

SVD Factorization for Tall-and-Fat Matrices on Map/Reduce Architectures

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Abstract

We demonstrate an implementation for an approximate rank- k SVD factorization, combining well-known randomized projection techniques with previously implemented map/reduce solutions in order to compute steps of the random projection based SVD procedure, such as QR and SVD. We structure the problem in a way that it reduces to Cholesky and SVD factorizations on $k \times k$ matrices computed on a single machine, greatly easing the computability of the problem.

1 Introduction

[1] presents many excellent techniques for utilizing map/reduce architectures to compute QR and SVD for the so-called tall-and-skinny matrices. QR factorization is turned into an $A^T A$ computation problem to be computed in parallel using map/reduce, and its key element the Cholesky decomposition, can be performed on a single machine. Let's use $C = A^T A$ and, since

$$C = A^T A = (QR)^T (QR) = R^T Q^T QR = R^T R$$

and because Cholesky factorization of an $n \times n$ symmetric positive definite matrix is

$$C = LL^T$$

where L is an $n \times n$ lower triangular matrix, and R is upper triangular, we can conclude if we factorize C into L and L^T , this implies $C = LL^T = RR^T$, we have a method of calculating R of QR using Cholesky factorization on $A^T A$. The key observation here is $A^T A$ computation results in an $n \times n$ matrix and if A is “skinny” then n is relatively small (in the thousands), then

Cholesky decomposition can be executed on a small $n \times n$ matrix on a single computer utilizing an already available function in a scientific computing library. Q is computed simply as $Q = AR^{-1}$. This again is relatively cheap because R is $n \times n$, the inverse is computed locally, matrix multiplication with A can be performed through map/reduce.

SVD is an additional step. SVD decomposition is

$$A = U\Sigma V^T$$

If we expand it with $A = QR$

$$QR = U\Sigma V^T$$

$$R = Q^T U \Sigma V^T$$

Let's call $\tilde{U} = Q^T U$

$$R = \tilde{U} \Sigma V^T$$

This means if we run a local SVD on R (we just calculated above with Cholesky) which is an $n \times n$ matrix, we will have calculated \tilde{U} , the real Σ , and real V^T .

Now we have a map/reduce way of calculating QR and SVD on $m \times n$ matrices where n is small.

1.1 Approximate rank-k SVD

Switching gears, we look at another method for calculating SVD. The motivation is while computing SVD, if n is large, creating a “fat” matrix which might have columns in the billions would require reducing the dimensionality of the problem. According to [2], one way to achieve is through random projection. First we draw an $n \times k$ Gaussian random matrix Ω . Then we calculate

$$Y = A\Omega$$

We perform QR decomposition on Y

$$Y = QR$$

Then form $k \times n$ matrix

$$B = Q^T A$$

Then we can calculate SVD on this small matrix

$$B = \hat{U} \Sigma V^T$$

Then form the matrix

$$U = Q \hat{U}$$

The main idea is based on

$$A = Q Q^T A$$

if replace Q which comes from random projection Y ,

$$A \approx \tilde{Q} \tilde{Q}^T A$$

Q and R of the projection are close to that of A . In the multiplication above R is called B where $B = \tilde{Q}^T A$, and,

$$A \approx \tilde{Q} B$$

then, as in [1], we can take SVD of B and apply the same transition rules to obtain an approximate U of A .

This approximation works because of the fact that projecting points to a random subspace preserves distances between points, or in detail, projecting the n -point subset onto a random subspace of $O(\log n / \epsilon^2)$ dimensions only changes the interpoint distances by $(1 \pm \epsilon)$ with positive probability [3]. It is also said that Y is a good representation of the span of A .

1.2 Combining Both Methods

Our idea was using approximate k -rank SVD calculation steps where $k \ll n$, and using map/reduce based QR and SVD methods to implement those steps. By utilizing random projection, we would be able to work in a smaller dimension which would translate to local Cholesky, and SVD calls on $k \times k$ matrices that can be performed in a speedy manner. Below we outline each map/reduce job.

Algorithm 1: Random Projection Job

```
input : A
output: Y
function MAP(key, value)
    Tokenize value and pick out id value pairs
    result  $\leftarrow$  zeros(1,k)
    for each  $j^{th}$  token  $\in$  value do
        Initialize seed with j
        r  $\leftarrow$  generate k random numbers
        result  $\leftarrow$  result + r  $\cdot$  token[j]
    end
    emit key, result
function REDUCE(key, value)
    noop
```

Each value of A will arrive to the algorithm as a key and value pair. Key is line number or other identifier per row of A . Value is a collection of id value pairs where id is column id this time, and value is the value for that column. Sparsity is handled through this format, if an id for a column does not appear in a row of A , it is assumed to be zero. The resulting Y matrix has dimensions $m \times k$.

Algorithm 2: $A^T A$ Cholesky Job

```
input : Y
output: R
function MAP(key k, val a)
    for i, row in enumerate( $a^T a$ ) do
        | emit i, row
    end
function REDUCE(key, value)
    | emit (k, sum( $\langle v_j^k \rangle$ ))
function FINAL LOCAL REDUCE (key, value)
    | result  $\leftarrow$  Cholesky( $A_{sum}$ )
    | emit (result)
```

The FINAL_LOCAL_REDUCE step is a function provided in most map/reduce frameworks, it is a central point that collects the output of all reducers, naturally a single machine which makes it ideal to execute the final Cholesky call on by now a very small ($k \times k$) matrix. The output is R .

Algorithm 3: Q Job

```
input :  $Y, R$ 
output:  $Q$ 
function  $INIT()$ 
|  $R_{inv} = R^{-1}$ 
function  $MAP(key, value)$ 
| for  $row$  in  $Y$  do
| | emit ( $key, row \cdot R_{inv}$ )
| end
```

There is no reducer in the Q Job, it is a very simple procedure, it merely computes multiplication between row of Y and a local matrix R . Matrix R is very small, $k \times k$, hence it can be kept locally in every node. The $INIT$ function is used to store the inverse of R locally, once the mapper is initialized, it will always use the same R^{-1} for every multiplication.

Algorithm 4: $A^T Q$ Job

```
input :  $AQ$ 
output:  $B^T$ 
function  $MAP(key, value)$ 
|  $left = row$  from  $A$ 
|  $right = row$  from  $Q$ 
| for  $nonzero\ j^{th}$   $cell$  in  $left$  do
| | emit  $j, left[j] \cdot right$ 
| end
function  $REDUCE(key, value)$ 
|  $result \leftarrow zeros(1, k)$ 
| for  $row$  in  $value$  do
| |  $result \leftarrow result + row$ 
| end
| emit  $key, result$ 
```

The job above takes an AQ matrix which is assumed to be a join between A and Q , per row, based on key. We split the row and deduce the A part and the Q part, then iterate cells of A one by one, which is assumed to be sparse, and multiply the entire row of Q . Then for each j^{th} non-zero cell of A , we multiply this value with the row from Q and emit the multiplication result with key j .

The $Q^T A$ job's formula can be seen at 1.1. For implementation purposes

we changed this formula into

$$B^T = A^T Q$$

because as output we needed to have a $n \times k$ matrix instead of a $k \times n$ one, which would allow us to use map/reduce SVD that translates into a local Cholesky and SVD on $k \times k$ matrices. Since we take SVD of B^T instead of B , that changes the output as well,

$$B = U \Sigma V^T$$

becomes

$$B^T = V \Sigma U^T$$

In other words, in order to obtain U of B , we need to take $(U_{BT}^T)^T$ from the SVD of B^T . This is how $A^T A$ Cholesky Job is called, this time with B^T as its input data.

Algorithm 5: $Q\tilde{U}$ Job

```

input : Q,R
output: U
function INIT()
  |  $\tilde{U} = \text{svd of } R$ 
function MAP(key, value)
  | for row in  $Q$  do
  |   | emit (key, row ·  $\tilde{U}$ )
  | end

```

The order of execution for everything is as follows:

Algorithm 6: Map/Reduce SVD

```

Y = Random Projection Job (A)
 $R_Y = A^T A$  Cholesky Job(Y)
 $Q_Y = Q$  Job
 $B^T = A^T Q$  Job
 $R_{BT} = A^T A$  Cholesky Job( $B^T$ )
 $U = Q\tilde{U}$  Job( $R_{BT}, Q$ )

```

1.3 Discussion

We performed our experiments on the Netflix dataset which has about 100 million from over 480,000 customers on 17770 movies. The implementation was programmed on Sasha distributed framework [5], and SVD calculation on the full dataset with $k = 7$ on two notebook computers, utilizing in total 6 cores took 20 minutes. Scipy SVD calculation on the same dataset is much faster, however, we need to stress our algorithms are prepared for cases where N is very large, i.e. in the billions. As such, for example during projection we did not simply create and pre-store a $n \times k$ random matrix and multiply multiple rows of A with this matrix. This would certainly be possible for Netflix data where n is relatively small, but would not work well in cases where A is “fat”. All code relevant for this paper can be found here [6].

There are only two passes necessary on the full dataset, and three passes on m rows but with reduced k dimensions this time. Perhaps predictably, the procedure spends most of its time at $A^T Q$ Job. This step performs not only a join between A and Q , it also emits k cells per non-zero value of A ’s rows, then creates partial sums these k vectors creating $n \times k$ result. If for simplicity we assume k non-zero cells in each A row, the complexity of this step would be $O(mk)$.

References

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