

Comparing Least Squares Calculations

Douglas Bates
R Development Core Team
Douglas.Bates@R-project.org

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Abstract

Many statistics methods require one or more least squares problems to be solved. There are several ways to perform this calculation, using objects from the base R system and using objects in the classes defined in the `Matrix` package.

We compare the speed of some of these methods on a very small example and on a example for which the model matrix is large and sparse.

1 Linear least squares calculations

Many statistical techniques require least squares solutions

$$\hat{\beta} = \arg \min_{\beta} \|\mathbf{y} - \mathbf{X}\beta\|^2 \quad (1)$$

where \mathbf{X} is an $n \times p$ model matrix ($p \leq n$), \mathbf{y} is n -dimensional and β is p dimensional. Most statistics texts state that the solution to (1) is

$$\hat{\beta} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{y} \quad (2)$$

when \mathbf{X} has full column rank (i.e. the columns of \mathbf{X} are linearly independent) and all too frequently it is calculated in exactly this way.

1.1 A small example

As an example, let's create a model matrix, `mm`, and corresponding response vector, `y`, for a simple linear regression model using the `Formaldehyde` data.

```
> data(Formaldehyde)
> str(Formaldehyde)

'data.frame':      6 obs. of  2 variables:
 $ carb   : num  0.1 0.3 0.5 0.6 0.7 0.9
 $ optden : num  0.086 0.269 0.446 0.538 0.626 0.782
```

```
> (m <- cbind(1, Formaldehyde$carb))
```

```
      [,1] [,2]
[1,]    1 0.1
[2,]    1 0.3
[3,]    1 0.5
[4,]    1 0.6
[5,]    1 0.7
[6,]    1 0.9
```

```
> (yo <- Formaldehyde$optden)
```

```
[1] 0.086 0.269 0.446 0.538 0.626 0.782
```

Using `t` to evaluate the transpose, `solve` to take an inverse, and the `%%` operator for matrix multiplication, we can translate 2 into the S language as

```
> solve(t(m) %% m) %% t(m) %% yo
```

```
      [,1]
[1,] 0.005085714
[2,] 0.876285714
```

On modern computers this calculation is performed so quickly that it cannot be timed accurately in R ¹

```
> system.time(solve(t(m) %% m) %% t(m) %% yo)
```

```
   user  system elapsed
    0         0         0
```

and it provides essentially the same results as the standard `lm.fit` function that is called by `lm`.

```
> dput(c(solve(t(m) %% m) %% t(m) %% yo))
```

```
c(0.00508571428571428, 0.876285714285715)
```

```
> dput(unname(lm.fit(m, yo)$coefficients))
```

```
c(0.00508571428571408, 0.876285714285715)
```

¹From R version 2.2.0, `system.time()` has default argument `gcFirst = TRUE` which is assumed and relevant for all subsequent timings

1.2 A large example

For a large, ill-conditioned least squares problem, such as that described in Koenker and Ng (2003), the literal translation of (2) does not perform well.

```
> library(Matrix)
> data(KNex, package = "Matrix")
> y <- KNex$y
> mm <- as(KNex$mm, "matrix") # full traditional matrix
> dim(mm)

[1] 1850  712

> system.time(naive.sol <- solve(t(mm) %*% mm) %*% t(mm) %*% y)

      user system elapsed 
1.464    0.024    1.489
```

Because the calculation of a “cross-product” matrix, such as $\mathbf{X}^\top \mathbf{X}$ or $\mathbf{X}^\top \mathbf{y}$, is a common operation in statistics, the `crossprod` function has been provided to do this efficiently. In the single argument form `crossprod(mm)` calculates $\mathbf{X}^\top \mathbf{X}$, taking advantage of the symmetry of the product. That is, instead of calculating the $712^2 = 506944$ elements of $\mathbf{X}^\top \mathbf{X}$ separately, it only calculates the $(712 \cdot 713)/2 = 253828$ elements in the upper triangle and replicates them in the lower triangle. Furthermore, there is no need to calculate the inverse of a matrix explicitly when solving a linear system of equations. When the two argument form of the `solve` function is used the linear system

$$(\mathbf{X}^\top \mathbf{X}) \hat{\boldsymbol{\beta}} = \mathbf{X}^\top \mathbf{y} \quad (3)$$

is solved directly.

Combining these optimizations we obtain

```
> system.time(cpod.sol <- solve(crossprod(mm), crossprod(mm,y)))

      user system elapsed 
1.537    0.011    1.550

> all.equal(naive.sol, cpod.sol)

[1] TRUE
```

On this computer (2.0 GHz Pentium-4, 1 GB Memory, Goto’s BLAS, in Spring 2004) the `crossprod` form of the calculation is about four times as fast as the naive calculation. In fact, the entire `crossprod` solution is faster than simply calculating $\mathbf{X}^\top \mathbf{X}$ the naive way.

```
> system.time(t(mm) %*% mm)
```

```

user  system elapsed
0.080  0.003  0.083

```

Note that in newer versions of R and the BLAS library (as of summer 2007), R's `%*%` is able to detect the many zeros in `mm` and shortcut many operations, and is hence much faster for such a sparse matrix than `crossprod` which currently does not make use of such optimizations. This is not the case when R is linked against an optimized BLAS library such as GOTO or ATLAS. Also, for fully dense matrices, `crossprod()` indeed remains faster (by a factor of two, typically) independently of the BLAS library:

```

> fm <- mm
> set.seed(11)
> fm[] <- rnorm(length(fm))
> system.time(c1 <- t(fm) %*% fm)

user  system elapsed
3.112  0.006  3.145

> system.time(c2 <- crossprod(fm))

user  system elapsed
1.48   0.00   1.48

> stopifnot(all.equal(c1, c2, tol = 1e-12))

```

1.3 Least squares calculations with Matrix classes

The `crossprod` function applied to a single matrix takes advantage of symmetry when calculating the product but does not retain the information that the product is symmetric (and positive semidefinite). As a result the solution of (3) is performed using general linear system solver based on an LU decomposition when it would be faster, and more stable numerically, to use a Cholesky decomposition. The Cholesky decomposition could be used but it is rather awkward

```

> system.time(ch <- chol(crossprod(mm)))

user  system elapsed
1.579  0.001  1.580

> system.time(chol.sol <-
+             backsolve(ch, forwardsolve(ch, crossprod(mm, y),
+             upper = TRUE, trans = TRUE)))

user  system elapsed
0.016  0.000  0.016

> stopifnot(all.equal(chol.sol, naive.sol))

```

The `Matrix` package uses the S4 class system (Chambers, 1998) to retain information on the structure of matrices from the intermediate calculations. A general matrix in dense storage, created by the `Matrix` function, has class `"dgeMatrix"` but its cross-product has class `"dpoMatrix"`. The `solve` methods for the `"dpoMatrix"` class use the Cholesky decomposition.

```
> mm <- as(KNex$mm, "dgeMatrix")
> class(crossprod(mm))

[1] "dpoMatrix"
attr(,"package")
[1] "Matrix"

> system.time(Mat.sol <- solve(crossprod(mm), crossprod(mm, y)))

   user   system elapsed 
 1.591    0.000    1.594 

> stopifnot(all.equal(naive.sol, unname(as(Mat.sol, "matrix"))))
```

Furthermore, any method that calculates a decomposition or factorization stores the resulting factorization with the original object so that it can be reused without recalculation.

```
> xpx <- crossprod(mm)
> xpy <- crossprod(mm, y)
> system.time(solve(xpx, xpy))

   user   system elapsed 
 0.106    0.000    0.107 

> system.time(solve(xpx, xpy)) # reusing factorization

   user   system elapsed 
 0.002    0.000    0.002
```

The model matrix `mm` is sparse; that is, most of the elements of `mm` are zero. The `Matrix` package incorporates special methods for sparse matrices, which produce the fastest results of all.

```
> mm <- KNex$mm
> class(mm)

[1] "dgCMatrix"
attr(,"package")
[1] "Matrix"

> system.time(sparse.sol <- solve(crossprod(mm), crossprod(mm, y)))
```

```

      user  system elapsed
0.005    0.001    0.006

> stopifnot(all.equal(naive.sol, unname(as(sparse.sol, "matrix"))))

```

As with other classes in the `Matrix` package, the `dsCMatrix` retains any factorization that has been calculated although, in this case, the decomposition is so fast that it is difficult to determine the difference in the solution times.

```

> xpx <- crossprod(mm)
> xpy <- crossprod(mm, y)
> system.time(solve(xpx, xpy))

```

```

      user  system elapsed
0.002    0.000    0.001

> system.time(solve(xpx, xpy))

```

```

      user  system elapsed
0.000    0.000    0.001

```

Session Info

```

> toLatex(sessionInfo())

• R version 2.7.2 Patched (2008-08-29 r46463), x86_64-unknown-linux-gnu
• Locale: C
• Base packages: base, datasets, grDevices, graphics, methods, stats, tools,
  utils
• Other packages: Matrix 0.999375-13, lattice 0.17-13
• Loaded via a namespace (and not attached): grid 2.7.2

> if(identical(1L, grep("linux", R.version[["os"]]))) { ## Linux - only ---
+   Scpu <- sfsmisc::Sys.procinfo("/proc/cpuinfo")
+   Smem <- sfsmisc::Sys.procinfo("/proc/meminfo")
+   print(Scpu[c("model name", "cpu MHz", "cache size", "bogomips")])
+   print(Smem[c("MemTotal", "SwapTotal")])
+ }

```

```

-
model name Dual-Core AMD Opteron(tm) Processor 2220
cpu MHz    2814.483
cache size 1024 KB
bogomips   5631.33
-
MemTotal   32967764 kB
SwapTotal  244187960 kB

```

References

John M. Chambers. *Programming with Data*. Springer, New York, 1998. ISBN 0-387-98503-4.

Roger Koenker and Pin Ng. SparseM: A sparse matrix package for R. *J. of Statistical Software*, 8(6), 2003.