

Sparsity-Preserving Difference of Positive Semidefinite Matrix Representation of Indefinite Matrices

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Abstract

We consider the problem of writing an arbitrary symmetric matrix as the difference of two positive semidefinite matrices. We start with simple ideas such as eigenvalue decomposition. Then, we develop a simple adaptation of the Cholesky that returns a difference-of-Cholesky representation of indefinite matrices. Heuristics that promote sparsity can be applied directly to this modification.

1 Introduction

Let $A \in \mathbf{S}^n$ be a real-valued symmetric matrix. It is always possible to write A as the difference $P_+ - P_-$ of two positive semidefinite matrices P_+ and P_- . Take, for example, $P_+ = A + tI$ and $P_- = tI$ for large enough $t > 0$. With this representation, one can rewrite an indefinite quadratic form $x^T A x$ as a difference-of-convex expression $x^T P_+ x - x^T P_- x$, which can be used in various algorithms for convex-concave programming [LB14, SDGB16]. In this note, we explore a number of different such representations and their properties.

1.1 Desired properties

In addition to the running time of the algorithm, there are several other properties that are important in typical applications.

Time complexity. Clearly, we want the algorithm for computing the representation to be fast. Asymptotic performance is important, but in practice, even with the same asymptotic complexity, one method may outperform another depending on how sparsity is exploited.

Memory usage. Ideally, representing P_+ and P_- should not cost much more than representing P itself. In the worst case, both P_+ and P_- are dense, and $2n^2$ floating point numbers must be stored. It is possible to save more space by exploiting the sparsity pattern of A , or representing the matrices P_+ and P_- implicitly, in a memory-efficient form.

Numerical stability. Due to the round-off errors of floating point numbers, the resulting representation may be numerically inaccurate. This can be particularly problematic when P_+ and P_- are stored implicitly (*e.g.*, via Cholesky factorization), rather than explicitly. Singular or badly conditioned matrices can often introduce big round-off errors, and we want the algorithm to be robust in such settings.

Additional curvature. In order for convex-concave procedure to perform better, we want P_+ and P_- to have as little “distortion” as possible, *i.e.*, we want the additional curvature measured by the nuclear norm

$$\|P_+\|_* + \|P_-\|_* - \|A\|_*$$

to be small. Since P_+ and P_- are required to be positive semidefinite, this quantity is equal to

$$\mathbf{Tr} P_+ + \mathbf{Tr} P_- - \|A\|_*.$$

2 Simple representations

Any indefinite matrix can be made positive semidefinite by adding a large enough multiple of the identity. Let $\lambda_{\min} < 0$ be the smallest eigenvalue of A . Then, for any $t \geq |\lambda_{\min}|$,

$$P_+ = A + tI, \quad P_- = tI$$

is a pair of positive semidefinite matrices whose difference is A . If the magnitude of the maximum eigenvalue $\lambda_{\max} > 0$ is smaller than that of λ_{\min} , then an alternative representation is also possible:

$$P_+ = tI, \quad P_- = tI - A,$$

where $t \geq \lambda_{\max}$. This representation is relatively easy to compute as it only requires a lower bound on $|\lambda_{\min}|$ or $|\lambda_{\max}|$. It also has a property that the sparsity of A is preserved as much as possible, in that no new off-diagonal nonzero entries are introduced in P_+ or P_- . Its disadvantage is the additional curvature it introduces:

$$\|P_+\|_* + \|P_-\|_* - \|A\|_* = 2t.$$

Another simple representation is based on the full eigenvalue decomposition of A . This representation preserves the norm of A and thus introduces no additional curvature. Let $A = Q\Lambda Q^T$ be the eigenvalue decomposition of A , where $\Lambda = \mathbf{diag}(\lambda_1, \dots, \lambda_n)$ is the eigenvalue matrix with

$$\lambda_1 \geq \dots \geq \lambda_k \geq 0 > \lambda_{k+1} \geq \dots \geq \lambda_n.$$

Then, Λ can be written as $\Lambda = \Lambda_+ - \Lambda_-$, where

$$\Lambda_+ = \mathbf{diag}(\lambda_1, \dots, \lambda_k, 0, \dots, 0), \quad \Lambda_- = \mathbf{diag}(0, \dots, 0, -\lambda_{k+1}, \dots, -\lambda_n).$$

Setting

$$P_+ = Q\Lambda_+Q^T, \quad P_- = Q\Lambda_-Q^T$$

then gives a difference of positive semidefinite matrix representation of A . In general, the cost of explicitly computing this representation is very high, as it not only requires the full eigenvalue decomposition, but also destroys the sparsity of A even when it is very sparse.

3 Cholesky-like representations

When A is positive semidefinite, there exists a unique lower triangular matrix $L \in \mathbf{R}^{n \times n}$ that satisfies $A = LL^T$. This representation is known as the *Cholesky factorization* of A . In the simplest form, the Cholesky algorithm can be described as a simple recursive algorithm. Formally, let $\mathbf{chol} : \mathbf{S}^n \rightarrow \mathbf{R}^{n \times n}$ that computes, given $A \in \mathbf{S}^n$, a lower triangular matrix $L = \mathbf{chol}(A)$ that satisfies $A = LL^T$. If A is 1-by-1, then L is simply given by $\sqrt{A_{11}}$. If A has two or more rows, let

$$A = \begin{bmatrix} a & v^T \\ v & M \end{bmatrix}$$

with $a \geq 0$, $v \in \mathbf{R}^{n-1}$, $M \in \mathbf{R}^{(n-1) \times (n-1)}$. If $a = 0$ is zero, then v must also equal zero, for otherwise A is indefinite. In this case, the Cholesky factorization is given by

$$\mathbf{chol} \left(\begin{bmatrix} 0 & 0 \\ 0 & M \end{bmatrix} \right) = \begin{bmatrix} 0 & \\ 0 & \mathbf{chol}(M) \end{bmatrix}.$$

If $a > 0$, the recursion is:

$$\mathbf{chol} \left(\begin{bmatrix} a & v^T \\ v & M \end{bmatrix} \right) = \begin{bmatrix} \sqrt{a} & \\ v/\sqrt{a} & \mathbf{chol}(M - vv^T/a) \end{bmatrix}.$$

The cost of computing a dense Cholesky factorization is $(1/3)n^3$ flops. In case A is sparse, various pivoting heuristics can be used to exploit the sparsity structure and speed up the computation.

Cholesky factorization does not exist when A has both positive and negative eigenvalues. However, the LDL decomposition, which is a close variant of the Cholesky factorization, exists for all symmetric matrices. It also has an additional computational advantage since there is no need to take square roots. The idea is to write A as LDL^T , where $L \in \mathbf{R}^{n \times n}$ is lower triangular with ones on the main diagonal, and $D \in \mathbf{R}^{n \times n}$ is block diagonal consisting of 1-by-1 or 2-by-2 blocks. In general, some additional computation is required to transform the LDL decomposition into the difference of two positive semidefinite matrices due to the 2-by-2 blocks in D . When D is diagonal (*i.e.*, no 2-by-2 blocks), then one can easily separate out the negative entries of D and the corresponding columns in L to write A as

$$A = L_1D_1L_1^T - L_2D_2L_2^T,$$

where D_1 and D_2 are diagonal matrices consisting of nonnegative entries only.

4 Difference-of-Cholesky representation

In this section, we describe a simple modification $\mathbf{chol2} : \mathbf{S}^n \rightarrow \mathbf{R}^{n \times n} \times \mathbf{R}^{n \times n}$ of the Cholesky algorithm that computes, given $A \in \mathbf{S}^n$, a pair of lower triangular matrices L_1 and L_2 such that

$$A = L_1 L_1^T - L_2 L_2^T,$$

where $(L_1, L_2) = \mathbf{chol2}(A)$. Let $a \geq 0$, $v \in \mathbf{R}^{n-1}$, and $M \in \mathbf{S}^{n-1}$. Below is a simple recursion for computing $\mathbf{chol2}$ when $a > 0$ is large enough:

$$\begin{aligned} \mathbf{chol2} \left(\begin{bmatrix} a & v^T \\ v & M \end{bmatrix} \right) &= \left(\begin{bmatrix} \sqrt{a} & \\ v/\sqrt{a} & S \end{bmatrix}, \begin{bmatrix} 0 & \\ 0 & T \end{bmatrix} \right) \quad (S, T) = \mathbf{chol2}(M - (1/a)vv^T), \\ \mathbf{chol2} \left(\begin{bmatrix} -a & v^T \\ v & M \end{bmatrix} \right) &= \left(\begin{bmatrix} 0 & \\ 0 & S \end{bmatrix}, \begin{bmatrix} \sqrt{a} & \\ -v/\sqrt{a} & T \end{bmatrix} \right) \quad (S, T) = \mathbf{chol2}(M + (1/a)vv^T). \end{aligned}$$

In this form, the algorithm is no different from computing the LDL decomposition and separating out positive and negative entries in D (assuming the LDL decomposition exists with a diagonal D). In case a is too small so that dividing by \sqrt{a} would give big round-off errors, the following recursion can be used, for any value of $\delta > 0$. Notice that with this recursion, the algorithm can proceed even when $a = 0$.

$$\mathbf{chol2} \left(\begin{bmatrix} a & v^T \\ v & M \end{bmatrix} \right) = \left(\begin{bmatrix} \sqrt{\delta + a} & \\ v_1 & S \end{bmatrix}, \begin{bmatrix} \sqrt{\delta} & \\ v_2 & T \end{bmatrix} \right) \quad (S, T) = \mathbf{chol2}(M - v_1 v_1^T + v_2 v_2^T).$$

Here, v_1 and v_2 are any vectors satisfying $\sqrt{\delta + a} v_1 - \sqrt{\delta} v_2 = v$. This introduces an additional degree of freedom, as we can freely choose v_1 or v_2 . For example, we can let $v_1 = 0$ or $v_2 = 0$. This way, it is possible to trade off the number of nonzero elements in L_1 against L_2 , which is a property that is not readily available in other representations discussed above. When we choose $v_1 = 0$, the recursion becomes

$$\mathbf{chol2} \left(\begin{bmatrix} a & v^T \\ v & M \end{bmatrix} \right) = \left(\begin{bmatrix} \sqrt{\delta + a} & \\ 0 & S \end{bmatrix}, \begin{bmatrix} \sqrt{\delta} & \\ -v/\sqrt{\delta} & T \end{bmatrix} \right) \quad (S, T) = \mathbf{chol2}(M + (1/\delta)vv^T).$$

For completeness, we show the recursion in the case of $A_{11} \leq 0$.

$$\mathbf{chol2} \left(\begin{bmatrix} -a & v^T \\ v & M \end{bmatrix} \right) = \left(\begin{bmatrix} \sqrt{\delta} & \\ v_1 & S \end{bmatrix}, \begin{bmatrix} \sqrt{\delta + a} & \\ v_2 & T \end{bmatrix} \right) \quad (S, T) = \mathbf{chol2}(M - v_1 v_1^T + v_2 v_2^T),$$

where v_1 and v_2 are any vectors satisfying $\sqrt{\delta} v_1 - \sqrt{\delta + a} v_2 = v$.

It is simple to modify this algorithm to return a pair of LDL factorizations to avoid computing square roots. With the additional parameter $\delta > 0$, both factorizations become positive definite and thus there will not be any 2-by-2 diagonal block in the factorizations.

Since the method is very close to the original Cholesky algorithm, and thus most extensions and techniques applicable to Cholesky algorithm or LDL decomposition naturally apply to the difference-of-Cholesky method. One such example is pivoting heuristics for LDL decomposition for avoiding round-off errors or ill-conditioned matrices, and at the same time, preserving the sparsity of the intermediate matrices as much as possible.

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