The Matrix Generalized Inverse Gaussian Distribution: Properties and Applications

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Abstract

While the Matrix Generalized Inverse Gaussian (MGIG) distribution arises naturally in some settings as a distribution over symmetric positive semi-definite matrices, certain key properties of the distribution and effective ways of sampling from the distribution have not been carefully studied. In this paper, we show that the MGIG is unimodal, and the mode can be obtained by solving an Algebraic Riccati Equation (ARE) equation [7]. Based on the property, we propose an importance sampling method for the MGIG where the mode of the proposal distribution matches that of the target. The proposed sampling method is more efficient than existing approaches [32, 33], which use proposal distributions that may have the mode far from the MGIG's mode. Further, we illustrate that the the posterior distribution in latent factor models, such as probabilistic matrix factorization (PMF) [25], when marginalized over one latent factor has the MGIG distribution. The characterization leads to a novel Collapsed Monte Carlo (CMC) inference algorithm for such latent factor models. We illustrate that CMC has a lower log loss or perplexity than MCMC, and needs fewer samples.

1 Introduction

Matrix Generalized Inverse Gaussian (MGIG) distributions [3, 10] are a flexible family of distributions over the space of symmetric positive definite matrices and has been recently applied as the prior for covariance matrix [21, 32, 33]. MGIG is a flexible prior since it contains Wishart, and Inverse Wishart distributions as special cases. We anticipate the usage of MGIG as prior for statistical machine learning models to grow with potential applications in Bayesian dimensionality reduction and Bayesian matrix completion. We illustrate some of these connections in Section 4.

Some properties of the MGIG distribution and its connection with Wishart distribution has been studied in [10, 27, 28]. However, to best of our knowledge, it is not yet known if the distribution is unimodal and, if it is unimodal, how to obtain the mode of MGIG. Besides, it is difficult to analytically calculate mean of the distribution and sample from the MGIG distribution. Monte Carlo methods like the importance sampling can in principle be applied to infer the mean of MGIG but one needs to design a suitable proposal distribution [22, 24].

There is only one important sampling procedure for estimating the mean of MGIG [32, 33]. In this approach, MGIG is viewed as a product of the Wishart and Inverse Wishart distributions and one of them is used as the proposal distribution. However, we illustrate that the mode of the proposal distribution in [32, 33] may be far away from the MGIG's mode. As a result, the proposal density is small in a region where the MGIG density is large yielding to an ineffective sampler and drastically wrong estimate of the mean (Figures 1 and 2).

In this paper, we first illustrate that the MGIG distribution is unimodal where the mode can be obtained by solving an *Algebraic Riccati Equation (ARE) [7]*. This characterization leads to an effective importance sampler for the MGIG distribution. More specifically, for estimating the expectation $\mathbb{E}_{X \sim MGIG}[g(X)]$, we select a proposal distribution over space of symmetric positive definite matrices like Wishart or Inverse Wishart distribution such that the mode of the proposal matches the mode of the MGIG. As a result, unlike the current sampler [32, 33], by aligning

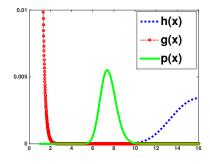


Figure 1: An illustration of bad proposal distribution in importance sampling. Let $p(x) = h^*(x)g^*(x)/Z_p \propto h(x)g(x)$. Note that $h(x) = h^*(x)/Z_h$ nor $g(x) = g^*(x)/Z_g$ need not be a good candidate proposal distribution to approximate p(x) since the mode of both h(x) and g(x) distribution is far away from p(x).

the shape of the proposal and the MGIG, the density of the proposal gets higher values in the high density regions of the target, yielding to a good approximation of $\mathbb{E}_{X \sim MGIG}[g(X)]$.

Further, we discuss a new application of the MGIG distribution in latent factor models such as probabilistic matrix factorization (PMF) [25] or Bayesian PCA (BPCA) [4]. In these settings, the given matrix $X \in \mathbb{R}^{N \times M}$ is approximated by a low-rank matrix $\hat{X} = UV^T$ where $U \in \mathbb{R}^{N \times D}$ and $V \in \mathbb{R}^{M \times D}$ with Gaussian priors over the latent matrices U and V. We show that after analytically marginalizing one of the latent matrices in PMF (or BPCA), the posterior over the other matrix has the MGIG distribution. This illustration yields to a novel Collapsed Monte Carlo (CMC) inference algorithm for PMF. In particular, we marginalize one of the latent matrices, say V, and propose a direct Monte Carlo sampling from the posterior of the other matrix, say U. Through extensive experimental analysis on synthetic, SNP, gene expression, and MovieLens datasets, we show that CMC has lower log loss or perplexity with fewer samples than Markov Chain Monte Carlo (MCMC) inference approach for PMF [26].

The rest of the paper is organized as follows. In Section 2, we cover background materials. In Section 3, we show that MGIG is unimodal and give a novel importance sampler for MGIG. We provide the connection of MGIG with PMF in Section 4, present the results in Section 5, and conclude in Section 6.

2 Background and Preliminary

In this section we provide some background on the relevant topics and tools that will be used in our analysis. We start by an introduction to importance sampling, MGIG distribution, a brief overview of the algebraic Riccati Equations (ARE), followed by describing the connection between Probabilistic Matrix Factorization and PCA.

Notations: Let \mathbb{S}_{++}^N and \mathbb{S}_{+}^N denote the space of symmetric $(N \times N)$ positive definite and positive semi-definite matrix, respectively. Denote 0_N as a matrix of all zeros $\{0\}^{N \times N}$. Let |.| denote the determinant of matrix, $\operatorname{Tr}(.)$ be the matrix trace. A matrix random variable $\Lambda \in \mathbb{S}_{++}^N$ has a Wishart distribution and is denoted as $\mathcal{W}_N(\Lambda | \Phi, \tau)$ where $\tau > N - 1$ and $\Phi \in \mathbb{S}_{++}^N$ [31]. A matrix random variable $\Lambda \in \mathbb{S}_{++}^N$ has an Inverse Wishart distribution and is denoted as $\mathcal{IW}_N(\Lambda | \Psi, \alpha)$ where $\alpha > N - 1$ and $\Psi \in \mathbb{S}_{++}^N$ is the scale matrix. Consider the matrix $X \in \mathbb{R}^{N \times M}$. We denote $\mathbf{x}_{:m}$ as the m^{th} column of X and \mathbf{x}_n as the n^{th} row of X.

2.1 Importance Sampling

Consider distribution $p(x) = \frac{1}{Z_p}p^*(x)$ where Z_p is the partition function which plays the role of a normalizing constant. Importance sampling is a general technique for estimating $\mathbb{E}_{x \sim p(x)}[f(x)]$ where sampling from p(x) (the target distribution) is difficult but we can evaluate the value of $p^*(x)$ at any given x [22]. The idea is to draw S samples $\{x_i\}_{i=1}^S$ from a similar but easier distribution denoted by proposal distribution $q(x) = \frac{1}{Z_q}q^*(x)$ and calculate

the expected value as follows

$$\mathbb{E}_{x \sim p}[f(x)] = \mathbb{E}_{x \sim q}\left[\frac{f(x)p(x)}{q(x)}\right] \approx \frac{\sum_{i=1}^{S} f(x_i)w(x_i)}{\sum_{i=1}^{S} w(x_i)},$$

where $w(x_i) = \frac{p^*(x_i)}{q^*(x_i)}$ is the weight of each sample *i*, and Z_q is the partition function.

The efficiency of importance sampling depends on how closely the proposal approximates the target in the shape. One way for monitoring the efficiency of importance sampling is the effective sample size measured as $ESS = \frac{(\sum_{i=1}^{S} w(x_i))^2}{\sum_{i=1}^{S} w^2(x_i)}$ [16]. If the proposal has the same shape as the target distribution, ESS achieves the maximum value. The other extreme happens if all but one of the importance weights are zero yielding to a minimum ESS value of one. Very small value of ESS indicates a big discrepancy between the proposal and target (for example when the mode of the proposal distribution is far away from the target's mode) leading to a drastically wrong estimate of $\mathbb{E}_{x\sim p}[f(x)]$ [22].

In particular, consider target distributions that can be decomposed as a product of two distributions, i.e., $p(x) \propto h(x)g(x)$. Naturally, one may choose one of the multiplicand of p(x) (h(x) or g(x)) as the proposal distribution since weight calculation becomes the evaluation at the other multiplicand. However, when mode of h(x) or g(x) is far away from the p(x)'s mode, neither of them are an appropriate candidate for the proposal distribution since the proposal density is small in a region where the target density is large (Figure 1). Thus it is quite possible that the sampler has a very low effective sample size (*ESS*) [16].

2.2 \mathcal{MGIG} Distribution

MGIG distribution was first introduced in [3] as a distribution over the space of symmetric ($N \times N$) positive definite matrices defined as follows.

Definition 2.1 (MGIG Distribution) Let Λ be a symmetric $(N \times N)$ positive definite matrix. A matrix-variate random variable Λ is MGIG distributed [3, 10] and is denoted as $\Lambda \sim MGIG_N(\Psi, \Phi, \nu)$ if the density of Λ is

$$f(\Lambda) = \frac{|\Lambda|^{\nu - (N+1)/2}}{|\frac{\Psi}{2}|^{\nu} B_{\nu}(\frac{\Phi}{2}\frac{\Psi}{2})} \exp\{\operatorname{Tr}(-\frac{1}{2}\Psi\Lambda^{-1} - \frac{1}{2}\Phi\Lambda)\}$$

where $B_{\nu}(.)$ is the matrix Bessel function [14] defined as

$$B_{\nu}\left(\frac{\Phi}{2}\frac{\Psi}{2}\right) = \left|\frac{\Phi}{2}\right|^{-\nu} \int_{\mathbb{S}^{N}_{++}} |S|^{-\nu - \frac{N+1}{2}} \exp\{\operatorname{Tr}\left(-\frac{1}{2}\Psi S^{-1} - \frac{1}{2}\Phi S\right)\} dS.$$
(1)

When N = 1, the MGIG is the generalized inverse Gaussian distribution GIG [15] which is often used as the prior in several domains [6, 13]. In the following, we show that if $\Psi = 0$, the MGIG distribution reduces to the Wishart, and if $\Phi = 0$, it becomes the Inverse Wishart distribution.

Proposition 1 [32, Proposition 2] If matrix $\Lambda \sim \mathcal{MGIG}_N(\Psi, \Phi, \nu)$, then $\Lambda^{-1} \sim \mathcal{MGIG}_N(\Phi, \Psi, -\nu)$.

Proof: The proof follows from the Bessel function property $B_{\delta}(WZ) = |WZ|^{-\delta}B_{-\delta}(ZW)$ [32].

Proposition 2 If matrix $\Lambda \sim \mathcal{MGIG}_N(\Psi, 0_N, \nu)$, and $-\nu > \frac{N-1}{2}$, then $\Lambda \sim IW_N(\Psi, -2\nu)$.

Proof: First note that If $-\nu > \frac{N-1}{2}$, then we have $B_{\nu}(0_N) = \Gamma_N(-\nu)$ [11]. Then, the proof simply follows from Definition 2.1.

Proposition 3 If matrix $\Lambda \sim \mathcal{MGIG}_N(0_N, \Phi, \nu)$, and $\nu > \frac{N-1}{2}$, then $\Lambda \sim W_N(\Phi^{-1}, 2\nu)$.

Proof: From Proposition 1, we have $\Lambda^{-1} \sim \mathcal{MGIG}_N(\Phi, 0_N, -\nu)$. Also, from Proposition 2, we have $\Lambda^{-1} \sim IW_N(\Phi, 2\nu)$. If matrix $\Lambda^{-1} \sim IW_N(\Phi, 2\nu)$ then $\Lambda \sim W_N(\Phi^{-1}, 2\nu)$. This completes the proof.

Sampling Mean of \mathcal{MGIG}: The sufficient statistics of \mathcal{MGIG} are $\log |\Lambda|$, Λ , and Λ^{-1} . It is, however, difficult to analytically calculate the expectations $\mathbb{E}_{\Lambda \sim \mathcal{MGIG}}[\Lambda]$ and $\mathbb{E}_{\Lambda \sim \mathcal{MGIG}}[\Lambda^{-1}]$. Importance sampling can be applied to

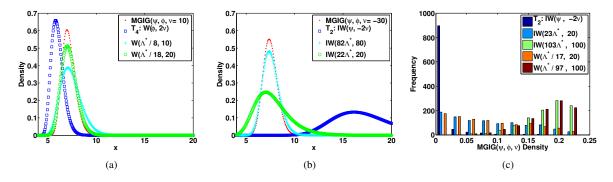


Figure 2: (a,b) Comparison of different proposal distribution (a) Wishart (\mathcal{W}) and (b) Inverse Wishart (\mathcal{IW}) for sampling mean of $\mathcal{MGIG}_1(\Psi, \Phi, \nu)$ where Λ^* is the mode of MGIG. The blue curves are the proposal distribution defined in [32, 33] which can not recover the mode of the \mathcal{MGIG} distribution. (c) Density of $\mathcal{MGIG}_2(\Psi, \Phi, \nu)$ for 1000 samples generated by each proposal distribution is calculated. More than 90% of samples generated by the previous proposal distribution in [32, 33] ($\mathcal{IW}(\psi, -2\nu)$) have zero \mathcal{MGIG} density leading to ESS = 40. Whereas, the new proposal distribution $IW(23\Lambda^*, 20)$ has the ESS = 550 which has a very similar shape to the target \mathcal{MGIG} distribution.

approximate those quantities. Note that based on the result of Proposition 1, the importance sampling procedure for estimating mean of \mathcal{MGIG} , i.e., $\mathbb{E}_{\Lambda \sim \mathcal{MGIG}}[\Lambda]$, can also be applied to infer the reciprocal mean i.e. $\mathbb{E}_{\Lambda \sim \mathcal{MGIG}}[\Lambda^{-1}]$.

An importance sampling procedure proposed in [32, 33], where the MGIG is viewed as a product of Inverse Wishart and Wishart distributions and one of the multiplicands is used as the natural choice of the proposal distribution. In particular, in [32, 33], the MGIG is viewed as

$$\mathcal{MGIG}_{N}(\Lambda|\Psi,\Psi,\nu) \propto \underbrace{e^{\mathrm{Tr}(-\frac{1}{2}\Phi\Lambda)}}_{T_{1}} \underbrace{\mathcal{IW}_{N}(\Lambda|\Psi,-2\nu_{u})}_{T_{2}}$$
(2)

$$\propto \underbrace{e^{\mathrm{Tr}(-\frac{1}{2}\Psi\Lambda^{-1})}}_{T_3} \underbrace{\mathcal{W}_N(\Lambda \mid \Phi, 2\nu_u)}_{T_s}.$$
(3)

Note that T_2 is the Inverse Wishart distribution and T_4 is the Wishart distribution, and there are efficient samplers for both of Wishart and Inverse Wishart distributions [29]. In [32, 33], authors advocate using T_2 (or T_4) as the proposal distribution which simplify the weight calculation to the evaluation of T_1 (or T_3). However, it is not studied how close T_2 (or T_4) are to the MGIG distribution in shape. For example, consider the 1-dimensional MGIG distribution

$$\mathcal{MGIG}_1(\Lambda \mid 35, 10, 10) \propto \underbrace{e^{\mathrm{Tr}(-\frac{35}{2}\Lambda^{-1})}}_{T_3} \underbrace{\mathcal{W}_1(\Lambda \mid 10, 20)}_{T_4}.$$
(4)

In [32, 33], $T_4 : W_1(\Lambda | 10, 20)$ is considered as the proposal distribution, but the mode of T_4 is far away from the mode of $\mathcal{MGIG}_1(\Lambda | 35, 10, 10)$ (Figure 2(a)). As a result, samples drawn from T_4 will be on the tail of the $\mathcal{MGIG}_1(\Lambda | 10, 20)$ distribution, and will end up getting low weights (importance) from the $\mathcal{MGIG}_1(\Lambda | 10, 20)$ distribution. Such a sampling procedure will be wasteful, i.e., drawing samples from the tails of the target \mathcal{MGIG}_1 distribution, leading to a very low *ESS*. Similar behavior is observed with several different choices of parameters for the \mathcal{MGIG} , here we only show three of them in Figure 2 due to the lack of space.

2.3 Algebraic Riccati Equation

An algebraic Riccati equation (ARE) is

$$A^T X + XA + XRX + Q = 0, (5)$$

where $A \in \mathbb{R}^{N \times N}$, $Q \in \mathbb{S}^{N}_{+}$, and $R \in \mathbb{S}^{N}_{+}$. We associate a $2N \times 2N$ matrix called the Hamiltonian matrix H with the ARE (5) as $H = \begin{bmatrix} A & R \\ -Q & -A^{T} \end{bmatrix}$. The Hamiltonian matrix has some useful properties appears in various control and

filtering problems of continuous time systems. In particular, the ARE (5) has a unique positive definite solution if and only if the associated Hamiltonian matrix H has no imaginary eigenvalues (Section 5.6.3 of [7]).

There have been offered various numerical methods to solve the ARE which can be reviewed in [1]. The key of numerical technique to solve ARE (5) is to convert the problem to a stable invariant subspace problem of the Hamiltonian matrix i.e., finding the invariant subspace corresponding to the eigenvalues of H with negative real parts. In particular, consider $V = \begin{bmatrix} X_1 \\ X_2 \end{bmatrix}$ to be a H-invariant subspace, i.e., $HV = V\Lambda$. Assume X_1 is invertible, we then post multiply by X_1^{-1} to obtain

$$HVX_1^{-1} = V\Lambda X_1^{-1} \Rightarrow \begin{bmatrix} A & R \\ -Q & -A^T \end{bmatrix} \begin{bmatrix} I \\ X \end{bmatrix} = \begin{bmatrix} I \\ X \end{bmatrix} X_1\Lambda X_1^{-1},$$
(6)

where $X = X_2 X_1^{-1}$. Multiplying both side by $\begin{bmatrix} -X & I \end{bmatrix}$, we have

$$\begin{bmatrix} -X & I \end{bmatrix} \begin{bmatrix} A & R \\ -Q & -A^T \end{bmatrix} \begin{bmatrix} I \\ X \end{bmatrix} = \begin{bmatrix} -X & I \end{bmatrix} \begin{bmatrix} I \\ X \end{bmatrix} X_1 \Lambda X_1^{-1} = 0.$$
(7)

Simplifying the left hand side we get the ARE (5) which implies that $X = X_2 X_1^{-1}$ is the solution of (5).

The usual ARE solvers such as the Schur vector method [17], SR methods [9], the matrix sign function [2, 12] require in general $O(n^3)$ flops [20]. For special cases, faster algorithms such as [20] can be applied which solves such an ARE with 20k dimensions in seconds. In this paper, we use Matlab ARE solver (*care*) to find the solution of ARE.

2.4 PMF, PPCA, and Bayesian PCA

Here, we giv a review of PMF [25], Probabilistic PCA (PPCA) [30], and Bayesian PCA (BPCA) [4], to illustrate the similarity and differences between the existing ideas and our approach. Table 1 provides a summary of the algorithms. A related discussion appears in [19]. All these models focus on an (partially) observed data matrix $X \in \mathbb{R}^{N \times M}$. Given latent factors $U \in \mathbb{R}^{N \times D}$ and $V \in \mathbb{R}^{M \times D}$, the rows of X are assumed to be generated according to $\mathbf{x}_{:m} = U\mathbf{v}_m^T + \epsilon$, where $\epsilon \in \mathbb{R}^N$. The different models vary depending on how they handle distributions or estimates of the latent factors U, V. Without loss of generality, for all the analysis through the paper, we are considering a fat matrix X where M > N.

PMF and BPMF: In PMF [25], one assumes independent Gaussian priors for all latent vectors \mathbf{u}_n and \mathbf{v}_m , i.e., $\mathbf{u}_n \sim \mathcal{N}(0, \sigma_u^2 \mathbb{I}), [n]_1^N$ and $\mathbf{v}_m \sim \mathcal{N}(0, \sigma_v^2 \mathbb{I}), [m]_1^M$. Then, one obtains the following posterior over (U, V)

$$p\left(U, V|X, \sigma^2, \sigma_u^2, \sigma_v^2\right) = \prod_{n,m} [\mathcal{N}(x_{nm} | \langle \mathbf{u}_n, \mathbf{v}_m \rangle, \sigma^2)]^{\delta_{nm}} \prod_n \mathcal{N}(\mathbf{u}_n | 0, \sigma_u^2 \mathbb{I}) \prod_m \mathcal{N}(\mathbf{v}_{:m} | 0, \sigma_v^2 \mathbb{I}) , \qquad (8)$$

where $\delta_{nm} = 0$ if x_{nm} is missing. PMF obtains point estimates (\hat{U}, \hat{V}) by maximizing the posterior (MAP), based on alternating optimization over U and V [25].

Bayesian PMF (BPMF) [26] considers independent Gaussian priors over latent factors with full covariance matrices, i.e., $\mathbf{u}_n \sim \mathcal{N}(0, \Sigma_u), [n]_1^N$ and $\mathbf{v}_m \sim \mathcal{N}(0, \Sigma_v), [m]_1^M$. Inference is done using Gibbs sampling to approximate the posterior P(U, V|X). At each iteration, U is sampled from the conditional probability of p(U|V, X), followed by sampling V from p(V|U, X) using the updated matrix U at the current iteration.

Probabilistic PCA: In PPCA [30], one assumes independent Gaussian prior over \mathbf{u}_n , i.e., $\mathbf{u}_n \sim \mathcal{N}(0, \sigma_u^2 \mathbb{I})$, but V is treated as a parameter to be estimated. In particular, in PPCA, V is chosen so as to maximize the marginalized likelihood of X given by

$$p(X|V) = \int_{U} p(X|U,V)p(U)dU = \prod_{n=1}^{N} \mathcal{N}(\mathbf{x}_{n}|0,\sigma_{u}^{2}VV^{T} + \sigma^{2}\mathbb{I}).$$
(9)

Interestingly, as shown in [30], the estimate \hat{V} can be obtained in closed form. For such a fixed \hat{V} , the posterior distribution over $U|X, \hat{V}$ can be obtained as:

$$p(U|X,\hat{V}) = \frac{p(X|U,\hat{V})p(U)}{p(X|\hat{V})} = \prod_{n=1}^{N} \mathcal{N}\left(\mathbf{u}_{n}|\Gamma^{-1}\hat{V}^{T}\mathbf{x}_{n},\sigma^{-2}\Gamma\right),$$
(10)

where $\Gamma = \hat{V}^T \hat{V} + \sigma_u^{-2} \sigma^{-2} \mathbb{I}$. Note that the posterior of the latent factor U in (10) depends on both X and \hat{V} . For applications of PPCA in visualization, embedding, and data compression, any point x_n in the data space can be

Table 1: Summary of low rank matrix factorization algorithms illustrated as the handled distribution where (.) is the inference procedure. CF denotes Closed Form. MCMC alternately sample both U and V from a Markov chain with the joint posterior p(U, V|X). CMC only samples the smaller U matrix directly from p(U|X).

Algorithm	Inference of U	Inference of V		
PPCA [30]	$p(U X, \hat{V})$ (CF)	Point Est. \hat{V} (ML)		
BPCA [4]	p(U, V X) (Approx.)	p(U, V X) (Approx.)		
PMF [25]	Point Est. (MAP)	Point Est. (MAP)		
BPMF [26]	p(U, V X) (MCMC)	p(U, V X) (MCMC)		
CMC-PMF (ours)	p(U X) (CMC)	p(V X) (CMC)		

summarized by its posterior mean $E[\mathbf{u}_n | \mathbf{x}_n, \hat{V}]$ and covariance $Cov(\mathbf{u}_n | \hat{V})$ in the latent space.

Bayesian PCA: In Bayesian PCA [4], one assumes independent Gaussian priors for all latent vectors \mathbf{u}_n and \mathbf{v}_m , i.e., $\mathbf{u}_n \sim \mathcal{N}(0, \sigma_u^2 \mathbb{I})$ and $\mathbf{v}_m \sim \mathcal{N}(0, \sigma_v^2 \mathbb{I})$, $[m]_1^M$. Bayesian posterior inference by Bayes rule considers p(U, V|X) = p(X|U, V)p(U)p(V)/p(X), which includes the intractable partition function

$$p(X) = \int_{U} \int_{V} p(X|U, V) p(U) p(V) dU dV.$$
(11)

The literature has considered approximate inference methods, such as variational inference [5], gradient descent optimization [19], MCMC [26], or Laplace approximation [4, 23].

While PPCA and Bayesian PCA were originally considered in the context of embedding and dimensionality reduction, PMF and BPMF have been widely used in the context of matrix completion where the observed matrix X has many missing entries. Nevertheless, as seen from the above exposition, the structure of the models are closely related (also see [19, 18]).

3 *MGIG* Properties and Sampling

Some properties of the MGIG distribution and its connection with Wishart distribution has been studied in [10, 27, 28]. However, to best of our knowledge, it is not yet known if the distribution is unimodal and how to obtain the mode of MGIG. In the following Lemma we show that the MGIG distribution is unimodal.

Lemma 4 Consider the MGIG distribution $MGIG_N(\Lambda|\Psi, \Phi, \nu)$. The mode of MGIG distribution is the solution of the following Algebraic Riccati Equation (ARE)

$$-2\alpha\Lambda + \Lambda\Phi\Lambda - \Psi = 0, \tag{12}$$

where $\alpha = (\nu - \frac{N+1}{2})$. ARE in (12) has a unique positive definite solution, thus the MGIG distribution is a unimodal distribution.

Proof: The log-density of $\mathcal{MGIG}_N(\Lambda|\Psi, \Phi, \nu)$ is

$$\log f(\Lambda) = \alpha \log |\Lambda| - \frac{1}{2} \operatorname{Tr}(\Psi \Lambda^{-1} + \Phi \Lambda) + C,$$
(13)

where $\alpha = (\nu - \frac{N+1}{2})$, and *C* is a constant which does not depend on Λ . The mode of \mathcal{MGIG}_N is obtained by setting derivative of (13) to zero. The derivative is a quadratic matrix equation as follows

$$\nabla f(\Lambda) = -2\alpha\Lambda + \Lambda\Phi\Lambda - \Psi = 0. \tag{14}$$

Note that (14) is a special case of ARE (5). The associated Hamiltonian matrix for (14) is $H = \begin{bmatrix} -\alpha \mathbb{I}_N & \Phi \\ \Psi & \alpha \mathbb{I}_N \end{bmatrix}$. Recall that ARE has a unique positive definite solution if and only if the associated Hamiltonian matrix H has no imaginary eigenvalues (Section 5.6.3 of [7]). Thus, to show the unimodality of \mathcal{MGIG} , it is enough to show that the corresponding characteristic polynomial $|H - \lambda \mathbb{I}_{2N}| = 0$ has no imaginary solution.

$$|H - \lambda \mathbb{I}_{2N}| = \begin{vmatrix} -(\alpha + \lambda)\mathbb{I}_N & \Phi \\ \Psi & (\alpha - \lambda)\mathbb{I}_N \end{vmatrix}$$

$$= |-(\alpha + \lambda)\mathbb{I}_{N}| |(\alpha - \lambda)\mathbb{I}_{N} + (\alpha + \lambda)^{-1}\Psi\Phi|$$

$$= |(\alpha - \lambda)\mathbb{I}_{N}| |-(\alpha + \lambda)\mathbb{I}_{N} - (\alpha - \lambda)^{-1}\Phi\Psi|$$

$$= \prod_{i=1}^{N} \{-(\alpha^{2} - \lambda^{2}) - \tilde{\lambda}_{i}\} = 0,$$
(15)

which yields to $\lambda^2 = \tilde{\lambda}_i + \alpha^2$ where $\tilde{\lambda}_i$ is the *i*th eigenvalue of $\Phi \Psi$. Note $\tilde{\lambda}_i > 0$ since Φ and Ψ are positive definite and product of two positive definite matrix has positive eigenvalue. As a result, (15) has no imaginary solution and H does not have any imaginary eigenvalue. As a result, ARE in (14) has a unique positive definite solution. This completes the proof.

Importance Sampling for \mathcal{MGIG} : Since \mathcal{MGIG} is a unimodal distribution, we propose an efficient importance sampling procedure for \mathcal{MGIG} by mode matching. We select a proposal distribution over space of positive definite matrices by matching the proposal's mode to the mode of \mathcal{MGIG} (mode matching) which aligns the proposal and \mathcal{MGIG} shapes. Mode matching is a good choice of the proposal as the proposal q(x) is large in a region where the target distribution \mathcal{MGIG} is large leading to a good estimate of the expectations $\mathbb{E}_{\Lambda \sim \mathcal{MGIG}}[\Lambda]$ or $\mathbb{E}_{\Lambda \sim \mathcal{MGIG}}[\Lambda^{-1}]$. An example of such proposal distribution is Inverse Wishart or Wishart distribution.

Let Λ^* be the mode of $\mathcal{MGIG}_N(\Lambda|\Psi, \Phi, \nu)$ which can be found by solving the ARE (14). The mode of Inverse Wishart $\mathcal{W}_N(\Lambda|\Sigma, \rho)$ distribution is $\Sigma^* = (\rho - N - 1)\Sigma$. To match the mode of $\mathcal{W}_N(\Lambda|\Sigma, \rho)$ with that of $\mathcal{MGIG}_N(\Lambda|\Psi, \Phi, \nu)$, we choose the scale parameter Σ of the Wishart distribution by setting $\Sigma^* = \Lambda^*$. In particular,

$$\Sigma^* = \Lambda^* = (\rho - N - 1)\Sigma \quad \Rightarrow \quad \Sigma = \frac{\Lambda^*}{\rho - N - 1}.$$
(16)

Thus, we suggest using $\mathcal{W}_N(\frac{\Lambda^*}{\rho-N-1},\rho)$ as the proposal distribution. At each iteration, we draw a sample $\Lambda_i \sim \mathcal{W}_N(\frac{\Lambda^*}{\rho-N-1},\rho)$, and calculate the importance weight as $w(\Lambda_i) = \frac{\mathcal{MGIG}_N(\Lambda_i|\Psi,\Phi,\nu)}{\mathcal{W}_N(\Lambda_i|\Sigma,\rho)}$. More specifically, the density of Wishart distribution is

$$q(\Lambda) = \frac{q^*(\Lambda)}{Z_q}, \quad \text{where} \quad q^*(\Lambda) = |\Lambda|^{\frac{\rho - N - 1}{2}} \exp\{-\frac{1}{2}\operatorname{Tr}(\Sigma^{-1}\Lambda)\}.$$
(17)

Then, the importance weight can be calculated as

$$w(\Lambda_i) = \frac{|\Lambda_i|^{\nu - (N+1)/2} \exp\{-\frac{1}{2} \operatorname{Tr}(\Psi \Lambda_i^{-1} + \Phi \Lambda_i)\}}{|\Lambda_i|^{\frac{\rho - N - 1}{2}} \exp\{-\frac{1}{2} \operatorname{Tr}(\Sigma^{-1} \Lambda_i)\}}$$
(18)

$$= |\Lambda_i|^{\nu - \frac{\rho}{2}} \exp\left\{-\frac{1}{2}\operatorname{Tr}\left(\Psi\Lambda_i^{-1} + [\Phi - \Sigma^{-1}]\Lambda_i\right)\right\}.$$
(19)

As a result, we can approximate the sample mean as

$$\mathbb{E}_{\Lambda \sim \mathcal{MGIG}}[f(\Lambda)] = \frac{\sum_{i=1}^{S} w(\Lambda_i) f(\Lambda_i)}{\sum_{j=1}^{S} w(\Lambda_j)}.$$
(20)

Note that the weight calculation requires to calculate the inverse and determinant of sampled matrix Λ_i . However, as illustrated in Algorithm 1, the random samples generator from W [29] returns the upper triangular matrix R where $\Lambda = R^T R$. Hence the inverse and determinant of Λ can be calculated efficiently from the inverse and diagonal of the triangular matrix R, respectively. Therefore, the cost of weight calculation is reduced to the cost of solving a linear system and upper triangular matrix production at each iteration.

A similar argument holds when the proposal distribution is an Inverse Wishart distribution. In particular, the mode of Inverse Wishart $\mathcal{IW}_N(\Sigma, \rho)$ distribution is $\frac{\Sigma}{\rho+N+1}$. Thus $\mathcal{IW}_N(\rho+N+1)\Lambda^*, \rho)$ is another suitable choice of the proposal distribution.

Figure 2 illustrates that the proposed importance sampling outperforms the one in [32, 33] for three examples of \mathcal{MGIG} . In particular, more than 90% of samples drawn from the proposal distribution T_2 in [32, 33] have zero weights leading to ESS = 40 (Figure 2 (c)). Whereas, our proposal distribution achieved ESS = 550 leading to a better approximation of the mean of \mathcal{MGIG} . Similar behavior is observed with several different choices of parameters for the \mathcal{MGIG} .

Algorithm 1 Random Generator of $W_N(\Lambda | \Sigma, \rho, L)$ [29]

1: Note $L^T L = \Sigma$ is the Cholesky factorization of Σ 2: $P_{ii} \sim \sqrt{\chi^2(\rho - (i - 1))}$ for all $i = 1 \cdots N$. 3: $P_{ij} \sim \mathcal{N}(0, 1)$ for i < j. 4: R = PL. 5: Return $\Lambda = R^T R$. 6: Return $\Lambda^{-1} = R^{-1} R^{-1}^T$. 7: Return $|\Lambda| = [\prod_{i=1}^N R_{ii}]^2$.

4 Connection of *MGIG* and Bayesian PCA

In this section, we illustrate that the mapping matrix V in Bayesian PCA can be marginalized or 'collapsed' yielding a Matrix Generalized Inverse Gaussian (MGIG) [3, 10] posterior distribution over the latent matrix U denoting as the marginalized posterior distribution. Then, we explain the derivation of the marginalized posterior for data with missing values, followed by a collapsed Monte Carlo Inference for PMF.

4.1 Closed form Posterior Distribution in Bayesian PCA

The key challenge in models such as Bayesian PCA or Bayesian PMF is that joint marginalization over both latent factors U, V is intractable. Probabilistic PCA gets around the problem by considering one of the variables, say V, to be a constant. In this section, we show that one can marginalize or 'collapse' one of the latent factors, say V, and obtain the marginalized posterior P(U|X) over the other variable denoted. In fact, we obtain the posterior with respect to the covariance structure $\Lambda_u = \beta_u \mathbb{I} + UU^T$, for a suitable constant β_u , which is sufficient to do Bayesian inference on new test points x_{test} .

We start with an outline of the analysis. Note that

$$p(U|X) \propto p(U)P(X|U) = p(U) \int_{V} P(X|U,V)p(V)dV , \qquad (21)$$

and, based on the posterior over U, one can obtain the probability on a new point as

$$p(x_{\text{test}}|X) = \int_{U} p(x_{\text{test}}|U)p(U|X)dU.$$
(22)

Next, we show that the posterior over U as in (21), rather the distribution over $\Lambda_u = \beta_u \mathbb{I} + UU^T$, can be derived analytically in *closed form*. The distribution is the Matrix Generalized Inverse Gaussian (\mathcal{MGIG}) distribution.

Now, similar to (9), marginalizing V gives

$$p(X | U) = \int_{V} p(X|U, V)p(V)dV$$
$$= \prod_{m=1}^{M} \int_{\mathbf{v}_{m}} \mathcal{N}\left(\mathbf{x}_{:m} | U\mathbf{v}_{m}^{T}, \sigma^{2}\mathbb{I}\right) \mathcal{N}\left(\mathbf{v}_{m} | 0, \sigma_{v}^{2}\mathbb{I}\right) \, \mathrm{d}\mathbf{v}_{n}$$
$$= \prod_{m=1}^{M} \mathcal{N}\left(\mathbf{x}_{:m} | 0, \sigma_{v}^{2}\Lambda_{u}\right),$$

where $\Lambda_u = \beta_v \mathbb{I} + UU^T$ and $\beta_v = \frac{\sigma^2}{\sigma_v^2}$. Then, the marginalized posterior of U is calculated as

$$p(U \mid X) \propto p(X \mid U) p(U) \propto |\Lambda_u|^{-M/2} \exp\left\{-\frac{1}{2\sigma_v^2} \sum_{m=1}^M \mathbf{x}_{:m}^T \Lambda_u^{-1} \mathbf{x}_{:m}\right\}$$
$$\times \exp\left\{-\frac{1}{2\sigma_u^2} \operatorname{Tr}(UU^T + \beta_u \mathbb{I} - \beta_u \mathbb{I})\right\}$$

 $\triangleright P$: upper triangular

$$= |\Lambda_{u}|^{-M/2} \exp\left\{\frac{-\operatorname{Tr}\left(\Lambda_{u}^{-1}\sum_{m=1}^{M}\mathbf{x}_{:m}\mathbf{x}_{:m}^{T}\right)}{2\sigma_{v}^{2}}\right\}$$

$$\times \exp\left\{\frac{-\operatorname{Tr}(\Lambda_{u})}{2\sigma_{u}^{2}}\right\} \times \exp\left\{\frac{\operatorname{Tr}(\beta_{u}\mathbb{I})}{2\sigma_{u}^{2}}\right\}$$

$$= |\Lambda_{u}|^{-M/2} \exp\left\{\operatorname{Tr}\left(-\frac{1}{2}\Lambda_{u}^{-1}\Psi_{u}-\frac{1}{2}\Lambda_{u}\Phi_{u}\right)\right\}$$
(23)

(24)

 $\sim \mathcal{MGIG}(\Lambda_u | \Psi_u, \Phi_u, \nu_u),$ where $\Psi_u = \frac{1}{\sigma_v^2} X X^T$, $\Phi_u = \frac{1}{\sigma_u^2} \mathbb{I}$, and $\nu_u = \frac{N-M+1}{2}$.

Therefore, by marginalizing or collapsing V, the posterior over $\Lambda_u = \beta_v \mathbb{I} + UU^T$ corresponding to the latent matrix U can be characterized exactly with a \mathcal{MGIG} distribution with parameters depending only on X. Note that this is in sharp contrast with (10) for PPCA, where the posterior covariance of \mathbf{u}_n is $\sigma^{-2}\Gamma$ which in turn depends on the point estimate for \hat{V} .

4.2 Posterior Distribution with Missing Data

In this section, we consider the matrix completion setting, when the observed matrix X has missing values. In presence of missing values, the likelihood of the observed sub-vector in any column of X is given as

$$p\left(\mathbf{x}_{n_m,m} \mid U, V\right) = \mathcal{N}\left(\mathbf{x}_{n_m,m} \mid \tilde{U}_m \mathbf{v}_m^T, \sigma^2 \mathbb{I}\right).$$
(25)

where n_m is a vector of size \tilde{N}_m containing indices of non-missing entries in column m of X, and \tilde{U}_m is a submatrix of U with size of $\tilde{N}_m \times D$ where each row correspond to a non-missing entry in the m^{th} column of X. The marginalized likelihood (25) can be written as

$$X|U) = \prod_{m=1}^{M} \mathcal{N}\left(\mathbf{x}_{n_m,m} \,|\, 0, \, \sigma_v^2 \Lambda_{un}\right), \tag{26}$$

where $\Lambda_{un} = \beta_v \mathbb{I} + \tilde{U}_n \tilde{U}_n^T$ and $\beta_v = \frac{\sigma^2}{\sigma_v^2}$. The marginalized posterior is given by

$$p(U \mid X) \propto \exp\left\{-\frac{1}{2\sigma_u^2}\operatorname{Tr}(UU^T)\right\}$$

$$\leq |\Lambda_{un}|^{-M/2} \exp\left\{-\frac{1}{2}\mathbf{x}_{n_m,m}^T \Lambda_{un}^{-1} \mathbf{x}_{n_m,m}\right\}.$$

$$(27)$$

As shown in (27), in presence of missing values, the posterior cannot be factorized as in (23) because each column $\mathbf{x}_{:m}$ contributes to different blocks Λ_{un} of Λ .

We propose to address the missing value issue by gap-filling. In particular, if one can obtain a good estimate of the covariance structure in X, so that $\Psi_u = \frac{1}{\sigma_v^2} X X^T$ in (24) can be approximated well, one can use the \mathcal{MGIG} posterior to do approximate inference. We consider two simple approaches to approximate the covariance structure of X: (i) by zero-padding the missing value matrix X (assuming E[X] = 0 or centering the data in practice), and estimating the covariance structure based on the zero-padded matrix, and (ii) by using a suitable matrix completion method, such as PMF, to get point estimates of the missing entries in X, and estimating the covariance structure based on the completed matrix. We experiment with both approaches in Section 5, and the zero-padded version seems to work quite well.

4.3 Collapsed Monte Carlo Inference for PMF

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Given that $\Lambda_u \sim \mathcal{MGIG}_N$, we predict the missing values as follows. Let $\mathbf{x} = [\mathbf{x}^o, \mathbf{x}^*] \sim \mathcal{N}(0, \Lambda)$, where $\mathbf{x}^o \in \mathbb{R}^p$ is the observed partition of $\mathbf{x} \in \mathbb{R}^N$ and $\mathbf{x}^* \in \mathbb{R}^{N-p}$ is missing. Accordingly, partition Λ as

$$\begin{array}{ccc}
p & N-p \\
\Lambda_{u} = \begin{pmatrix} \Lambda_{oo} & \Lambda_{o*} \\
\Lambda_{*o} & \Lambda_{**} \end{pmatrix} p \\
N-p
\end{array}$$
(28)

Algorithm 2 CMC Inference for PMF

1: Construct zero-padded matrix Z from $X \in \mathbb{R}^{N \times M}$. 2: Let $\Psi_u = \frac{ZZ^T}{\sigma_v^2}$, $\Phi_u = \frac{\mathbb{I}}{\sigma_u^2}$, and $\nu_u = \frac{N-M+1}{2}$. 3: Solve (14) to find mode Λ^* of $\mathcal{MGIG}(\Psi_u, \Phi_u, \nu_u)$. 4: Let $L^T L = \Lambda^*$ be the Cholesky factorization of Λ^* . 5: Let $\tilde{L} = \frac{L}{\sqrt{\rho - M - 1}}$. 6: for $t = 1 \cdots T$ do 7: Let $\Lambda^{(t)} \sim \mathcal{W}_N(\frac{\Lambda^*}{\rho - M - 1}, \rho, \tilde{L})$ 8: Let $w^t = \frac{\mathcal{MGIG}_N(\Lambda^{(t)}|\Psi_u, \Phi_u, \nu_u)}{\mathcal{W}_N(\Lambda^{(t)}|\frac{\Lambda^*}{\rho - M - 1}, \rho, \tilde{L})}$. 9: Let $\mu^t = \Lambda_{*o}^{(t)} \Lambda_{oo}^{(t)-1} \mathbf{x}^o$. 10: Let $\Sigma^t = \Lambda_{**}^{(t)} - \Lambda_{*oo}^{(t)} \Lambda_{oo}^{(t)-1} \Lambda_{o*}^{(t)}$. 11: Let $\bar{\mu} = \bar{\mu} + w^t \mu^t$. 12: Let $\bar{\Sigma} = \bar{\Sigma} + w^t \Sigma^t$. 13: $\tilde{\mu}^* = \frac{\bar{\Sigma}}{\sum_{t=1}^T w^t}$. 14: $\tilde{\Sigma}^* = \frac{\bar{\Sigma}}{\sum_{t=1}^T w^t}$. 15: Report the distribution of $\mathbf{x}^* \sim \mathcal{N}(\tilde{\mu}^*, \tilde{\Sigma}^*)$. 16: Set the point estimate of \mathbf{x}^* as μ^* .

▷ Algorithm 1

Then the conditional probability of \mathbf{x}^* given \mathbf{x}^o and Λ is

$$p(\mathbf{x}^* | \mathbf{x}^o, \Lambda) \sim \mathcal{N}(\mu^*, \Sigma^*),$$

$$\mu^* = \Lambda_{*o} \Lambda_{oo}^{-1} \mathbf{x}^o,$$

$$\Sigma^* = \Lambda_{**} - \Lambda_{*o} \Lambda_{oo}^{-1} \Lambda_{*o}.$$
(29)

where $\mathbf{y} = \Lambda_{*o}\Lambda_{oo}^{-1}$ is the solution of the linear system $\Lambda_{oo}\mathbf{y} = \Lambda_{*o}^T$ and can be calculated efficiently. Since sampling from \mathcal{MGIG} is difficult, we propose to use importance sampling to infer the missing values as

$$p(x_n^*|x_n^o) = \mathbb{E}_{\Lambda \sim \mathcal{MGIG}} \left[p(x_n^*|x_n^o, \Lambda) \right] = \mathbb{E}_{\Lambda \sim q} \left[\frac{p(x_n^*|x_n^o, \Lambda) \mathcal{MGIG}_N(\Lambda | \Psi_u, \Phi_u, \nu_u)}{q(\Lambda)} \right],$$

where q is the proposal distribution as discussed above and sampling $\Lambda^{(t)}$ from q yields to the estimate of

$$\tilde{\mu}^{*} = \frac{\sum_{t=1}^{T} \Lambda_{*o}^{(t)} \Lambda_{oo}^{(t)} \mathbf{x}^{o} w(\Lambda^{(t)})}{\sum_{t=1}^{t} w(\Lambda^{(t)})}$$

$$\tilde{\Sigma}^{*} = \frac{\sum_{t=1}^{T} [\Lambda_{**}^{(t)} - \Lambda_{*o}^{(t)} \Lambda_{oo}^{(t)} \mathbf{\Lambda}_{*o}^{(t)}] w(\Lambda^{(t)})}{\sum_{t=1}^{t} w(\Lambda^{(t)})}.$$
(30)

Algorithm 2 in appendix illustrates the summary of the collapsed Monte Carlo (CMC) inference for predicting the missing values. A practical approximation to avoid the calculations in Lines 9-12 of Algorithm 2 at each iteration is to simply estimate the mean of the posterior $\bar{\Lambda} = \frac{\sum_{t=1}^{T} \Lambda^{(t)} w^t}{\sum_{t=1}^{T} w^t}$ with samples drawn from the proposal distribution (line 6), then do the inference based on $\bar{\Lambda}$. As it is shown in Section 5, if the degrees of freedom ν_u is small, the mode is close to the mean and the approximation using $\bar{\Lambda}$ works well.

5 Experimental Results

We compared the performance of MCMC and CMC on both log loss and running times.

5.1 Datasets

We evaluated the models on 4 datasets: 1) **SNP**: single nucleotide polymorphism (SNP) is important for identifying gene-disease associations where the data usually has 5 to 20% of genotypes missing [8]. We used phased SNP dataset for chromosome 13 of the CEU population¹. We randomly dropped 20% of the entries. 2) **Gene Expression:** DNA microarrays provides measurement of thousands of genes under a certain experimental condition where suspicious values are usually regarded as missing values. Here we used gene expression dataset for Breast Cancer (BRCA)². We randomly dropped 20% of the entries. 3) **MovieLens:** we used MovieLens³ dataset with 1M rating represented as a fat matrix $X \in \mathbb{R}^{N \times M}$ where M = 3900 movies and N = 6040 users. 4) **Synthetic:** first the latent matrices U and V are generated by randomly choosing each $\{\mathbf{u}_n\}_{n=1}^N$ and $\{\mathbf{v}_m\}_{m=1}^M$ from $\mathcal{N}(0, \sigma_u^2 \mathbb{I})$ and $\mathcal{N}(0, \sigma_v^2 \mathbb{I})$, respectively. Then, matrix X is built by sampling each x_{nm} from $\mathcal{N}(\langle \mathbf{u}_n, \mathbf{v}_m \rangle, \sigma^2)$. The parameters are set to N = 100, M = 6000, $\sigma_u^2 = \sigma_v^2 = 0.05$, and $\sigma^2 = 0.01$. We dropped random entries using Bernoulli distributions with $\delta = 0.1, 0.2$.

5.2 Methodology

We compared CMC with MCMC inference for PMF. Gibbs sampling with diagonal covariance prior over the latent matrices is used for MCMC. For the model evaluation, average of log loss (LL) is reported over 5-fold cross-validation. LL measures how well a probabilistic model q predicts the test sample defined as $LL = -\frac{1}{T} \sum_{i=1}^{N} \sum_{j=1}^{M} \delta_{ij} \log q(x_{ij})$ where $q(x_{ij})$ is the inferred probability and T is the total number of observed values. A better model q assign higher probability $q(x_{ij})$ to observed test data, and have a smaller value of LL.

LL Percentile: For any posterior model q(x), a test data point x_{test} with low $q(x_{test})$ has large log loss, and high $q(x_{test})$ has low log loss. To comparatively evaluate the posteriors obtained from MCMC and CMC, we consider their log loss percentile plots. For any posterior, we sort all the test data points in ascending order of their log loss, and plot the mean log loss in 10 percentile batches. More specifically, the first batch corresponds to the top 10% of data points with the lowest log loss, the second batch corresponds to the top 20% of data points with the lowest log loss (including the first 10% percentile), and so on.

5.3 Results

We summarize the results from different aspects:

Log loss: CMC has a small log loss across all percentile batches, whereas log loss of MCMC increases exponentially (linear increase in the log scale) for percentile batches with higher log loss i.e., smaller predicting probability, (Figure 3). Thus, MCMC assigned extremely low probability to several test points as compared to CMC. Figure 4(a) illustrates that log loss of MCMC continues to decrease with growing sample size up to 2000 samples, implying that MCMC has not yet converged to the equilibrium distribution. Note that log loss of CMC with 200 samples (Figure 4(b)) is 10 times less than log loss of MCMC with 2000 samples. We also compared the results with the previous proposal [32, 33], and observed that for MovieLens the results are worse than our proposed result as they achieved Inf LL on the last batch. Effective number of samples: For the synthetic, SNP, and gene expression datasets, we generated 10,000 samples using MCMC. The burn-in period is set to 500 with a lag of 10 yielding to 1000 effective samples. For the MovieLens, we generated 5,000 samples using MCMC with the burn-in period of 1000 and a lag of 2 yielding to 2000 effective samples. We initialized the latent matrices U and V with the factors estimated by PMF, to help the convergence of MCMC. Sample size in CMC procedure is set to 1,000 for all datasets. Note that MCMC alternately sample both latent matrices U and V from a Markov chain and the quality of the posterior improves with increasing number of samples. For the proposed CMC procedure, the bigger matrix V is marginalized and only samples from the smaller U matrix is drawn directly from the true posterior distribution. Hence, CMC has considerably improved sample utilization. **Initialization:** As discussed in Section 4.2, in order to use the MGIG posterior for inference, the covariance structure of matrix X should be estimated. Here we evaluate two approaches to approximate the covariance structure of X: (i) by zero-padding the missing value matrix X, and (ii) by computing the point estimates of the missing entries in X with

¹http://hapmap.ncbi.nlm.nih.gov/downloads/phasing/

²http://cancergenome.nih.gov/

³www.movielens.umn.edu

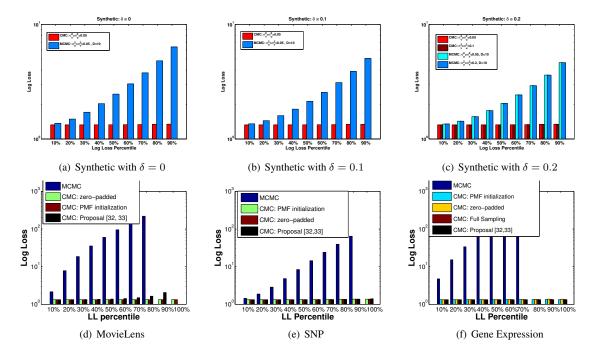


Figure 3: Log loss (LL) of CMC and MCMC for different log loss percentile on different datasets presented in the log scale (δ denotes the missing proportion). CMC consistently achieves lower LL compared to MCMC. LL of MCMC increases exponentially (linearly in log scale) by adding data points with higher log loss. Proposal in [30,31] achieved infinity LL for MovieLens. Empty bar represents infinity LL (e.g. 90% and 100% percentile in (d)

PMF. CMC with zero-padded initialization has a similar log loss behavior as point estimate initialization with PMF (Figures 3 (d-f)).

Full sampler vs Mean sampler: Figure 3(f) shows the result of the full sampler (Algorithm 2), and the mean sampler (approximating the inference by estimating $\overline{\Lambda} = \mathbb{E}_{\Lambda \sim MGIG}[\Lambda]$ as discussed in Section 4.3) on gene expression data. Since the log losses are similar with both samplers, and the behavior is typical, we presented log loss results on the other datasets only based on the mean sampler, which is around 100 times faster.

Comparison of inferred posterior distributions: To emphasize the importance of choosing the right measure for comparison, e.g., log loss vs RMSE, we illustrate the inferred posterior distributions over several missing entries/ratings in MovieLens obtained from MCMC and CMC in Figure 5. Note that the scales for CMC (red) and MCMC (blue) are different. Overall, the posterior from CMC tends to be more conservative (not highly peaked), and obtains lower log loss across a range of test points. Interestingly, as shown in Figure 5(a), MCMC can make mistakes with high confidence, i.e., predicts 5 stars with a peaked posterior whereas the true rating is 3 stars. Such troublesome behavior is correctly assessed with log loss, but not by RMSE since it does not consider the confidence in the prediction. As shown in Figure 5(d), for some test points, both MCMC and CMC inferred similar posterior distributions with a bias difference where the mean of CMC is closer to the true value.

Time Comparison: We have compared running time in both serial and in parallel over 1000 steps yielding to 200 and 1000 samples for MCMC and CMC, respectively. We implement the algorithms in Matlab. The computation time is estimated on a PC with a 3.40 GHz Quad core CPU and 16.0G memory. The average run time results are reported in Table 2. For Synthetic, SNP, and gene expression datasets, MCMC converges very slowly. For MovieLens dataset, the running time of both are very close but note that MCMC requires more number of samples for convergence than CMC (Figure 4).

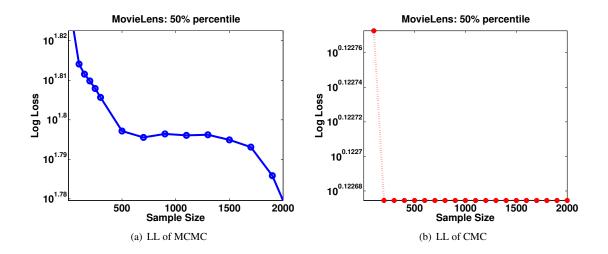


Figure 4: LL of CMC and MCMC for different sample size of MovieLens data in the log scale. LL of both CMC and MCMC is decreasing by adding more samples. LL of MCMC is in magnitude 10 times more than CMC.

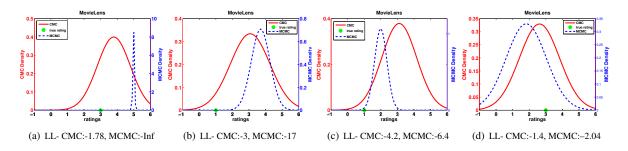


Figure 5: Density of CMC and MCMC for several data input on MovieLens data. CMC provide distributions with lower LL compared to MCMC e.g. in (a) LL of MCMC is -Inf whereas LL of CMC is -1.78.

6 Conclusion

We studied the \mathcal{MGIG} distribution and provided certain key properties with a novel sampling technique from the distribution and its connection with the latent factor models such as PMF or BPCA. With showing that the \mathcal{MGIG} distribution is unimodal and the mode can be obtained by solving an ARE, we proposed an new importance sampling approach to infer the mean of \mathcal{MGIG} . The new sampler, unlike the existing sampler [32, 33], chooses the proposal distribution to have the same mode as the \mathcal{MGIG} . This characterization leads to a far more effective sampler than [32, 33] since the new sampler align the shape of the proposal to the target distribution. Although, the \mathcal{MGIG} distribution has been recently applied to Bayesian models as the prior for the covariance matrix, here, we introduced a novel application of the \mathcal{MGIG} in PMF or BPCA. We showed that the posterior distribution in PMF or BPCA with Gaussian priors, has the \mathcal{MGIG} distribution. This illustration, yields to a new CMC inference algorithm for PMF.

Acknowledgment

The research was supported by NSF grants IIS-1447566, IIS-1447574, IIS-1422557, CCF-1451986, CNS- 1314560, IIS-0953274, IIS-1029711, NASA grant NNX12AQ39A, and gifts from Adobe, IBM, and Yahoo. F. F. acknowledges the support of DDF (2015-2016) from the University of Minnesota.

Table 2: Time Comparison of CMC and MCMC on different datasets. At each step of MCMC, rows of U and V can be sampled in parallel denoted by MCMC parallel. The running time is reported over 1000 steps for both methods. Note that the effective number of samples of MCMC is less than 1000 and more steps is required to obtain enough samples. The number of iterations for convergence of CMC is much less than 1000 (Figure 4).

Dataset	Size	MCMC (1000 steps, 200 samples)		CMC (1000 steps, 1000 samples)	
		Serial	Parallel	Serial	Parallel
Synthetic	100× 6,000	728s	404s	6s	48
SNP	120×104,868	12,862s	5,859s	75s	22s
Gene Expression	591× 17,814	3,478s	2,278s	140s	90s
MovieLens	3,233× 6,040	2,350s	2,100s	5,387s	2,058s

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