlo(MC) method which is guaranteed by central limit theorem is not enough for high dimensional multivariate random variable. Genz and Bretz (2009) claimed independent sample points is the reason of slow convergence. *Quasi-Monte Carlo*(QMC) methods uses deterministic sequences of sample points. Via employing low discrepancy sets for sequence, QMC is asymptotically efficient than MC. Since square root of prime numbers is irrational and linear independent over the rational numbers, K_N defined below is low-discrepancy sets.

$$K_N = \{i\mathbf{q} \bmod 1, i = 1, \cdots, N\},$$

where $\mathbf{q} = \sqrt{\mathbf{p}}$ and $\mathbf{p}$ is set of prime numbers. Selecting K_N shifted with $\mathbf{\Delta} \sim U[0,1]^n$ as sample points sequence, we have been implemented QMC.

$$L_N = \{\mathbf{z} + \mathbf{\Delta} \bmod 1 : \mathbf{z} \in K_N\}$$

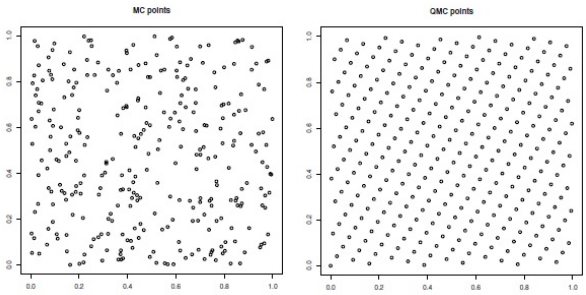


Figure 1: Comparison of MC and QMC sample points(Genz & Bretz, 2009)

Cholesky decomposition and few tranformation gives (2), and algorithm implemented (2) at $L_N \times ns$ times.

$$\begin{aligned}
\mathbf{\Phi}_n(\mathbf{a} \le \mathbf{x} \le \mathbf{b}; \mathbf{\Sigma}) &= \mathbf{\Phi}_n(a \le \mathbf{L}\mathbf{y} \le \mathbf{b}; I_n) \\
&= \int_{a_1 \le l_{11} y_1 \le b_1} \phi(y_1) \cdots \int_{a_n \le \mathbf{l}_n^t \mathbf{y} \le b_n} \phi(y_n) d\mathbf{y} \\
&= \int_{\tilde{a}_1}^{\tilde{b}_1} \phi(y_1) \int_{\tilde{a}_2(y_1)}^{\tilde{b}_2(y_1)} \phi(y_2) \cdots \int_{\tilde{a}_n(y_1,\cdots,y_{n-1})}^{\tilde{b}_n(y_1,\cdots,y_{n-1})} \phi(y_n) d\mathbf{y} \\
\text{with } \tilde{a}_i(y_1, \cdots, y_{i-1}) &= \frac{a_i - \sum_{j=1}^{i-1} l_{ij} y_j}{l_{ii}} \text{ and } (\tilde{b}_i(y_1, \cdots, y_{i-1})) = \frac{b_i - \sum_{j=1}^{i-1} l_{ij} y_j}{l_{ii}}
\end{aligned}$$

$$
\begin{aligned}
&= \int_{\Phi(\tilde{a}_1)}^{\Phi(\tilde{b}_1)} \int_{\Phi(\tilde{a}_2(\Phi^{-1}(z_1)))}^{\Phi(\tilde{b}_2(\Phi^{-1}(z_1)))} \cdots \int_{\Phi(\tilde{a}_n(\Phi^{-1}(z_1),\cdots,\Phi^{-1}(z_{n-1})))}^{\Phi(\tilde{b}_n(\Phi^{-1}(z_1),\cdots,\Phi^{-1}(z_{n-1})))} d\mathbf{z}(y_i = \Phi^{-1}(z_i)) \\
&= (e_1 - d_1) \int_0^1 (e_2(w_1) - d_2(w_1)) \cdots \\
&\int_0^1 (e_n(w_1, \cdots, w_{n-1}) - d_n(w_1, \cdots, w_{n-1}))) \int_0^1 d\mathbf{w} \\
&\text{with } z_i = d_i + (e_i - d_i) w_i
\end{aligned} \tag{2}
$$

Algorithm 1 Multivariate Normal Probability with Quasi Monte Carlo Method

procedure MVN($\boldsymbol{\mu}, \boldsymbol{\Sigma}, \mathbf{a}, \mathbf{b}, ns, N$)
  $\mathbf{L} = \text{cholesky}(\boldsymbol{\Sigma})$
  $\mathbf{a} = \mathbf{a} - \boldsymbol{\mu}$; $\mathbf{b} = \mathbf{b} - \boldsymbol{\mu}$
  $T = 0, N = 0, V = 0$
  $\mathbf{p} =$ vector of primes less than $\frac{5n \log n + 1}{4}$;$\mathbf{q} = \sqrt{\mathbf{p}}$
  $\mathbf{P} = \mathbf{1}_{ns}$
  $ans = 0$
  for $i = 1, \cdots, ns$ **do**
    $I_i = 0$, $\boldsymbol{\Delta} \sim U(0,1)^n$
    for $j = 1, \cdots, N$ **do**
      $\mathbf{X}[1:n, j] = (j+1)\mathbf{q} + \boldsymbol{\Delta}$
      $\mathbf{X}[1:n, j] = 2|\mathbf{X}[1:n, j] - \text{floor}(\mathbf{X}[1:n, j])| - 1$
    end for
    sample $= \mathbf{O}_{n,N}$
    $\mathbf{s}, \mathbf{c}, \mathbf{d}, \mathbf{dc}, \mathbf{P} = \mathbf{0}_N$
    for $j = 1, \cdots, n$ **do**
      if $j > 1$ **then**
        $c = \min(1, c + X[j-1, :] \odot dc)$
        sample$[i-1, 1:N] = \Phi^{-1}(c)$
        $s =$ **sample**$[1:i-1, 1:N]^T L[1:i-1, i]$
      end if
      $\mathbf{P}* = \Phi(\frac{b-s}{L[i,i]}) - \Phi(\frac{a-s}{L[i,i]})$
    end for
    ans+ $= \text{mean}(\mathbf{P})$
  end for
  return ans$/ns$
end procedure

2.2 Conditioning Approximation

We can exploit Cholesky factors from LDL decomposition rather than dealing with original covariance matrix. Mendell and Elston (1974) and Kamakura (1989) developed conditioning method to calculated cdf of multivariate truncated normal distribution. Trinh and Genz (2015) employ bivariate blocking method for efficient calculation while accuracy is preserved

$$\mathbf{\Sigma} = \begin{pmatrix} \mathbf{\Sigma}_{1,1} & \mathbf{R}^T \\ \mathbf{R} & \hat{\mathbf{\Sigma}} \end{pmatrix}, \text{ with } \mathbf{L} = \begin{pmatrix} \mathbf{I}_2 & \mathbf{O} \\ 1:\mathbf{M} & \mathbf{L} \end{pmatrix} \text{ and } \mathbf{D} = \begin{pmatrix} \mathbf{D}_1 & \mathbf{O} \\ \mathbf{O} & \widehat{\mathbf{D}} \end{pmatrix},$$

where $\mathbf{\Sigma}_{1,1}, \mathbf{D}_1$ is a 2×2 matrix. From $\mathbf{D}_1 = \mathbf{\Sigma_{1,1}}$, $\mathbf{M} = \mathbf{R}\mathbf{D}_1^{-1}$, $\widehat{\mathbf{D}} = \hat{\mathbf{\Sigma}} - \mathbf{M}\mathbf{D}_1\mathbf{M}^T$, we can obtain bivariate LDL decomposition of $\mathbf{\Sigma}$ inductively.

With transformation $\mathbf{y} = L\mathbf{x}$, $\mathbf{a} \leq \mathbf{x} \leq \mathbf{b}$ is tranformed to $a_j - \sum_{m=1}^{j-1} l_{jm}x_m = \alpha_j \leq x_j \leq b_j - \sum_{m=1}^{j-1} l_{jm}x_m = \beta_j$ for $j = 1, \cdots, n$. Then, with $k = \frac{n}{2}$ and $\mathbf{x}_{2k} = (x_{2k-1}, x_{2k})^T$

$$\begin{aligned} \mathbf{\Phi}_n(\mathbf{a}, \mathbf{b}; \mathbf{0}, \mathbf{\Sigma}) = \frac{1}{\sqrt{|\mathbf{D}|(2\pi)^n}} \int_{\alpha_1}^{\beta_1} \int_{\alpha_2}^{\beta_2} e^{-\frac{1}{2}\mathbf{x_2}^T\mathbf{D}_1^{-1}\mathbf{x}_2} \\ \cdots \int_{\alpha_{2k-1}}^{\beta_{2k-1}} \int_{\alpha_{2k}}^{\beta_{2k}} e^{-\frac{1}{2}\mathbf{x_{2k}}^T\mathbf{D}_1^{-1}\mathbf{x}_{2k}} \end{aligned} \tag{3}$$

Cao et al. (2019) generalizes bivariate method of Trinh and Genz (2015) to d-dimensional. Algorithms and details are following. When $s = \frac{m}{d}$ is integer, results of Algorithm 2, $\mathbf{L}, \mathbf{D}$ can

Algorithm 2 LDL decomposition

procedure LDL($\mathbf{\Sigma}$)
  $\mathbf{L} \leftarrow \mathbf{I}_m, \mathbf{D} \leftarrow \mathbf{O}_m$
  for $i = 1 : d : m - d + 1$ **do**
    $\mathbf{D}[i : i + d - 1, i : i + d - 1] \leftarrow \mathbf{\Sigma}[i : i + d - 1, i : i + d - 1]$
    $\mathbf{L}[i + d : m, i : i + d - 1] \leftarrow \mathbf{\Sigma}[i + d : m, i : i + d - 1]\mathbf{D}^{-1}[i : i + d - 1, i : i + d - 1]$
    $\mathbf{\Sigma}[i + d : m, i + d : m] \leftarrow \mathbf{\Sigma}[i + d : m, i + d : m] - \mathbf{L}[i + d : m, i : i + d - 1]\mathbf{D}^{-1}[i : i + d - 1, i : i + d - 1]\mathbf{L}[i : i + d - 1, i + d : m]$
    if $i + d < m$ **then**
      $\mathbf{D}[i + d : m, i + d : m] \leftarrow \mathbf{\Sigma}[i + d : m, i + d : m]$
    end if
  end for
  return L and **D**
end procedure

be written as

$$\mathbf{L} = \begin{pmatrix} \mathbf{I}_d & \mathbf{O}_d & \cdots & \mathbf{O}_d \\ \mathbf{L}_{2,1} & \ddots & \ddots & \vdots \\ \vdots & \ddots & \mathbf{I}_d & \mathbf{O}_d \\ \mathbf{L}_{s,1} & \cdots & \mathbf{L}_{s,s-1} & \mathbf{I}_d \end{pmatrix}, \mathbf{D} = \begin{pmatrix} \mathbf{D}_1 & \mathbf{O}_d & \cdots & \mathbf{O}_d \\ \mathbf{O}_d & \ddots & \ddots & \vdots \\ \vdots & \ddots & \mathbf{D}_{s-1} & \mathbf{O}_d \\ \mathbf{O}_d & \cdots & \mathbf{O}_d & \mathbf{D}_s \end{pmatrix}$$

with d-dimensional identitiy matrix $\mathbf{I}_d$ and d-dimensional zero matrix $\mathbf{O}_d$ and d-dimensional positive-definite matrix $\mathbf{D}_1, \cdots, \mathbf{D}_s$. Algorithm 2 is still valid when m is not multiple of d if we allow $\mathbf{L}, \mathbf{D}$ to have non-d dimensional matrix block as last row.

As in (3), tranformation, $Y = LX$ provides m-dimensional multivariate normal prabability as the product of s d-dimensional multivariate normal probabilities as below.

$$\mathbf{\Phi_m}(\mathbf{a}, \mathbf{b}; \mathbf{0}, \mathbf{\Sigma}) = \int_{\alpha_1}^{\beta_1} \phi_d(\mathbf{y}_1; \mathbf{D}_1) \int_{\alpha_2}^{\beta_2} \phi_d(\mathbf{y}_2; \mathbf{D}_2) \cdots \int_{\alpha_s}^{\beta_s} \phi_d(\mathbf{y}_s; \mathbf{D}_s) d\mathbf{y}_s \cdots d\mathbf{y}_2 d\mathbf{y}_1, \quad (4)$$

where $\boldsymbol{\alpha}_i = \mathbf{a}_i - \sum_{j=1}^{i-1} \mathbf{L}_{ij}\mathbf{y}_j, \boldsymbol{\beta}_i = \mathbf{b}_i - \sum_{j=1}^{i-1} \mathbf{L}_{ij}\mathbf{y}_j$ Equation (4) is implemented as below.

Algorithm 3 d-dimensional conditioning algorithm

procedure CMVN($\mathbf{\Sigma}, \mathbf{a}, \mathbf{b}, d$)
  $\mathbf{y} \leftarrow \mathbf{0}, P \leftarrow 1$
  for $i = 1 : s$ **do**
    $j \leftarrow (i-1)d$
    $\mathbf{g} \leftarrow \mathbf{L}[j+1 : j+d, 1 : j]\mathbf{y}[1 : j]$
    $\boldsymbol{\alpha} \leftarrow \mathbf{a}[j+1 : j+d] - \mathbf{g}$
    $\boldsymbol{\beta} \leftarrow \mathbf{b}[j+1 : j+d] - \mathbf{g}$
    $\mathbf{D}' \leftarrow \mathbf{D}[j+1 : j+d, j+1 : j+d]$
    $P \leftarrow P \cdot \mathbf{\Phi}_d(\boldsymbol{\alpha}, \boldsymbol{\beta}; \mathbf{0}, \mathbf{D}')$
    $\mathbf{y}[j+1 : j+d] \leftarrow E[\mathbf{Y}']$
  end for
  return P and $\mathbf{y}$
end procedure

2.3 Multidimensional Truncated Expectations

In algorithm 3, approximation of $\mathbf{\Phi}_d$ and $E[Y']isrequired.$ $\mathbf{\Phi}_d$ is possibly obtained with quasi monte calro method proposed by Genz (1992), and Kan and Robotti (2017) provides methods to calculate $E[Y']$. The truncated expectation can be expressed by

$$E(X^{e_j}) = \frac{1}{\mathbf{\Phi}(\mathbf{a}, \mathbf{b}; \boldsymbol{\mu}, \mathbf{\Sigma})} \int_{\mathbf{a}}^{\mathbf{b}} x_j \phi_d(\mathbf{x}; \boldsymbol{\mu}, \mathbf{\Sigma}) d\mathbf{x} = \frac{1}{\mathbf{\Phi}(\mathbf{a}, \mathbf{b}; \boldsymbol{\mu}, \mathbf{\Sigma})} F_j^d(\mathbf{a}, \mathbf{b}; \boldsymbol{\mu}, \mathbf{\Sigma})$$

Theorem 1. *(Kan & Robotti, 2017)*

$$F_j^d(\mathbf{a}, \mathbf{b}; \boldsymbol{\mu}, \boldsymbol{\Sigma}) = \mu_j \boldsymbol{\Phi}_d(\mathbf{a}, \mathbf{b}; \boldsymbol{\mu}, \boldsymbol{\Sigma}) + \mathbf{e}_j^T \boldsymbol{\Sigma} \mathbf{c}$$

,where c is a vector with lth component defined as

$$\begin{aligned}
c_l &= \phi_1(a_l; \mu_l, \sigma_l^2)\Phi_{d-1}(\mathbf{a}_{-l}, \mathbf{b}_{-l}; \hat{\boldsymbol{\mu}}^1, \hat{\boldsymbol{\Sigma}}_l) \\
&\quad - \phi_1(b_l; \mu_l, \sigma_l^2)\Phi_{d-1}(\mathbf{a}_{-l}, \mathbf{b}_{-l}; \hat{\boldsymbol{\mu}}^2, \hat{\boldsymbol{\Sigma}}_l) \\
\hat{\boldsymbol{\mu}}_l^1 &= \mu_{-l} + \boldsymbol{\Sigma}_{-l,l} \frac{a_l - \mu_l}{\sigma_l^2}, \\
\hat{\boldsymbol{\mu}}_l^2 &= \mu_{-l} + \boldsymbol{\Sigma}_{-l,l} \frac{b_l - \mu_l}{\sigma_l^2}, \\
\hat{\boldsymbol{\Sigma}}_l &= \boldsymbol{\Sigma}_{-l,-l} - \frac{1}{\sigma_l^2} \boldsymbol{\Sigma}_{-l,l} \boldsymbol{\Sigma}_{l,-l}
\end{aligned}$$

Proof. Derivative of the multivariate normal density satisfies below

$$-\frac{\partial \phi_n(\mathbf{x}; \boldsymbol{\mu}, \boldsymbol{\Sigma})}{\partial \mathbf{x}} = \boldsymbol{\Sigma}^{-1}(\mathbf{x} - \mu)\phi_n(\mathbf{x}; \boldsymbol{\mu}, \boldsymbol{\Sigma}) \tag{5}$$

With integration (5) from $\mathbf{a}$ to $\mathbf{b}$,

$$\boldsymbol{c} = \boldsymbol{\Sigma}^{-1} \begin{bmatrix} F_1^d - \mu_1 \Phi_{d-1} \\ F_2^d - \mu_1 \Phi_{d-1} \\ \vdots \\ F_d^d - \mu_1 \Phi_{d-1} \end{bmatrix} \tag{6}$$

Using the fact that

$$\begin{aligned}
\phi_n(\mathbf{x}; \boldsymbol{\mu}, \boldsymbol{\Sigma})|_{x_j = a_j} &= \phi_1(a_j; \mu_j, \sigma_j^2)\phi_{n-1}(\mathbf{x}_{-j}; \hat{\boldsymbol{\mu}}_j^1 \hat{\boldsymbol{\Sigma}}^1) \\
\phi_n(\mathbf{x}; \boldsymbol{\mu}, \boldsymbol{\Sigma})|_{x_j = b_j} &= \phi_1(b_j; \mu_j, \sigma_j^2)\phi_{n-1}(\mathbf{x}_{-j}; \hat{\boldsymbol{\mu}}_j^2 \hat{\boldsymbol{\Sigma}}^1),
\end{aligned}$$

(6) becomes

$$\begin{aligned}
c_l &= \phi_1(a_l; \mu_l, \sigma_l^2)\Phi_{d-1}(\mathbf{a}_{-l}, \mathbf{b}_{-l}; \hat{\boldsymbol{\mu}}^1, \hat{\boldsymbol{\Sigma}}_l) \\
&\quad - \phi_1(b_l; \mu_l, \sigma_l^2)\Phi_{d-1}(\mathbf{a}_{-l}, \mathbf{b}_{-l}; \hat{\boldsymbol{\mu}}^2, \hat{\boldsymbol{\Sigma}}_l)
\end{aligned}$$

□

Theorem 1 has same form with bivariate version of Trinh and Genz (2015) with $d = 2$ and it allows us to calculate $E[Y']$ in Algorithm 3 with $\boldsymbol{\Phi}$ which can be obtained with quasi monte calro method proposed by Genz (1992)

2.4 Multidimensional Conditioning Approximation with Univariate Reordering

It is known that appropriate integration order on conditioning algorithm possibly improves estimation accuracy, by reducing overall variation. Schervish (1984) originally proposed to arrange variables having relatively short integration interval width than other variables should be integrated later. Also, Gibson, Glasbey, and Elston (1994) suggested variables which have smallest expected values should be placed in outermost postion of the whole integration. Since, inner integrals which have smaller variation have the most influence with this order, overall variance decreases. Trinh and Genz (2015) also employs this ordering, and Cao et al. (2019) generalized it to d-dimensional problem.

Algorithm 4 d-dimensional conditioning algorithm with univariate reordering

procedure RCMVN($\mathbf{\Sigma}, \mathbf{a}, \mathbf{b}, d$)
  $\mathbf{y} \leftarrow \mathbf{0}, \mathbf{C} \leftarrow \mathbf{\Sigma}$
  for $i = 1 : m$ **do**
    if $i > 1$ **then**
      $\mathbf{y}[i-1] \leftarrow \frac{\phi(a') - \phi(b')}{\Phi(b') - \Phi(a')}$
    end if
    $j \leftarrow \text{argmin}_{i \le j \le m}\{\Phi(\frac{\mathbf{b}[j] - \mathbf{C}[j,1:i-1]\mathbf{y}[1:i-1]}{\sqrt{\mathbf{\Sigma}[j,j] - \mathbf{C}[j,1:i-1]\mathbf{C}^T[j,1:i-1]}}) - \Phi(\frac{\mathbf{a}[j] - \mathbf{C}[j,1:i-1]\mathbf{y}[1:i-1]}{\sqrt{\mathbf{\Sigma}[j,j] - \mathbf{C}[j,1:i-1]\mathbf{C}^T[j,1:i-1]}})\}$
    $\mathbf{\Sigma}[:,(i,j)] \leftarrow \mathbf{\Sigma}[:,(j,i)]; \mathbf{\Sigma}[(i,j),:] \leftarrow \mathbf{\Sigma}[(j,i),:]$
    $\mathbf{C}[:,(i,j)] \leftarrow \mathbf{C}[:,(j,i)]; \mathbf{C}[(i,j),:] \leftarrow \mathbf{C}[(j,i),:]$
    $\mathbf{a}[(i,j)] = \mathbf{a}[(j,i)]$
    $\mathbf{b}[(i,j)] = \mathbf{b}[(j,i)]$
    $\mathbf{C}[i,i] \leftarrow \sqrt{\mathbf{\Sigma}[i,i] - \mathbf{C}[i,1:i-1]\mathbf{C}^T[i,1:i-1]}$
    $\mathbf{C}[j,i] \leftarrow \frac{\mathbf{\Sigma}[j,i] - \mathbf{C}[i,1:i-1]\mathbf{C}^T[j,1:i-1]}{\mathbf{C}[i,i]}$, for $j = i+1, \cdots, m$
    $a' = \frac{\mathbf{a}[i] - \mathbf{C}[i,1:i-1]y[1:i-1]}{\mathbf{C}[\mathbf{i},\mathbf{i}]}$
    $b' = \frac{\mathbf{b}[i] - \mathbf{C}[i,1:i-1]y[1:i-1]}{\mathbf{C}[\mathbf{i},\mathbf{i}]}$
  end for
  return CMVN($\mathbf{\Sigma}, \mathbf{a}, \mathbf{b}, d$) as in Algorithm 3
end procedure

3 Hierarchical-Block Approximations

In this section, we suggest methods to solve the n-dimensional MVN problem with the hierarchical covariance matrix using the d-dimensional conditioning method with that of the Monte Carlo-based method for solving the m-dimensional MVN problems presented by the diagonal blocks.

3.1 Hierarchical Cholesky Decomposition

Hackbusch (2015) proposed adopting hiarchical matrix and its Cholesky decomposition. We have applied low rank approximation to each block of its decomposition to enhance computation efficiency and to save memory cost while accuracy is preserved. $A = LU$have the structure

$$\begin{pmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{pmatrix} = \begin{pmatrix} L_{11} & O \\ L_{21} & L_{22} \end{pmatrix} \begin{pmatrix} L_{11}^T & L_{12}^T \\ O & L_{22}^T \end{pmatrix}$$

with lower triangular matrix L_{11}, L_{22}. It comprises four tasks to complete the decomposition:

(a) compute L_{11} via Cholesky decomposition of A_{11}

(b) compute L_{12} from $L_{21}L_{11}^T = A_{21}$

(c) low rank approximation of $L_{12} = UV^T$

(d) compute L_{22} via Cholesky decomposition of $A_{22} - L_{21}L_{21}^T$

(a) and (d) are solved with hierachical Cholesky decomposition itself, and (b) is easy since it has triangular form. For (c), one needs to use low-rank approximation of SVD, i.e. $A = UDV^T = \sum_{i=1}^{n} d_i u_i v_i^T \approx \sum_{i=1}^{k} d_i u_i v_i^T$. Algorithm for the hierachical Cholesky decomposition of $n \times n$ matrix into $m \times m$ blocks is stated below.

Algorithm 5 Hierachical Cholesky decomposition

procedure HCHOL(A, n,m,rank)
  for $i = 1 : log_2(\frac{n}{m})$ **do**
    $nb = n/2^i$
    x = 0, y = nb
    for $j = 1 : 2^{i-1}$ **do**
      $\mathbf{U}, \mathbf{D}, \mathbf{V} = lowrankSVD(A[xbegin + 1 : xbegin + nb, ybegin + 1 : ybegin + nb], rank)$
      $\mathbf{A}[x + 1 : x + nb, y + 1 : y + rank] = \mathbf{UD}$
      $\mathbf{A}[x + 1 : x + nb, y + rank + 1 : y + nb] = \mathbf{O}$
      $\mathbf{A}[y + 1 : y + nb, x + 1 : x + rank] = \mathbf{VD}$
      $\mathbf{A}[y + 1 : y + nb, x + rank + 1 : x + nb] = \mathbf{O}$
      $x+ = 2nb, y+ = 2nb$
    end for
  end for
end procedure

3.2 The Hierarchical-Block Conditioning Method

Let $\phi_m(\mathbf{x}; \mathbf{\Sigma})$ be a pdf of m-dimensional normal distribution $N(\mathbf{0}, \mathbf{\Sigma})$ and $(\mathbf{B}, \mathbf{U}\mathbf{V}^T)$ be the hierarchical Cholesky decompostion of the covariance matrix $\mathbf{\Sigma}$. Then, we can express (1) as

$$\Phi_n(\mathbf{a}, \mathbf{b}; \mathbf{0}, \mathbf{\Sigma}) = \int_{\mathbf{a}_1'}^{\mathbf{b}_1'} \phi_m(\mathbf{x}_1; \mathbf{B}_1\mathbf{B}_1^T) \cdots \int_{\mathbf{a}_r'}^{\mathbf{b}_r'} \phi_r(\mathbf{x}_r; \mathbf{B}_r\mathbf{B}_r^T) d\mathbf{x}_r \cdots d\mathbf{x}_1. \tag{7}$$

Where $\mathbf{a}'$, $\mathbf{b}'$, $i = 1, \cdots, r$, are the corresponding segments of the updated $\mathbf{a}$ and $\mathbf{b}$. Specifficaly, we can compute n-dimensional MVN problem using hierarchical structure as algorithm 6.

Algorithm 6 Hierarchical-block conditioning algorithm

procedure `HMVN`(a, b, $\mathbf{\Sigma}$, d)
  $\mathbf{x} \leftarrow \mathbf{0}$ and $P \leftarrow 1$
  $[\mathbf{B}, \mathbf{UV}] \leftarrow$ `choldecomp_hmatrix`($\mathbf{\Sigma}$)
  for $i = 1 : r$ **do**
    $j \leftarrow (i-1)m$
    if $i > 1$ **then**
      $o_r \leftarrow$ row offset of $\mathbf{U}_{i-1}\mathbf{V}_{i-1}^T$
      $o_c \leftarrow$ column offset of $\mathbf{U}_{i-1}\mathbf{V}_{i-1}^T$
      $l \leftarrow \dim(\mathbf{U}_{i-1}\mathbf{V}_{i-1}^T)$
      $\mathbf{g} \leftarrow \mathbf{U}_{i-1}\mathbf{V}_{i-1}^T\mathbf{x}[o_c + 1 : o_c + l]$
      $\mathbf{a}[o_r + 1 : o_r + l] = \mathbf{a}[o_r + 1 : o_r + l] - \mathbf{g}$
      $\mathbf{b}[o_r + 1 : o_r + l] = \mathbf{a}[o_r + 1 : o_r + l] - \mathbf{g}$
    end if
    $\mathbf{a}_i \leftarrow \mathbf{a}[j + 1 : j + m]$
    $\mathbf{b}_i \leftarrow \mathbf{b}[j + 1 : j + m]$
    $P = P * \Phi_m(\mathbf{a}_i, \mathbf{b}_i; \mathbf{0}, \mathbf{B}_i\mathbf{B}_i^T)$
    $\mathbf{x}[j + 1 : j + m] \leftarrow \mathbf{B}_i^{-1}E(\mathbf{X}_i)$
  end for
end procedure

Note the probability value $\Phi_m(\mathbf{a}_i, \mathbf{b}_i; \mathbf{0}, \mathbf{B}_i\mathbf{B}_i^T)$ can be computed using QMC (`HMVN`, Method 1 in Cao et al. (2019)), d-dimensional conditioning algorithm (`HCMVN`, Method 2 in Cao et al. (2019)) or with d-dimensional conditioning algorithm with univariate reordering (`HRCMVN`, Method 3 in Cao et al. (2019)). These methods are more effective and can easily be parallelized compared to the classical methods.

3.3 Computational Complexity

To compare computational complexity, we decomposed the complexity of Algorithm 6 into three parts and listed the complexity for each part in Table 1, where $M(\cdot)$ denotes the complexity of the QMC simulation in the given dimension.

	MVN prob	Trunc exp	Upd limits
`HMVN`	$\frac{n}{m}M(m)$	$2nM(m) + O(nm^2)$	$O(mn + knlog(n/m))$
`HCMVN`	$\frac{n}{d}M(d) + O(m^2n)$	$2nM(d) + O(nd^2)$	$O(mn + knlog(n/m))$
`HRCMVN`	$\frac{n}{d}M(d) + O(m^2n)$	$2nM(d) + O(nd^2)$	$O(mn + knlog(n/m))$

Table 1: Complexity decomposition of the `HMVN`, `HCMVN`, and `HRCMVN`

The three parts of the complexity are the calculation of the MVN probability (MVN prob), the calculation of the truncated expectations (Trunc exp), and the update of the integration limits with truncated expectations (Upd limits), respectively. The latter two share the same asymptotic order in all three complexity terms. The updating cost is independent to the method. The complexity of univariate reordering is $O(m^2n)$, which is same as that of computing the MVN probabilities in `HCMVN`. Complexity from univariate reordering results in an identical major complexity component for `HCMVN` and `HRCMVN`. Since `HCMVN` and `HRCMVN` perform the QMC simulation in d-dimensions, the choice of m does not affect the complexity of `HCMVN` and `HRCMVN`.

4 Block Reordering

In sum, value of probability based on n-dimensioned multivariate normal random variable comprises of m multiplications of d-dimensional integrals. The idea arose from the construction of hierarchical Cholesky decomposition of covariance matrix, which enables concentration of high correlation values in the block diagonal area. As a consequence, correlation within blocks(or, group of compositions) are high while correlation between blocks(between groups) are low. Recall the `RCMVN` algorithm(3) : as computing each d-dimensional integral values, integration variables were arranged in order of increasing order of `CMVN` probability values, from outer to inner. Trinh and Genz (2015) discovered that this reordering improves overall accuracy. In this sense, the authors adopted block reordering procedure. Briefly speaking, this procedure permutes the block of LDL-decomposed covariance matrix, in order of `RCMVN` probability values of each blocks. On the top left corner, the block with minimal probability value get its place. Algorithm 7 is the block reordering algorithm introduced in Cao et al. (2019).

Sort function arranges elements in the vector 'ind' in an increasing order based on $\mathbf{P}$. Also, G means the intrinsic geometry of data. In practice, we set the geometry as 2D isotropic exponential covariance model, assuming data observation occured in unit square grid, indices arranged based on Morton order of level 1. The paper implemented the comparison between computing `HMVN`, `HCMVN`, `HRCMVN` values with or without block reordering procedure. Commonly,

Algorithm 7 Blockwise reordering

procedure BLOCKREORDER(G, ρ, a, b, m, ind)
  G, ρ, a, b, m, ind given, $\mathbf{P} \leftarrow 0$
  for $i = 1 : m : n - m + 1$ **do**
    $\mathbf{s} \leftarrow ind[i : i + m - 1]$
    $\mathbf{A} \leftarrow \rho(G, \mathbf{s})$
    $a' \leftarrow a[\mathbf{s}]$
    $b' \leftarrow b[\mathbf{s}]$
    $\mathbf{P} \leftarrow [\mathbf{P}, \texttt{RCMVN}(\mathbf{A}, a', b', 1).P]$
  end for
  sort(ind, **P**, m)
  return ind
end procedure

block reordering procedure places on the way before implementing hierarchical decomposition. For example, one can derive Algorithm 8 as a `HCMVN` procedure with block reordering.

Algorithm 8 Hierarchical-block conditioning algorithm with Block Reordering

procedure HCMVN_BRO($a,\ b,\ \Sigma,\ d$)
  $\mathbf{x} \leftarrow \mathbf{0}$, $P \leftarrow 1$, ind $\leftarrow [1, \ldots, n]$
  $[\mathbf{B}, \mathbf{UV}] \leftarrow$ `choldecomp_hmatrix`(Σ)
  $\mathbf{B} \leftarrow$ `Blockreorder`(G, ρ, a, b, m, ind)
  for $i = 1 : r$ **do**
    $j \leftarrow (i - 1)m$
    if $i > 1$ **then**
      $o_r \leftarrow$ row offset of $\mathbf{U}_{i-1}\mathbf{V}_{i-1}^T$
      $o_c \leftarrow$ column offset of $\mathbf{U}_{i-1}\mathbf{V}_{i-1}^T$
      $l \leftarrow \dim(\mathbf{U}_{i-1}\mathbf{V}_{i-1}^T)$
      $\mathbf{g} \leftarrow \mathbf{U}_{i-1}\mathbf{V}_{i-1}^T\mathbf{x}[o_c + 1 : o_c + l]$
      $\mathbf{a}[o_r + 1 : o_r + l] = \mathbf{a}[o_r + 1 : o_r + l] - \mathbf{g}$
      $\mathbf{b}[o_r + 1 : o_r + l] = \mathbf{a}[o_r + 1 : o_r + l] - \mathbf{g}$
    end if
    $\mathbf{a}_i \leftarrow \mathbf{a}[j + 1 : j + m]$
    $\mathbf{b}_i \leftarrow \mathbf{b}[j + 1 : j + m]$
    $P = P * \Phi_m(\mathbf{a}_i, \mathbf{b}_i; \mathbf{0}, \mathbf{B}_i\mathbf{B}_i^T)$
    $\mathbf{x}[j + 1 : j + m] \leftarrow \mathbf{B}_i^{-1}E(\mathbf{X}_i)$
  end for
end procedure

Block reordering aims for improving accuracy rather than shortening computation time. According to the simulation result introduced in Cao et al. (2019), the extra time used for running block reordering is relatively small compared to the total time costs.

5 Numerical Examples

In this section, we show you the results of implementing and experimenting with the methods described above. The implementation was done in julia=1.2.0. Code is made available in the github repository[1].

5.1 Cholesky Factorization

The *chol* function from **LinearAlgebra** package, the *dpotrf* from **LAPACK** package, and hierarchical Cholesky decomposition which suggested by Hackbusch (2015) are implemented. Exponential covariance matrix, $\mathbf{\Sigma}_{ij} = exp(-\|\mathbf{s}_i - \mathbf{s}_j\|/\beta)$ is set with $\beta = 0.3$. n points, $\mathbf{s}_1, \cdots, \mathbf{s}_n$ is evenly distributed over unique square with Morton's order which defined recursively as described in figure 2.

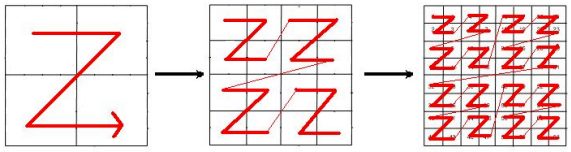


Figure 2: Morton's order(Salem & Arab, 2016)

With various n, three Cholesky methods are applied and results are below table 2. In low rank approximation at algorithm 5, rank is about $n^{1/4}$.

n	256	1024	4096	16384
chol	0.001s	0.0097s	0.414s	156.3s
dpotrf	0.0007s	0.0132s	0.431s	154.1s
hierarchical Cholesky	0.153s	0.076s	0.916s	37.3s
Error of hierarchical Cholesky	1.06e-7	9.97e-7	1.11e-3	1.87e-3

Table 2: Excution times for Cholesky factorization

Hierarchical Cholesky decomposition is more efficient than other classical Cholesky method with large dimension. Hierarchical Cholesky decomposition provides $\mathbf{\Sigma} \approx L_H L_H^T$. Its relative error is defined as $\frac{\|\mathbf{\Sigma} - L_H L_H^T\|_2}{\|\mathbf{\Sigma}\|_2}$, and table 2 ensures accuracy of hierarchical Cholesky decomposition proposed by Hackbusch (2015).

[1] `https://github.com/kw-lee/AdvStatComp_HDP`

5.2 Multivariate Normal Probabilities

To implement `*MVN` functions, we need to calculate n-dimensional normal probability (1),

$$\Phi_n(a, b; 0, \mathbf{\Sigma}) = \int_a^b \frac{1}{\sqrt{(2\pi)^n |\mathbf{\Sigma}|}} \exp\left(-\frac{1}{2}\mathbf{x}^T \mathbf{\Sigma}^{-1} \mathbf{x}\right) d\mathbf{x},$$

numerically. We implement `mvn`, the function that calculate multivariate normal probabilities using Richtmyer QMC method introduced in subsection 2.1. Varying sample size N and dimension d, two Monte Carlo methods are compared and results are below table 3. We generate N samples from $N(0, I_d)$ and set $\mathbf{a}_i = -\infty$ and $\mathbf{b}_i = 0$, i.e. true probabilities are $1/2^d$s, and repeat 20 times. Relative errors and computation times of each method are formulated.

(n, d)	4	8	12	16	20
Classical Monte Carlo					
500	12.2% 0.294ms	56.8% 0.016ms	161.9% 0.018ms	100.0% 0.019ms	100.0% 0.019ms
1000	9.5% 0.046ms	50.6% 0.041ms	193.8% 0.028ms	100.0% 0.028ms	100.0% 0.034ms
1500	8.9% 0.055ms	38.7% 0.046ms	150.2% 0.042ms	100.0% 0.048ms	100.0% 0.045ms
2000	5.4% 0.070ms	26.5% 0.065ms	102.4% 0.072ms	100.0% 0.058ms	100.0% 0.055ms
2500	5.1% 0.073ms	32.0% 0.092ms	100.1% 0.081ms	100.0% 0.083ms	100.0% 0.076ms
Richtmyer Quasi-Monte Carlo					
500	0.0% 0.058ms	0.0% 0.003ms	0.0% 0.006ms	0.0% 0.006ms	0.0% 0.011ms
1000	0.0% 0.003ms	0.0% 0.009ms	0.0% 0.013ms	0.0% 0.017ms	0.0% 0.020ms
1500	0.0% 0.006ms	0.0% 0.011ms	0.0% 0.016ms	0.0% 0.019ms	0.0% 0.030ms
2000	0.0% 0.011ms	0.0% 0.012ms	0.0% 0.013ms	0.0% 0.025ms	0.0% 0.036ms
2500	0.0% 0.009ms	0.0% 0.022ms	0.0% 0.033ms	0.0% 0.038ms	0.0% 0.056ms

Table 3: Richtmyer Quasi-Monte Carlo and classical Monte Carlo

Note QMC is superior to MC in every criterion. All the multivariate normal distribution probabilities required in the next algorithms are calculated using the `mvn` function.

5.3 d-dimensional Conditioning Algorithm without/with Reordering

Haar distribution is defined with a uniform distribution in the unitary $N \times N$ matrices group, $U(N)$. Stewart (1980) provides how to sample from Haar distribution with theorem 2

Theorem 2. *Stewart (1980) Let the independent vectors $x_1, \cdots, x_n$ be distributed $N(0, \sigma^2\mathbf{I})$. For $j = 1, 2, \cdots, n-1$, let $\mathbf{H}_{x_j}$ be the Householder transformation that reduces x_j to $r_{jj}e_1$, where r_{ij} is obtained in QR decomposition of $[x_1, \cdots, x_n]$ Let $\mathbf{H}_j = diag(\mathbf{I}_{j-1}, \bar{\mathbf{H}}_j)$. Let $\mathbf{D} = diag(sign(r_{11}), \cdots, sign(r_{nn}))$. Then the product $\mathbf{Q} = \mathbf{DH_1} \cdots \mathbf{H_{n-1}}$ follows Haar Distribution.*

We simulates 250 MVN problems with various values of m and d. $\mathbf{\Sigma} = \mathbf{QJQ}^T$ is simulated with $\mathbf{Q} \sim Haardistribution$ and $J = diag(j_i)$ where $j_1, \cdots, j_m \sim U(0, 1)$. Integration limits $a_i = -\infty$ and $b_i \sim (U, m)$ for $i = 1 \cdots, m$ are chosen. Estimated value is compared with approximated value obtained via quasi monte carlo method with a sample size of 10^4, which ensures error below 10^{-4}, and relative error and spent time is formulated below.

(m, d)	1	2	4	8	16
Without univariate reordering					
16	3.7% 0.029ms	3.5% 0.201ms	3.6% 0.431ms	3.8% 0.676ms	2.9% 1.372ms
32	2.4% 0.001ms	2.9% 0.390ms	2.9% 0.833ms	3.3% 1.283ms	2.7% 2.545ms
64	1.9% 0.004ms	2.1% 0.762ms	2.1% 1.686ms	1.8% 2.545ms	1.9% 5.004ms
128	1.3% 0.024ms	1.5% 1.505ms	1.3% 3.333ms	1.2% 5.146ms	1.4% 10.548ms
With univariate reordering					
16	3.3% 0.007ms	3.1% 0.203ms	3.3% 0.439ms	3.6% 0.680ms	2.7% 1.363ms
32	2.3% 0.004ms	2.6% 0.393ms	2.6% 0.841ms	3.2% 1.289ms	2.6% 2.544ms
64	2.0% 0.014ms	2.1% 0.773ms	2.1% 1.695ms	1.9% 2.552ms	1.9% 5.022ms
128	1.2% 0.097ms	1.5% 1.593ms	1.4% 3.462ms	1.2% 5.268ms	1.4% 10.7861ms

Table 4: Errors and execution times of the d-dimensional conditioning method

Estimation error tended to decrease as d increases with each m since lager d implers less discarded correlation information. Spent time grows to a linear fashion with m while it grows exponentially with d.

5.4 Hierarchical-Block Approximations

In this section, we implement three methods in the section 3 and compare theirs performance

- M1, `HMVN()`: Calculate multivariate normal probabilities using hierarchical-block approximation
- M2, `HCMVN()`: Calculate multivariate normal probabilities using hierarchical-block conditioning approximation
- M3, `HRCMVN()`: Calculate multivariate normal probabilities using hierarchical-block conditioning approximation with univarite reordering

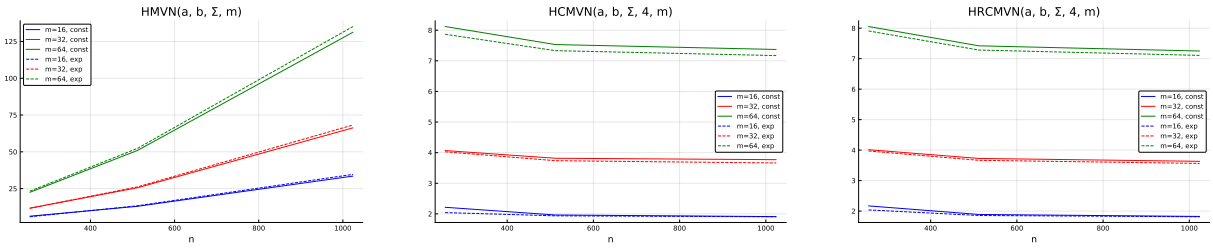
We use 20 as the sample size instead of 250 as in Table 4 because the covariance structure is fixed, leading to a much smaller standard deviation for the estimators. We simulates two spatial problems with various values of m and n.

1. Constant covariance matrix: $k(x_i, x_j) = \theta + (1-\theta)\delta_{ij}$ for some $|\theta| < 1$.
2. 1D exponential covariance matrix: $k(x_i, x_j) = \exp(-d_{ij}/\beta)$ for some $\beta > 0$, where d_{ij} is the distance between x_i and x_j.

We set the integration limits $a_i = -\infty$ and $b_i \sim (U, n)$ for $i = 1 \cdots, n$, $\theta = 0.7$, $d_{ij} = 1$, and $\beta = 10$ as in Cao et al. (2019). Estimated value is compared with approximated value obtained via QMC with a sample size of 10^4. In this simulation, we fix $d = 4$ for `HCMVN` and `HRCMVN`. Table 5 and Figure 3 are errors and execution times under the constant covariance structure and 1D exponential covariance structure respectively.

m	16			32			64		
n	256	512	1024	256	512	1024	256	512	1024
Constant covariance structure									
M1	8.22%	7.11%	8.66%	8.94%	7.88%	6.68%	10.58%	8.05%	9.78%
M2	8.37%	7.08%	8.60%	8.91%	7.77%	6.61%	10.58%	8.26%	9.91%
M3	8.51%	7.10%	8.70%	9.51%	7.92%	7.00%	10.68%	7.94%	9.63%
1D exponential covariance matrix									
M1	2.87%	0.00%	0.01%	0.07%	1.31%	0.00%	2.65%	0.27%	0.57%
M2	3.28%	0.01%	0.90%	0.07%	1.31%	0.01%	2.65%	0.28%	0.57%
M3	4.73%	0.09%	2.11%	2.17%	1.90%	0.16%	3.72%	1.25%	0.66%

Table 5: Relative errors under the constant covariance structure and 1D exponential covariance structure



(a) M1 (b) M2 (c) M3

Figure 3: Execution time (seconds) under the constant covariance structure and 1D exponential covariance structure

Note the execution times of M2 and M3 are significantly smaller than that of M1 even their performances are similar.

Next, we conducted computer simulations with a 2D exponential covariance matrix, based on the sample points arranged by Morton's order. We fix $m = 8$ for 2D covariance structure and examine the efficiency of our algorithm, with $d = 1, 2, 4$. To test sensitivity with respect to correlation strength, we perform the estimation under $\beta = 0.3, 0.1$, and 0.03, where each values represent strong, medium, and weak correlation strengths. We set n to 16, 64, 256 and other settings are same as above. Table 6 presents the results.

n	*compress*	`mvn`	`HMVN`	$\texttt{HCMVN}_1$	$\texttt{HCMVN}_2$	$\texttt{HCMVN}_4$
$\beta = 0.3$						
16	0.89	0.00ppm	53.68ppm	2139.98ppm	1723.46ppm	276.37ppm
64	0.56	0.00ppm	143.88ppm	167.26ppm	167.69ppm	169.31ppm
256	0.28	0.00ppm	215.10ppm	213.41ppm	213.41ppm	213.41ppm
$\beta = 0.1$						
16	0.89	0.00ppm	0.00ppm	0.84ppm	0.60ppm	0.02ppm
64	0.56	0.00ppm	0.00ppm	1.61ppm	0.09ppm	0.01ppm
256	0.28	0.00ppm	0.00ppm	0.02ppm	0.02ppm	0.02ppm
$\beta = 0.03$						
16	0.89	0.00ppm	0.00ppm	0.00ppm	0.00ppm	0.00ppm
64	0.42	0.00ppm	0.00ppm	0.00ppm	0.00ppm	0.00ppm
256	0.20	0.00ppm	0.00ppm	0.00ppm	0.00ppm	0.00ppm

Table 6: Relative errors and efficiency of the two-level hierarchical-block conditioning methods

In Table 6, $\texttt{HCMVN}_d$ denotes `HCMVN` function with conditioning parameter d and

$$compress = \frac{\text{Total memory size of the } \mathcal{H} \text{ matrix}}{\text{Memory size of the covariance matrix } \boldsymbol{\Sigma}}.$$

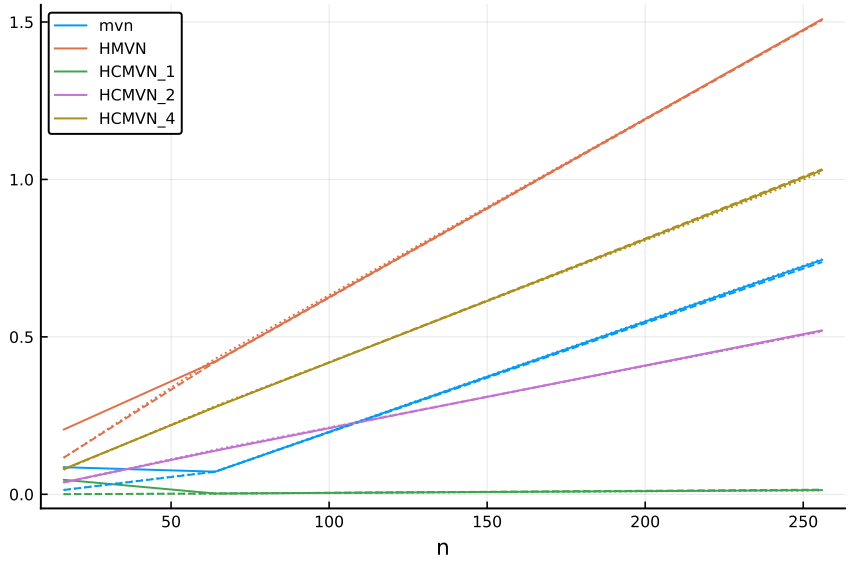


Figure 4: Execution time (seconds) under the constant covariance structure and 2D exponential covariance structure; solid line: $\beta = 0.3$, dashed line: $\beta = 0.1$, dotted line: $\beta = 0.03$

In this experiment, Cao et al. (2019) mentioned

> It is worth mentioning that the correlation strength is essentially increased when n increases while β remains unchanged because the samples are from the unit hypercube. Also the increase of d will reduce the estimation error but is still unable to reach a satisfactory level. The method, when used without a reordering strategy, does not produce sufficiently accurate results. This motivated the development of the reordering strategy described in the next section

with extremely large size simulation. But, in our case, the phenomenon stated above could not be observed due to shortage of computing resource we had.

6 Conclusion

So far, our group comprehended and emulated the results of approximation of high-dimensional multivariate normal probabilities which comprises three concepts: hierarchical representation, d-dimensional conditioning, and block reordering. For computer simulation, our group used Julia. In terms of computing, our group reproduced all the procedures mentioned in Cao et al. (2019) such as `CMVN`, `RCMVN`, `HCMVN`, `HRCMVN`, and block reordering. The numbers including running time, error rate, etc were not exactly in line with Cao et al. (2019). Even though we followed the streamline of the published pseudocodes of each methods, it might be the case that the difference of computing environment of our group and the authors produce the difference.

By using distinct programming language, possessing different computers with unequal quality of CPUs, generating rule of random numbers (e.g. seed number), etc.

In Cao et al. (2019), the experiments were done by setting covariance structure by 2D or 1D exponential spatial model along with Morton ordering, which is feasible to take advantage of hierarchical decomposition for covariance matrix. Although Cao et al. (2019) suggested that in the case of completely random, non-hierarchical method might show better performance in terms of computing time, it seems rational that the hierarchical decomposition method is effective approach for the case of smooth covariance function. The procedure of d-dimensional conditioning and block reordering scheme improved accuracy of estimated value under the exponential covariance structure, with negligible amount of computing time and cost. The integrated value is computed by multiplyng truncated expectation values, computed based on the principle of Quasi-Monte Carlo simulation. Hence, it remains further topic of research to delve into the methodology of estimating the truncated expectations of multivariate normal random variables. Furthermore, considering that our approximation method dealt with the case of covariance structure that m divides n. This means that $m \times m$ block matrices can fit the diagonal line of the original covariance matrix. Therefore, it might be worth studying deeply about the issue when m does not divide n, so there exist remnants on diagonal locations.

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