GPUFish: A Parallel Computing Framework for Matrix Completion from A Few Observations

Charlie Hubbard and Chinmay Hegde
Electrical and Computer Engineering Department
Iowa State University

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Abstract

The problem of recovering a data matrix from a small sample of observed entries, also known as *matrix completion*, arises in several real-world applications including recommender systems, sensor localization, and system identification. We introduce GPUFish, a parallel computing software framework for solving very large-scale matrix completion problems. GPUFish is modular, tunable, inherently parallelizable, and leverages the massive number of multiple concurrent kernel executions possible on a modern GPU.

The algorithmic core of GPUFish is an optimized implementation of the Jellyfish framework [1] which employs parallel stochastic gradient descent for solving the matrix completion problem. GPUFish enables the user to fine-tune the loss function to domain-dependent problems, thus extending the matrix completion framework to non-numeric observations. As a stylized application, we demonstrate how to adapt GPUFish to solve the *1-bit matrix completion* problem where the matrix observations are binary [2]. Our results demonstrate that we achieve a 100x speedup over existing serial algorithms for this problem, with only a minimal loss in prediction accuracy, using a standard workstation equipped with a single GPU.

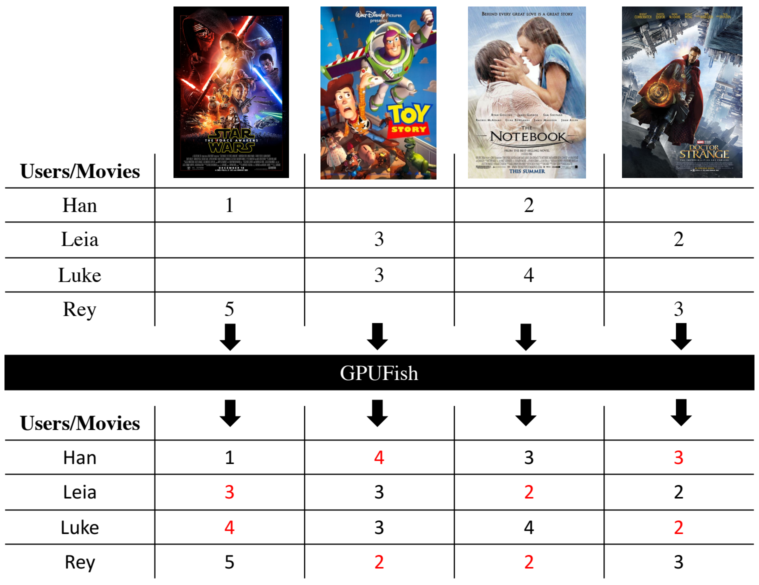
1 Introduction

1.1 Motivation

The problem of recovering a data matrix from a small sample of its entries, also called the *matrix completion* problem, arises in several real-world applications including content recommender systems, sensor localization, and system identification.

The matrix completion problem rose to prominence during the Netflix Prize [3]. The problem faced by Netflix was the following: given a subset of movie ratings provided by users, how best to predict future (unknown) movie ratings? Put differently, imagine a large ratings matrix $\mathbf{M}$ with rows representing users and columns representing movies. Given a partially observed subset of the entries of $\mathbf{M}$, the goal was to fill in the rest of the missing (unobserved) entries.

This problem poses three central challenges. First, for a content provider such as Netflix, even the most active users can only rate a small fraction of the movies available, and therefore the matrix of *observed* ratings is extremely sparse. Without additional information, the task of recovering $\mathbf{M}$ would seem impossible. However, the recent, large body of work in matrix completion has shown that as long as the matrix $\mathbf{M}$ possess a *sufficiently low rank*, we can recover the missing entries of $\mathbf{M}$ via a convex optimization procedure [4–7].



Users/Movies				
Han	1		2	
Leia		3		2
Luke		3	4	
Rey	5			3

Users/Movies				
Han	1	4	3	3
Leia	3	3	2	2
Luke	4	3	4	2
Rey	5	2	2	3

Figure 1: *In a collaborative filtering environment, one can use* GPUFish *to predict user-movie ratings and complete an incomplete ratings matrix.*

Second, for large-scale content providers such as Netflix, Amazon, and Spotify, their popularity, and sheer amount of content available, implies that the number of users and the number of items can both be in the order of hundreds of millions (as of December 2015, Amazon had over 300 million registered users). Matrices this large (greater than a few thousand rows/columns) cause problems for typical matrix completion methods, and convex optimization approaches are not particularly suitable. To resolve this, a non-convex, incremental heuristic for matrix completion was introduced in [1]. This method, termed as Jellyfish, achieves this speed-up by using a specific randomized version of *incremental gradient descent*, which allows data points to be processed in parallel with no fine-grained memory locking.

Third, the application of standard approaches for matrix completion to the problem of content recommendation is not seamless. The matrix completion literature assumes that the entries of the matrix are *real-valued*; however, the ratings provided by users of content providers are almost always "quantized" to some finite set of integers (for example, Netflix ratings range from 1 to 5, while Pandora only allows a binary like/dislike system.) Treating such *categorical* ratings as if they were quantized versions of a "true" real number creates a number of issues; for example, if a user's "true" rating of a particular movie in Netflix is 7.8 but we cap the reported rating at a maximum of 5, then we have introduced a significant amount of observation noise that is unaccounted for during the recovery of the remaining ratings. To remedy this, the framework of *1-Bit matrix completion* has been presented in [2] and outperforms contemporary matrix completion methods by intrinsically modeling the ratings as non-numeric entities. However, the challenge now is to solve an *even* more complicated convex optimization procedure, and again the issue of scalability in this setting is further exacerbated.

1.2 Our contributions

In this technical report, we introduce GPUFish, a parallel computing software framework for solving matrix completion problems for arbitrary data types. To the best of our knowledge, our proposed framework is the first to extend and massively parallelize generic matrix completion solution approaches.

GPUFish is modular, tunable, and leverages the massive number of multiple concurrent kernel executions possible on a modern GPU. As a stylized application, we demonstrate how to adapt GPUFish to solve the 1-bit matrix completion problem where the matrix observations are binary [2]. Our results demonstrate that we achieve a 150x speedup over existing serial algorithms, while maintaining comparable prediction accuracy. Our work demonstrates that a standard workstation equipped with a single GPU can be effectively deployed to solve very large scale matrix completion problems.

A CUDA implementation of GPUFish is available for download at https://github.com/cghubbard/gpu-fish.

1.3 Our techniques

The algorithmic core of GPUFish is an optimized implementation of the Jellyfish framework [1]. Similar to the approach proposed in [1], our approach also employs a randomized, incremental stochastic gradient descent; this enables us to work in the factorized space, never having to store the entire ratings matrix in memory during the training process.

However, GPUFish generalizes the previous approach in two distinct ways: (i) GPUFish enables the user to transparently adapt to domain-dependent problems, thus extending the matrix completion framework to numeric as well as non-numeric observations. (ii) GPUFish enables the user to leverage the full parallel processing power of a GPU, and can concurrently process hundreds of available samples in the training phase; this considerably accelerates training time over known existing approaches.

2 Application: Scalable Collaborative Filtering

As a stylized application, we describe an instantiation of GPUFish for solving large scale instances of the matrix completion (also sometimes called *collaborative filtering*) problem where the user ratings are available in the form of binary (like/dislike) observations.

2.1 Setup: 1-bit matrix completion

We adopt the 1-bit matrix completion model of [2]. Our goal is to complete any missing entries of a rank-r matrix $\mathbf{M}$ with n_r rows and n_c columns, given an observed subset of its entries, denoted by $\Omega \subseteq [n_r] \times [n_c]$. Here, the entries of $\mathbf{M}$ represent the underlying interest (or "enjoyment") level that a user i has in item j.

However, in a departure from classical matrix completion, we do not get to directly observe the entries of $\mathbf{M}$. Instead, consider any twice-differentiable function $p : \mathbb{R} \to [0, 1]$. We record observations $\mathbf{Y}$ such that:

$$Y_{i,j} = \begin{cases} +1 & \text{with probability } p(M_{i,j}), \\ -1 & \text{with probability } 1 - p(M_{i,j}), \end{cases} \quad \text{for} \quad (i,j) \in \Omega. \tag{2.1}$$

In other words, $\mathbf{Y}$ is a matrix of identical size as $\mathbf{M}$, where the entry $Y_{i,j}$ is $+1$ with high probability if user i "enjoys" item j (i.e., $M_{i,j}$ is high), and -1 otherwise. As with previous work in matrix completion, it is important that Ω is chosen *uniformly at random*; this can be implemented, for example, if any $(i,j) \in \{1, \ldots, n_r\} \times \{1, \ldots, n_c\}$ is independently included in Ω with probability $\frac{E[|\Omega|]}{n_r n_c}$.

In [2], the *Probit* and *Logit* functions, often employed in model fitting in statistics, are explored as natural functions to model the underlying distribution of the entries of $\mathbf{Y}$. Suppose we focus on the Logit function $p(x) = \frac{e^x}{1+e^x}$. To recover an estimate of $\mathbf{M}$ we can maximize the log-likelihood function of the optimization variable $\mathbf{X}$ over the set of observations Ω. Denote $\mathbb{1}_A$ as the indicator function over a Boolean condition A. Then the log-likelihood function corresponding to the Logit model is given by:

$$\mathcal{L}_{\Omega,\mathbf{Y}}(\mathbf{X}) := \sum_{(i,j)\in\Omega} \left(\mathbb{1}_{Y_{i,j}=1}\log(p(X_{i,j})) + \mathbb{1}_{Y_{i,j}=-1}\log(1-p(X_{i,j}))\right). \tag{2.2}$$

The estimate of $\mathbf{M}$, therefore, is given by the solution to the constrained optimization problem[1]:

$$\begin{gathered}\widehat{\mathbf{M}} = \underset{\mathbf{X}}{\operatorname{argmax}}\ \mathcal{L}_{\Omega,\mathbf{Y}}(\mathbf{X}),\\ \text{s.t. } \operatorname{rank}(\mathbf{X}) \le r\,.\end{gathered} \tag{2.3}$$

2.2 Factorized version of optimization problem

The optimization problem (2.3) is non-convex, due to the presence of the rank constraint on $\mathbf{X}$. The standard method adopted in matrix completion approaches is to perform a *nuclear norm relaxation* of the rank constraint. However, nuclear norm-regularized matrix recovery formulations can incur a high running time [1, 4, 6].

In order to resolve this issue, we adopt the Jellyfish approach of [1]. Jellyfish can be used to solve problems of the form:

$$\text{minimize} \sum_{(i,j)\in\Omega} f_{ij}(X_{ij}) + P(\mathbf{X}), \tag{2.4}$$

where f is any convex loss function of a scalar and $P : \mathbb{R}^{n_r\times n_c} \to \mathbb{R}$ is a matrix regularizer that encourage low-rank solutions. In our implementation, we use the γ_2-norm as a regularizer [8]. The γ_2-norm is defined as the infimum of the matrix maximum-row-norms of the factors of $\mathbf{X}$, measured over all possible factorizations of $\mathbf{X}$:

$$\|\mathbf{X}\|_{\gamma_2} := \inf\left\{\max\left(\|\mathbf{L}\|^2_{2,\infty}, \|\mathbf{R}\|^2_{2,\infty}\right) : \mathbf{X} = \mathbf{L}\mathbf{R}^*\right\}, \tag{2.5}$$

Here, $\|\cdot\|_{2,\infty}$ denotes the maximum row-norm of any matrix, $\mathbf{A}$:

$$\|\mathbf{A}\|_{2,\infty} := \max_j \left(\sum_k \mathbf{A}^2_{jk}\right)^{1/2}. \tag{2.6}$$

Assuming that the decision variable $\mathbf{X}$ is at most rank-r, we can rewrite it at $X = \mathbf{L}\mathbf{R}^*$, where the size of L and R are $n_r \times r$ and $n_c \times r$, respectively. Note that explicit storage of $\mathbf{X}$ requires memory capacity proportional to $n_r n_c$, which is infeasible for most matrices encountered in large-scale collaborative filtering applications. Instead, by writing our decision variable as $\mathbf{L}\mathbf{R}^*$, we only incur a memory requirement proportional to $(n_r + n_c)r$, a significant reduction.

We now consider a constrained version of (2.4) (where the regularization term is explicitly bounded by a parameter B):

$$\text{minimize} \sum_{(i,j)\in\Omega} f_{ij}(X_{ij}) \qquad \text{subject to} \qquad \|\mathbf{X}\|_{\gamma_2} \le \mathrm{B}\,. \tag{2.7}$$

The optimal value of B is empirically chosen on a per dataset basis.

We replace f by the negative log-likelihood function specified in 2.3, and also assume the factorized version of the γ_2-norm defined above. With a bit of algebraic simplification, we obtain the *bilinear* optimization problem:

[1]To be precise, the problem formulation in [2] also included a boundedness constraint on $\|\mathbf{M}\|_\infty$, but we omit that constraint here.

$$\text{minimize} \sum_{(i,j)\in\Omega} -\mathcal{L}(\mathbf{L}\mathbf{R}^*) \quad \text{subject to} \quad \|\mathbf{L}\|_{2,\infty}^2 \leq \mathrm{B},\ \|\mathbf{R}\|_{2,\infty}^2 \leq \mathrm{B}. \tag{2.8}$$

To solve (2.8), we adopt the *incremental projected gradient descent* approach of [1]. We alternately update $\mathbf{L}$ (resp., $\mathbf{R}$) while keeping $\mathbf{R}$ (resp., $\mathbf{L}$) fixed. In each iteration, the updates to $\mathbf{L}$ and $\mathbf{R}$ are given by [1]:

$$\begin{aligned} \mathbf{L}_{i_k}^{(k+1)} &= \Pi_{\mathrm{B}}\left(\mathbf{L}_{i_k} - \alpha_k \mathcal{L}'(\mathbf{L}_{i_k}^{(k)}\mathbf{R}_{j_k}^{(k)*})\mathbf{R}_{j_k}^{(k)}\right) \\ \mathbf{R}_{i_k}^{(k+1)} &= \Pi_{\mathrm{B}}\left(\mathbf{R}_{i_k} - \alpha_k \mathcal{L}'(\mathbf{L}_{i_k}^{(k)}\mathbf{R}_{j_k}^{(k)*})\mathbf{L}_{j_k}^{(k)}\right) \end{aligned} \tag{2.9}$$

where the projection operator Π onto the constraint set in (2.8) admits the closed form expression:

$$\Pi_B(v) = \begin{cases} \frac{\sqrt{B}v}{\|v\|} & \|v\|^2 \geq \mathrm{B} \\ v & \text{otherwise} \end{cases}. \tag{2.10}$$

Here $\mathbf{L}_i$ is the i^{th} row of $\mathbf{L}$ and $\mathbf{R}_j$ is the j^{th} row of $\mathbf{R}$ so $\mathbf{L}_{i_k}^{(k)}\mathbf{R}_{j_k}^{(k)*}$ is the estimated value of matrix $\mathbf{M}_(i,j)$. The step size parameter in the gradient descent iteration, α_k, is a positive scalar that decreases by a constant amount at every iteration.

2.3 Parallelization

The above gradient descent formulation of the matrix recovery has several computational advantages. Primarily, we observe that the updates performed in (2.9) operate on highly *local* portions of the matrices $\mathbf{L}$ and $\mathbf{R}$. That is any pair $(i,j) \in \Omega$ will only read from and write to the rows $\mathbf{L}_i$ and $\mathbf{R}_j$. Given a pair of points from Ω, (i_1, j_1) and (i_2, j_2) we could perform the gradient updates for these points in parallel as long as $i_1 \neq i_2$ and $j_1 \neq j_2$; they are entirely unrelated. In the same manner, if we had two sets of points $S_1 = \{(i,j) : i \in I_1, j \in J_1\}$ and $S_2 = \{(i,j) : i \in I_2, j \in J_2\}$ with $I_1 \cap I_2 = \emptyset$ and $J_1 \cap J_2 = \emptyset$, the gradient updates for each set could be run, in principle, completely in parallel. This is the intuition exploited in [1]; however, they have focused on standard matrix completion as a special case, and also assume a standard multi-core computing model.

We first describe the scheme for sample ordering, called *cyclic partitioning*, developed in depth in [1]. We introduce some terminology. Any two (row or column) index sets S_1 and S_2 are said to be overlapping if either $I_1 \cap I_2 \neq \emptyset$ or $J_1 \cap J_2 \neq \emptyset$. Therefore, if the observed data points in Ω were suitably partitioned into non-overlapping groups, then each group could be *independently* processed.

A simple way to group the data is to divide our matrix $\mathbf{M}$ into four smaller blocks. An illustration is displayed in Fig. 2. For consistency with [1] we will refer to these blocks as *chunks* and index any chunk C as $C_{a,b}$ where a and b are row and column indices of the chunk in the partitioned matrix. From Fig. 2, it is clear that the blocks on the diagonal of $\mathbf{M}$, $\mathbf{B_{1,1}}$ and $\mathbf{B_{2,2}}$, are non-overlapping, as are the off-diagonal blocks, $\mathbf{B_{1,2}}$ and $\mathbf{B_{2,1}}$. It is also clear that any two chunks $C_{a,b}$ and $C_{a',b'}$ are overlapping if $a = a'$ or $b = b'$.

We know that non-overlapping chunks can be safely processed in parallel; so we will define two *rounds* of chunks where $R_1 = \{C_{1,1}, C_{2,2}\}$ and $R_2 = \{C_{2,1}, C_{1,2}\}$; in this way we are free to process the chunks in each round in parallel as they are non-overlapping. If we process the rounds sequentially, no two parallel processes will ever be writing or reading from the same rows of $\mathbf{R}$ or $\mathbf{L}$ at the same time and we can eschew any *locking* delays between the different processes.

Extending our example, we observe that if we have the means to process p chunks in parallel we will need to divide our matrix into p^2 chunks and divide the chunks into p rounds. Before we can determine the appropriate chunk for the data points $(i,j) \in \Omega$ we generate random permutations of the row and column indices of our matrix $\mathbf{M}$, π_{row} and π_{col} to ensure that the data points in any chunk differ between subsequent

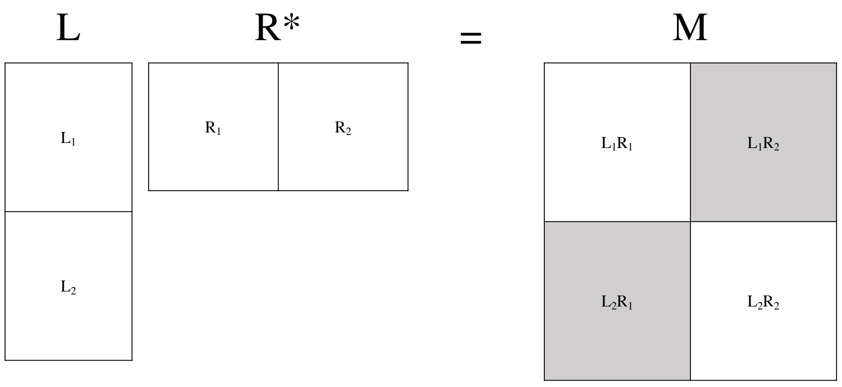


Figure 2: *A chunking of our matrix. Non-overlapping chunks are of the same color and are grouped into rounds. Here we have 4 chunks in 2 rounds.*

passes over that data set. In addition, we use *without-replacement* sampling to determine the order that observed samples are placed in chunks. Again, from [1] we place any data point $(i, j) \in \Omega$ in the chunk $C_{a,b}$ according to the following *shuffling rule*:

$$a = \left[\frac{p}{n_r}(\pi_{row}(i) - 1)\right] + 1 \text{ and } b = \left[\frac{p}{n_c}(\pi_{col}(j) - 1)\right] + 1. \tag{2.11}$$

With the entire data set placed into chunks we are ready to perform our parallel gradient updates.

3 GPUFish

3.1 Optimized computation

Thus far, our approach is a straightforward adaptation of Jellyfish for the 1-bit matrix completion problem. However, in contrast with [1], we will perform our updates on a graphics processing unit (GPU) which, unlike a traditional CPU, can perform simultaneous computations on different parts of the data.

We provide a high level description of the organization of a GPU. Each process instantiated on the GPU is known as a *kernel*. A kernel can be executed in parallel across several threads of the GPU. The programmer (or compiler) groups the parallel threads into *blocks* and the blocks into a grid of blocks. When launching a kernel on the GPU, the user controls the number of blocks to launch as well as the number of threads per block to launch. Each thread launched by the kernel executes an instance of that kernel. Threads in a block execute concurrently. The execution of thread blocks is performed by *streaming multiprocessors*, or SMs for short. The number of blocks that can be executed in parallel by a single SM depends on the resources used by each block, the resources available in each SM, and the number of SMs in the GPU.

We leverage this architecture for our incremental gradient descent algorithm. Suppose that we have divided Ω into p^2 chunks. We will launch a single kernel for each of the p rounds we have created. As noted above, the kernels must be launch sequentially to perform the parallel updates without fine-grained locking. Each round will contain p chunks so we will instantiate our kernel with p blocks. Each block will be responsible for performing gradient updates (2.9) for all data points (samples) in the corresponding chunk. Each block of the kernel will contain r worker threads, where r is the rank of $\mathbf{M}$. Each thread, t_k, in a given block will be

Algorithm 1 GPUFish

```
Given: a data set $\Omega$
1: Permute rows and columns of $\mathbf{M}$, shuffle $\Omega$
2: Separate $\Omega$ into $p^2$ chunks
3: Round[i] = $p$ chunks s.t. all chunks are non-overlapping
4: Transfer data for Round[1] to GPU
5: for i = 1 to $p$ in parallel do
6:     Launch GPU_Gradient_Updates kernel with $p$ blocks and $r$ threads per block
7:     Transfer data for Round[i+1] to GPU overwriting the data from Round[i-1]
8: end for
```

Algorithm 2 GPU_Gradient_Updates

```
Given: $p$ chunks
1: for each of $p$ chunks in parallel do
2:     for each data point $(i, j, rating)$ in the chunk do
3:         apply (2.9) to $\mathbf{L}$ and $\mathbf{R}$
4:     end for
5: end for
```

responsible for updating $\mathbf{L}_{ik}$ and $\mathbf{R}_{jk}$, that is the k^{th} entry in the rows of $\mathbf{L}$ and $\mathbf{R}$ being updated by 2.9 according to the data point $(i, j, Y_{i,j})$. In this way, we not only perform the gradient updates for a large number of data points, but also update *in parallel* the r entries of any row of $\mathbf{L}$ or $\mathbf{R}$. In contrast with [1], using this procedure we get an r-fold speedup *per round*.

We can further optimize running time as follows. While a given kernel (corresponding to one of the rounds) is being processed by the GPU, we simultaneous loading the data required to execute the next kernel onto the GPU. At the completion of the given we remove its data from the GPU and continue to the next round. The process of chunking our data and then performing parallel gradient updates over p kernels is known as an *epoch*. Because each epoch requires a new shuffle of our dataset, we begin each epoch by launching a separate CPU thread to compute the shuffle required for the next epoch; this extra CPU thread is executed in parallel with the GPU kernel launches being handled by the main CPU.

The procedure above is an adaptation of JELLYFISH for the GPU, which we will call GPUFISH. Algorithm 1 describes the overall action of a single epoch of GPUFISH.

3.2 Data management

We discuss some specific schemes for managing the various observations and variables that a practical implementation of GPUFISH would encounter. As mentioned above, to compute our gradient updates (2.9) we launch p blocks each with r threads; where r is the rank of our matrix. Each block is responsible for the serial processing of all the points in a single chunk and the threads allocated to each block allow us to load, update and store in memory the relevant rows $\mathbf{L}$ and $\mathbf{R}$ in a single step.

Before the first epoch, the matrices $\mathbf{L}$ and $\mathbf{R}$ are loaded into the *global memory* of the GPU where they can be accessed by all threads of the GPU. We initialize $\mathbf{L}$ and $\mathbf{R}$ with uniformly distributed random entries from $[-0.5, 0.5]$, we scale these entires by $\frac{1}{sqrt(n_r \times n_c)}$. Thread access to global memory is generally slow, so rather than make repeated calls to global memory we begin by loading the relevant rows of $\mathbf{L}$ and $\mathbf{R}$ into *shared memory* on the GPU. This memory is shared only between the threads of each block and access to it is significantly faster than global memory. After completing our computation of (2.8) from our copies of $\mathbf{L}$ and $\mathbf{R}$ in shared memory we write the our updates to $\mathbf{L}$ and $\mathbf{R}$ back to global memory.

In addition to making use of the GPU's faster shared memory, we also make use of the ability of the GPU's

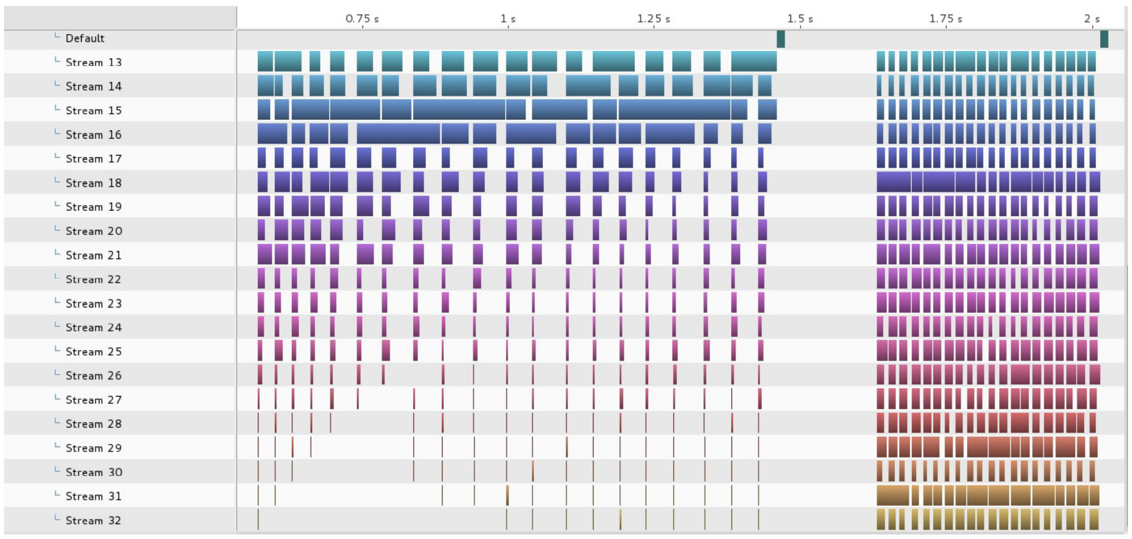


Figure 3: *A visualization of two epochs. Each bar represents gradient updates as performed by a single chunk. Here* $p = 20$ *so there are 20 rounds, each containing 20 chunks; each of the 20 chunks is processed in parallel. This image was produced by NVIDIA Visual Profiler, to generate it Algorithm 1 was modified to launch* p *individual kernels on* p *streams in place of one kernel with* p *blocks.*

ability to transfer data from the while processing a kernel(s). Rather than transfer the entire permuted data set onto the GPU, at the beginning of each epoch we transfer the data needed for the first round of gradient updates and launch the kernel responsible for performing updates on the data. As this kernel processes the first round we gather the data required to process round two and load it onto the GPU. During the processing of round two we overwrite the samples corresponding to the first round with the data for the next (third round). This procedure is repeated until the epoch has finished. While providing an obvious speedup over performing all of the data transfers at once, this data management scheme also enables us to only have two rounds worth of data (approximately $\frac{2\times\|\Omega\|}{p}$ data points) on the GPU at any one. This enables GPUFish to process *very large data sets* even on memory-limited GPUs.

In Fig. 3 we provide a visualization of the execution of two epochs of GPUFish. We execute the first epoch without permuting the rows and columns of Ω and note the irregular sizes of the chunks. Before the second epoch begins, we shuffle the data before partitioning it into chunks. The shuffling process has spread the data points in Ω evenly across the chunks, resulting in a decreased runtime for the epoch.

4 Performance Evaluation

4.1 Experimental setup

All experiments were performed on a Dell workstation equipped with: a 6-core Xeon E5-2620 v3 CPU, 64GB of RAM, a 256GB Class 30 SSD, and an NVIDIA GeForce GTX 1080 GPU. For our experiments, we use Linux 3.10.0-327 along with NVCC V8.0.26.

4.2 Low rank matrix recovery

We begin by examining the sample complexity required to successfully recover the underlying matrix M (Here, we work in the 1-bit matrix completion setting where successful "recovery" is defined as estimating a matrix from the signs of a subset of its observations).

We describe the experimental setup. A random $n_r \times n_c$ matrix $\mathbf{M}$ was formed such that $\mathbf{M} = \mathbf{M}_L\mathbf{M}_R^*$ where $\mathbf{M}_L$ is $n_r \times r$ and $\mathbf{M}_R$ is $n_c \times r$; the entires of $\mathbf{M}_L$ and $\mathbf{M}_R$ were independently sampled from a uniform distribution on $[-\frac{1}{2}, \frac{1}{2}]$. Here $n_r = n_c = 4000$. Entries of $\mathbf{M}$ were drawn at random for both the training set (the size of which varied) and the test set (1000 entries). The input parameters for our model — the maximum row sum of $\mathbf{M}$ and the gradient step size α — were determined using a grid search. The input rank to the model was the (known) true rank of $\mathbf{M}$, though overestimating the rank seemed to have little effect on our results. To measure accuracy of our model we record the percentage of samples in our test set whose sign is correctly predicted by the sign of $f(\hat{\mathbf{M}})$ where $\hat{\mathbf{M}}$ is our estimate of $\mathbf{M}$. Figure 1 displays results for the $r = 1$ and $r = 3$ cases.

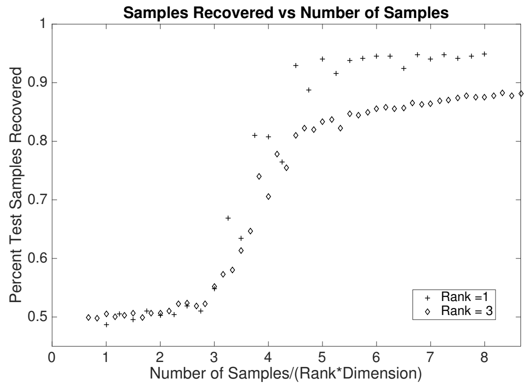


Figure 4: *Percentage of test samples recovered as a function of the number of samples input into* GPUFish. *Here the number of samples is given as a fraction of the rank of the matrix ($r = 1$ and $r = 3$) and the dimension ($d = 4000$).*

4.3 Collaborative filtering with real data

In our next batch of experiments we test the ability of GPUFish to make predictions in the collaborative filtering environment on real-world data. Specifically we make predictions about user interest in movies for the Movielens (100k , 1m and 20m) data set [9]. Where possible we compare our results to those produced from the code released with [2].

We transform the user-movie ratings from the Movielens data set (integers in $[1, 5]$) to one-bit observations by subtracting the average over all ratings (approximately 3.5) from each rating and recording the sign. Our input parameters, including rank, are again determined by a grid search. Each instance of GPUFish was terminated after 20 epochs. For each Movielens data set (100k, 1M and 20M) we remove 5,000 ratings for testing purposes, and train the model with the remaining ratings. In Table 1 we present the percentage of one-bit ratings correctly recovered by GPUFish as a function of the original rating. We also display the overall percentage of ratings correctly recovered as well as the runtime of the algorithm.

In Table 2 we present the present the results of GPUFish as run on the Movielens 20M data set. Here users are allowed to rate movies on a scale from $[0.5, 1, 1.5, \ldots, 5]$.

Empirically we were able to determine the number of blocks per kernel (the number of chunks in a round) that results in the smallest run time. The results are presented in Figure 4.3. For each epoch we perform two processes in parallel: gradient updates on the GPU and the permuting and chunking Ω; the run time of each epoch is the max of the time taken by either of these two processes. Examining Figure 4.3 we see that executing GPUFish with a larger number of blocks per kernel can only decrease our runtime to the extent

Original Rating	1	2	3	4	5	Overall	Runtime(s)
GPUFish: ML 100k	80%	77%	58%	71%	87%	**72%**	**0.30**
1-Bit: ML 100k	79%	73%	58%	75%	89%	**73%**	47
GPUFish: ML 1m	86%	74%	55%	75%	92%	**74%**	**1.1**
1-Bit: ML 1m	84%	76%	53%	77%	94%	**75%**	3130

Table 1: *A comparison between 1-bit matrix completion from [2] and the 1-bit matrix completion implemented in* GPUFish*.* GPUFish *produces results on par with the traditional 1-bit approach and is able to do so in a fraction of the runtime.*

Original Rating	0.5	1	1.5	2	2.5	3	3.5	4	4.5	5	Overall
GPUFish: ML 20m	84%	85%	89%	81%	85%	68%	63%	67%	82%	88%	74%

Table 2: *The results of* GPUFish *operating on the almost 20 million entires of the of the Movielens 20m data set. Runtime: 30 seconds.*

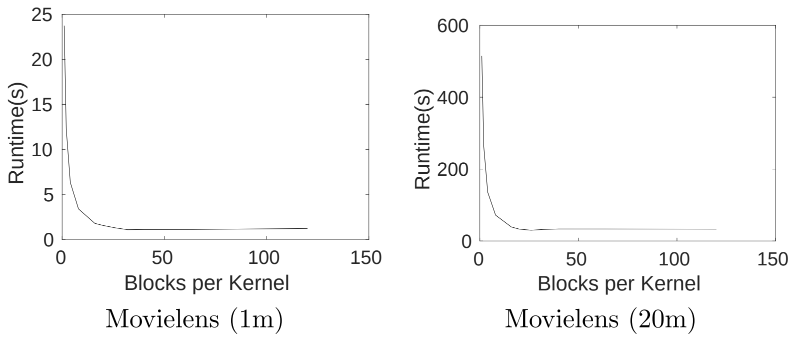


Figure 5: The runtime of 20 epochs of GPUFish vs the number of blocks per kernel

that it is no longer determined by the execution of gradient updates. At approximately 30 blocks per kernel our gradient updates can be performed faster than our permutations and chunking and we no longer see a decrease in runtime.

4.4 Effect of chunking

We now present preliminary results relating to the effect of chunking on the ability of GPUFish to make accurate predictions. For both the Movielens 1m and 20m data sets GPUFish was run as described in Algorithm 1 and then run with a modified algorithm where the data was permuted and chunked prior to epoch one and never again. Recall that chunking for epoch *t+1* is performed in parallel with the gradient updates for epoch *t*; ideally these steps would take equal amounts of time but, as shown in Table 3, we find that after the initial permutation of data additional permutations significantly increase the time per epoch of GPUFish, but have little effect on the accuracy of our predictions.

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GPUFish	Data set	Accuracy	Runtime (s)	Time per epoch (s)
w/ chunking	ML 1m	74%	1.1	0.055
w/o chunking	ML 1m	74%	0.48	0.024
w/ chunking	ML 20m	74%	30	1.5
w/o chunking	ML 20m	74%	6.5	0.33

Table 3: GPUFish *run with and without between-round chunking on the Movielens 1m and 20m data sets. Removing between-round chunking had no effect on accuracy and significantly decreased runtime.*

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