

# Cholesky and LDL decomposition in R

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In LU decomposition we have factored the matrix into two matrices L and U such that  $A = LU$ . L represents the lower triangular matrix and U represents the upper triangular matrix. Where L have diagonal elements as 1, U has diagonal elements not necessarily 1. In symmetric positive definite matrix, L is lower triangular matrix and U is upper triangular matrix. We can factorize a symmetric positive definite matrix into two matrices L and D such that  $A = LDL^T$ . L represents the lower triangular matrix and D represents the diagonal matrix. Whereas cholesky decomposition is a factorization of matrix  $A = U^T U$ . where U is upper triangular matrix and  $U = \sqrt{(D)}L^T$ .

Writing the code in R

```
Cholesky <- function(M){
  # Check whether the matrix is Positive Symmetric or not
  # Symmetric
  for(i in 1:nrow(M)){
    for(j in 1:ncol(M)){
      if(M[i,j] != M[j,i]){
        stop("Matrix is not symmetric")
      }
    }
  }

  # Check whether the matrix is Positive Definite or not
  if(M[1,1] <= 0){
    stop("Matrix is not Positive Definite")
  }
  for(i in 2:nrow(M))
  {
    if(det(M[1:i,1:i]) <= 0){
      stop("Matrix is not Positive Definite")
    }
  }

  # LU Decomposition
  LU_decomposition <- function(M){
    L <- 1
    if(is.matrix(M)){
      n <- ncol(M) # Number of columns
      m <- nrow(M) # Number of rows
      s <- min(n,m)
      L <- diag(x = 1 , nrow = s, ncol = s) # Lower triangular matrix
      pivot <- M[1,1] # Pivot element
      if(pivot == 0){
        stop("Pivot element is zero,Permutate the matrix")
      }
      for(i in 2:s){
```

```

    L[i,1] <- M[i,1]/pivot
    M[i,] <- M[i,] - (M[i,1]/pivot) * M[1,]
  }
  K <- LU_decomposition(M[-1,-1])
  M[-1,-1] <- K[[2]]
  L[-1,-1] <- K[[1]]
  }
  list(L = L, U = M)
}
# Cholesky Decomposition
D <- LU_decomposition(M)
L <- D$L
U <- D$U
for(i in 1:nrow(L)){
  for(j in 1:ncol(L)){
    if(L[i,j] < 0){
      L[i,j] <- -sqrt(-L[i,j])
    }
    else{
      L[i,j] <- sqrt(L[i,j])
    }
  }
}
A <- L
diag(A) <- sqrt(diag(U))
A
}

```

Example

```

M <- matrix(c(2,-1,0,-1,2,-1,0,-1,2),nrow = 3, ncol = 3,byrow = TRUE)
Cholesky(M)

```

```

##           [,1]      [,2]      [,3]
## [1,]  1.4142136  0.0000000  0.0000000
## [2,] -0.7071068  1.2247449  0.0000000
## [3,]  0.0000000 -0.8164966  1.1547010

```