ldl( ) — Bunch–Kaufman decomposition

Description Syntax Remarks and examples Conformability Diagnostics Also see

Description

`ldl(`A`,` L`,` D`,` p`)` returns the Bunch–Kaufman decomposition (with diagonal pivoting) of A in a permuted lower-triangular matrix L and a symmetric block-diagonal matrix D with 1×1 and 2×2 diagonal blocks, along with a permutation vector p.

With the permutation vector, L`[`p`, .]` becomes a lower-triangular matrix with unit diagonal.

Up to roundoff error, the returned results are such that

$$A[p,p] = L[p,.]*D*L[p,.]'$$

`ldl(`A`,` L`,` D`)` is similar to `ldl(`A`,` L`,` D`,` p`)`, but the permutation vector p is omitted from the output.

Up to roundoff error, the returned results are such that

$$A = L*D*L'$$

Syntax

void `ldl(`*numeric matrix* A`,` L`,` D`)`

void `ldl(`*numeric matrix* A`,` L`,` D`,` p`)`

where

1. A is symmetric (Hermitian) indefinite.
2. the types of L, D, and p are irrelevant; results are returned there.

Remarks and examples

The Bunch–Kaufman decomposition is a generalization of the Cholesky decomposition.

Bunch–Kaufman decomposition of matrix A can be written as

$$PAP' = PLDL'\ P'$$

where P is a permutation matrix that permutes the rows of A.

L is the permuted lower-triangular matrix. With the permutation matrix P, PL is a lower-triangular matrix with unit diagonal.

D is the symmetric block-diagonal matrix D with 1×1 and 2×2 diagonal blocks.

Rather than returning P directly, returned is p corresponding to P. Lowercase p is a column vector that contains the subscripts of the rows in the desired order. That is,

$$PL = L[p,.]$$

The advantage of this is that p requires less memory than P, and the reorganization, should it be desired, can be performed more quickly; see [M-1] **Permutation**.

Example 1: Bunch–Kaufman decomposition

The Bunch–Kaufman decomposition of A can be written as

$$A = L * D * L'$$

`ldl(`A`,` L`,` D`)` will make this calculation:

```
: A
[symmetric]
       1   2   3
  +-------------+
1 |  2          |
2 |  3   2      |
3 |  4   1   2  |
  +-------------+

: ldl(A, L = ., D = ., p = .)
: L
                 1              2              3
  +-----------------------------------------------+
1 |              1              0              0  |
2 |  -.1666666667     .8333333333              1  |
3 |              0              1              0  |
  +-----------------------------------------------+

: D
[symmetric]
                 1              2              3
  +-----------------------------------------------+
1 |              2                                |
2 |              4              2                 |
3 |              0              0   1.666666667   |
  +-----------------------------------------------+

: p
       1
  +----+
1 |  1 |
2 |  3 |
3 |  2 |
  +----+

: mreldif(A, L * D * L')
  1.11022e-16
: mreldif(A[p, p], L[p, .] * D * L[p, .]')
  1.11022e-16
```

Conformability

`ldl(`A`, `L`, `D`, `p`)`:

input:

A:	$n \times n$	

output:

L:	$n \times n$	
D:	$n \times n$	
p:	$n \times 1$	(optional)

Diagnostics

`ldl(`A`, `L`, `D`, `p`)` returns missing results if A contains missing values.

Also see

[M-5] **cholesky( )** — Cholesky square-root decomposition

[M-4] **Matrix** — Matrix functions