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 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. 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 if A is "skinny" then n is relatively small (in the thousands), then Cholesky

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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 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

Our idea was using approximate k-rank SVD calculation steps where $k << n$, 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 ← zeros(1,k)
> > **for** *each jth token $\in$ value* **do**
> > > Initialize seed with j
> > > r ← generate k random numbers
> > > result ← 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 ← 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 jth non-zero cell of A, we multiply this value with the row from Q and emit the multiplication result with key j.

This job's formula in 1.1 is described $Q^T A$. 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

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   input : Q,R
   output: U
   function *INIT()*
     | $\tilde{U}$ = svd of R
   function *MAP(key, value)*
     for *row in Q* **do**
       | **emit** *(key, row $\cdot \tilde{U}$)*
     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, map/reduce environment is a streaming environment which needs to process in record-by-record basis. Fortunately exactly for the same reasons a map/reduce algorithm can scale horizontally, being able to process records in the billions proportional to the number of nodes in a cluster whereas single machine algorithm would not. 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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