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

Burak Bayramlı

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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 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. The idea is based on the fact that QR factorization can be turned into an $A^T A$ computation problem computer in parallel, en masse using map/reduce, and through this to a Cholesky decomposition performed on a single machine. Since

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

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

$$A = LL^T$$

where L is an $n \times n$ lower triangular matrix, and R is upper triangular, we can conclude if we factorize A into L and L^T, this implies $LL^T = RR^T$, 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 an $n \times n$ matrix and

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if A is "skinny" then n is relatively small (in the thousands), and Cholesky decomposition can be executed on a small $n \times n$ matrix on a single computer. Q is computed simply as $Q = AR^{-1}$. This again is relatively cheap because R is $n \times n$, the inverse is computed locallly, 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 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

$$A = QQ^T A$$

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

What if n is also very large? In this case local Cholesky or SVD computations would take a long time as well. Our idea was using approximate k-rank SVD where $k << n$, before map/reduce based QR and SVD methods presented in section 1, to reduce dimension before using map/reduce methods presented in Section 1, this way, we are again able to work with small matrices locally, $k \times k$ this time on which Cholesky, SVD can be performed. 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 jth 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($< v_j^k >$)
    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 a $k \times k$ 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 job, 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** : A,Q
> **output**: B^T
> **function** *REDUCE (key, value)*
> > **for** *row in value* **do**
> > > **if** *row is from A* **then**
> > > > $left = row$
> > >
> > > **end**
> > > **if** *row is from Q* **then**
> > > > $right = row$
> > >
> > > **end**
> >
> > **end**
> > **for** *nonzero j^{th} cell in left* **do**
> > > **emit** *j, left[j] $\cdot$ right*
> >
> > **end**
>
> **function** *REDUCESUM (key, value)*
> > result $\leftarrow$ zeros(1,k)
> > **for** *row in value* **do**
> > > result $\leftarrow$ result $+ row$
> >
> > **end**
> > **emit** *key, result*

The job above takes A and Q matrices at the same time. Both of these matrices are based on the same key (line number, of preexisting id) and we need to join them first. If a mapper is a pass-through mapper, in other words if it does not exist, it is assumed to simply re-emit the key and value,

which will, indirectly force matching rows with the same id from A and Q to be sent to the first reducer. Then for each unique id, the first reducer gets exactly two rows. This is an indirect way of performing a join in map/reduce environment.

We detect if this row is a Q or an A because we will iterate cells of A which is assumed to be sparse. Then for each jth non-zero cell of A, we multiply this value with the matching row of Q and emit this multiplication result with key j.

References

[1] Gleich, Benson, Demmel, *Direct QR factorizations for tall-and-skinny matrices in MapReduce architectures*

[2] N. Halko, *Randomized methods for computing low-rank approximations of matrices*

[3] S. Dangupta, A. Gupta *An Elementary Proof of a Theorem of Johnson and Lindenstrauss*