# Sparse Cholesky decomposition (sksparse.cholmod)

New in version 0.1.

## Overview

This module provides efficient implementations of all the basic linear algebra operations for sparse, symmetric, positive-definite matrices (as, for instance, commonly arise in least squares problems).

Specifically, it exposes most of the capabilities of the CHOLMOD package, including:

- Computation of the Cholesky decomposition LL' = A or LDL' = A (with fill-reducing permutation) for both real and complex sparse matrices A, in any format supported by scipy.sparse. (However, CSC matrices will be most efficient.)
- A convenient and efficient interface for using this decomposition to solve problems of the form Ax = b.
- The ability to perform the costly fill-reduction analysis once, and then re-use it to efficiently decompose many matrices with the same pattern of non-zero entries.
- In-place 'update' and 'downdate' operations, for computing the Cholesky decomposition of a rank-k update of A and of product AA'. So, the result is the Cholesky decomposition of A + CC' (or AA' + CC'). The last case is useful when the columns of A become available incrementally (e.g., due to memory constraints), or when many matrices with similar but non-identical columns must be factored.
- Convenience functions for computing the (log) determinant of the matrix that has been factored.
- A convenience function for explicitly computing the inverse of the matrix that has been factored (though this is rarely useful).

# Quickstart

If A is a sparse, symmetric, positive-definite matrix, and b is a matrix or vector (either sparse or dense), then the following code solves the equation Ax = b:

```
from sksparse.cholmod import cholesky
factor = cholesky(A)
x = factor(b)
```

If we just want to compute its determinant:

```
factor = cholesky(A)
ld = factor.logdet()
```

(This returns the log of the determinant, rather than the determinant itself, to avoid issues with underflow/overflow. See logdet(), log().)

If you have a least-squares problem to solve, minimizing  $||Mx - b||^2$ , and M is a sparse matrix, the solution is  $x = (M'M)^{-1}M'b$ , which can be efficiently calculated as:

```
from sksparse.cholmod import cholesky_AAt
# Notice that CHOLMOD computes AA' and we want M'M, so we must set A = M'!
factor = cholesky_AAt(M.T)
x = factor(M.T * b)
```

However, you should be aware that for least squares problems, the Cholesky method is usually faster but somewhat less numerically stable than QR- or SVD-based techniques.

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# Top-level functions

All usage of this module starts by calling one of four functions, all of which return a **Factor** object, documented below.

Most users will want one of the cholesky functions, which perform a fill-reduction analysis and decomposition together:

sksparse.cholmod.cholesky(A, beta=0, mode="auto",  $ordering\_method="default"$ ,  $use\ long=None$ )

Computes the fill-reducing Cholesky decomposition of

$$A + \beta I$$

where A is a sparse, symmetric, positive-definite matrix, preferably in CSC format, and beta is any real scalar (usually 0 or 1). (And I denotes the identity matrix.)

Only the lower triangular part of A is used.

mode is passed to analyze().

ordering\_method is passed to analyze().

use long is passed to analyze().

**Returns:** A **Factor** object represented the decomposition.

sksparse.cholmod.cholesky\_AAt(A, beta=0, mode="auto",  $ordering\_method="default"$ ,  $use\ long=None$ )

Computes the fill-reducing Cholesky decomposition of

$$AA' + \beta I$$

where A is a sparse matrix, preferably in CSC format, and beta is any real scalar (usually 0 or 1). (And I denotes the identity matrix.)

Note that if you are solving a conventional least-squares problem, you will need to transpose your matrix before calling this function, and therefore it will be somewhat more efficient to construct your matrix in CSR format (so that its transpose will be in CSC format).

mode is passed to analyze AAt().

ordering method is passed to analyze\_AAt().

use\_long is passed to analyze\_AAt().

**Returns:** A **Factor** object represented the decomposition.

However, some users may want to break the fill-reduction analysis and actual decomposition into separate steps, and instead begin with one of the analyze functions, which perform only fill-reduction:

sksparse.cholmod.analyze(A, mode="auto",  $ordering\_method="default"$ ,  $use\ long=None$ )

Computes the optimal fill-reducing permutation for the symmetric matrix A, but does *not* factor it (i.e., it performs a "symbolic Cholesky decomposition"). This function ignores the actual contents of the matrix A. All it cares about are (1) which entries are non-zero, and (2) whether A has real or complex type.

**Parameters:** • A - The matrix to be analyzed.

mode - Specifies which algorithm should be used to (eventually) compute the Cholesky decomposition - one of "simplicial", "supernodal", or

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- "auto". See the CHOLMOD documentation for details on how "auto" chooses the algorithm to be used.
- ordering\_method Specifies which ordering algorithm should be used to (eventually) order the matrix A - one of "natural", "amd", "metis", "nesdis", "colamd", "default" and "best". "natural" means no permutation. See the CHOLMOD documentation for more details.
- **use\_long** Specifies if the long type (64 bit) or the int type (32 bit) should be used for the indices of the sparse matrices. If use long is None try to estimate if long type is needed.

#### **Returns:**

A Factor object representing the analysis. Many operations on this object will fail, because it does not yet hold a full decomposition. Use Factor.cholesky\_inplace() (or similar) to actually factor a matrix.

sksparse.cholmod.analyze AAt(A, mode="auto", ordering method="default", use long=None)

Computes the optimal fill-reducing permutation for the symmetric matrix AA', but does not factor it (i.e., it performs a "symbolic Cholesky decomposition"). This function ignores the actual contents of the matrix A. All it cares about are (1) which entries are non-zero, and (2) whether A has real or complex type.

- **Parameters: A** The matrix to be analyzed.
  - mode Specifies which algorithm should be used to (eventually) compute the Cholesky decomposition - one of "simplicial", "supernodal", or "auto". See the CHOLMOD documentation for details on how "auto" chooses the algorithm to be used.
  - ordering method Specifies which ordering algorithm should be used to (eventually) order the matrix A - one of "natural", "amd", "metis", "nesdis", "colamd", "default" and "best". "natural" means no permutation. See the CHOLMOD documentation for more details.
  - **use long** Specifies if the long type (64 bit) or the int type (32 bit) should be used for the indices of the sparse matrices. If use long is None try to estimate if long type is needed.

#### **Returns:**

A Factor object representing the analysis. Many operations on this object will fail, because it does not yet hold a full decomposition. Use Factor.cholesky\_AAt\_inplace() (or similar) to actually factor a matrix.

#### Note:

Even if you used cholesky() or cholesky AAt(), you can still call cholesky inplace() or cholesky\_AAt\_inplace() on the resulting Factor to quickly factor another matrix with the same non-zero pattern as your original matrix.

# Factor objects

class sksparse.cholmod.Factor

A Factor object represents the Cholesky decomposition of some matrix A (or AA'). Each **Factor** fixes:

- A specific fill-reducing permutation
- A choice of which Cholesky algorithm to use (see analyze())
- Whether we are currently working with real numbers or complex

Given a **Factor** object, you can:

- · Compute new Cholesky decompositions of matrices that have the same pattern of non-zeros
- · Perform 'updates' or 'downdates'

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- Access the various Cholesky factors
- · Solve equations involving those factors

## Factoring new matrices

## Factor.cholesky\_inplace(A, beta=0)

Updates this Factor so that it represents the Cholesky decomposition of  $A + \beta I$ , rather than whatever it contained before.

A must have the same pattern of non-zeros as the matrix used to create this factor originally.

#### Factor.cholesky\_AAt\_inplace(A, beta=0)

The same as cholesky\_inplace(), except it factors  $AA' + \beta I$  instead of  $A + \beta I$ .

## Factor.cholesky(A, beta=0)

The same as **cholesky\_inplace()** except that it first creates a copy of the current **Factor** and modifies the copy.

**Returns:** The new Factor object.

#### Factor.cholesky\_AAt(A, beta=0)

The same as **cholesky\_AAt\_inplace()** except that it first creates a copy of the current **Factor** and modifies the copy.

**Returns:** The new Factor object.

## **Updating/Downdating**

Factor.update\_inplace(C, subtract=False)

Incremental building of AA' decompositions.

Updates this factor so that instead of representing the decomposition of A (AA'), it computes the decomposition of A+CC' (AA'+CC') for subtract=False which is the default, or A-CC' (AA'-CC') for subtract=True. This method does not require that the **Factor** was created with **cholesky\_AAt()**, though that is the common case.

The usual use for this is to factor AA' when A has a large number of columns, or those columns become available incrementally. Instead of loading all of A into memory, one can load in 'strips' of columns and pass them to this method one at a time.

Note that no fill-reduction analysis is done; whatever permutation was chosen by the initial call to **analyze()** will be used regardless of the pattern of non-zeros in C.

## Accessing Cholesky factors explicitly

## Note:

When possible, it is generally more efficient to use the solve\_... functions documented below rather than extracting the Cholesky factors explicitly.

#### Factor.P()

Returns the fill-reducing permutation P, as a vector of indices.

The decomposition LL' or LDL' is of:

```
A[P[:, np.newaxis], P[np.newaxis, :]]
(or similar for AA').
```

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## Factor.**D**()

Converts this factorization to the style

$$LDL' = PAP'$$

or

$$LDL' = PAA'P'$$

and then returns the diagonal matrix D as a 1d vector.

## Note:

This method uses an efficient implementation that extracts the diagonal D directly from CHOLMOD's internal representation. It never makes a copy of the factor matrices, or actually converts a full LL' factorization into an LDL' factorization just to extract D.

## Factor.L()

If necessary, converts this factorization to the style

$$LL' = PAP'$$

or

$$LL' = PAA'P'$$

and then returns the sparse lower-triangular matrix L.

## Warning:

The L matrix returned by this method and the one returned by  $\underline{L}\underline{D}()$  are different!

## Factor. LD()

If necessary, converts this factorization to the style

$$LDL' = PAP'$$

or

$$LDL' = PAA'P'$$

and then returns a sparse lower-triangular matrix "LD", which contains the D matrix on its diagonal, plus the below-diagonal part of L (the actual diagonal of L is all-ones).

See  $L_D()$  for a more convenient interface.

#### Factor.L\_D()

If necessary, converts this factorization to the style

$$LDL' = PAP'$$

or

$$LDL' = PAA'P'$$

and then returns the pair (L, D) where L is a sparse lower-triangular matrix and D is a sparse diagonal matrix.

## Warning:

The L matrix returned by this method and the one returned by L() are different!

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# Solving equations

All methods in this section accept both sparse and dense matrices (or vectors) b, and return either a sparse or dense x accordingly.

All methods in this section act on LDL' factorizations by default. Thus L refers by default to the matrix returned by  $\mathbf{L}_{0}$ , not that returned by  $\mathbf{L}_{0}$  (though conversion is not performed unless necessary).

#### Factor. $solve_A(b)$

Solves a linear system.

Parameters: b - right-hand-side

**Returns:** math:x, where Ax = b (or AA'x = b, if

you used cholesky\_AAt()).

<u>\_\_call\_\_()</u> is an alias for this function, i.e., you can simply call the <u>Factor</u> object like a function to solve Ax = b.

## Factor.\_\_call\_\_(b)

Alias for solve\_A().

## Factor.solve\_LDLt(b)

Solves a linear system.

Parameters: b - right-hand-side

**Returns:** math:x, where LDL'x = b.

(This is different from  $\underline{\text{solve\_A()}}$  because it does not correct for the fill-reducing permutation.)

## Factor. $solve_LD(b)$

Solves a linear system.

**Parameters: b** - right-hand-side

**Returns:** math:x, where LDx = b.

## Factor. $solve_DLt(b)$

Solves a linear system.

**Parameters: b** - right-hand-side

**Returns:** math:x, where DL'x = b.

## Factor. $solve_L(b)$

Solves a linear system.

**Parameters:** • **b** – right-hand-side

• **use\_LDLt\_decomposition** – If True, use the *L* of the *LDL'* decomposi-

tion. If False, use the  $\it L$  of the  $\it LL'$  decomposition.

**Returns:** math:x, where Lx = b.

#### Factor. $solve_Lt(b)$

Solves a linear system.

**Parameters:** • **b** - right-hand-side

ullet use LDLt\_decomposition - If True, use the L of the LDL' decomposi-

tion. If False, use the  $\it L$  of the  $\it LL'$  decomposition.

**Returns:** math:x, where L'x = b.

## Factor. $solve_D(b)$

Returns x, where Dx = b.

Factor.apply\_P(b)

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```
Returns x, where x = Pb.
```

## Factor.apply\_Pt(b)

Returns x, where x = P'b.

## Convenience methods

## Factor.logdet()

Computes the (natural) log of the determinant of the matrix A.

If f is a factor, then f.logdet() is equivalent to np.sum(np.log(f.D())).

New in version 0.2.

## Factor.det()

Computes the determinant of the matrix A.

Consider using <u>logdet()</u> instead, for improved numerical stability. (In particular, determinants are often prone to problems with underflow or overflow.)

New in version 0.2.

## Factor.slogdet()

Computes the log-determinant of the matrix A, with the same API as numpy.linalg.slogdet().

This returns a tuple (sign, logdet), where sign is always the number 1.0 (because the determinant of a positive-definite matrix is always a positive real number), and logdet is the (natural) logarithm of the determinant of the matrix A.

New in version 0.2.

## Factor.inv()

Returns the inverse of the matrix A, as a sparse (CSC) matrix.

## Warning:

For most purposes, it is better to use **solve()** instead of computing the inverse explicitly. That is, the following two pieces of code produce identical results:

```
x = f.solve(b)
x = f.inv() * b # DON'T DO THIS!
```

But the first line is both faster and produces more accurate results.

Sometimes, though, you really do need the inverse explicitly (e.g., for calculating standard errors in least squares regression), so if that's your situation, here you go.

New in version 0.2.

#### Factor.copy()

Copies the current Factor.

Returns: A new Factor object.

# Error handling

class sksparse.cholmod.CholmodError

class sksparse.cholmod.CholmodNotPositiveDefiniteError

class sksparse.cholmod.CholmodNotInstalledError

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 $class \verb| sksparse.cholmod.CholmodOutOfMemoryError| \\$ 

class sksparse.cholmod.CholmodTooLargeError

class sksparse.cholmod.CholmodNotPositiveDefiniteError

class sksparse.cholmod.CholmodInvalidError

class sksparse.cholmod.CholmodGpuProblemError

Errors detected by CHOLMOD or by our wrapper code are converted into exceptions of type **CholmodError** or an appropriated subclass.

class sksparse.cholmod.CholmodWarning

Warnings issued by CHOLMOD are converted into Python warnings of type **CholmodWarning**.

#### class sksparse.cholmod.CholmodTypeConversionWarning

CHOLMOD itself supports matrices in CSC form with 32-bit integer indices and 'double' precision floats (64-bits, or 128-bits total for complex numbers). If you pass some other sort of matrix, then the wrapper code will convert it for you before passing it to CHOLMOD, and issue a warning of type **CholmodTypeConversionWarning** to let you know that your efficiency is not as high as it might be.

## Warning:

Not all conversions currently produce warnings. This is a bug.

Child of CholmodWarning.

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