Matrix Completion with Weighted Constraint for Haplotype Estimation

S. Majidian, M. Mohades, and M.H. Kahaei

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1 abstract

A new optimization design is proposed for matrix completion by weighting the measurements and deriving the corresponding error bound. Accordingly, the Haplotype reconstruction using nuclear norm minimization with Weighted Constraint (HapWeC) is devised for haplotype estimation. Computer simulations show the outperformance of the HapWeC compared to some recent algorithms in terms of the normalized reconstruction error and reconstruction rate.

2 Introduction

Matrix completion has already been applied to collaborative filtering, system identification, global positioning, and remote sensing problems. A model defined for matrix completion is [1]

$$Y_{ij} = M_{ij} + Z_{ij} \quad \forall (i,j) \in \Omega \tag{1}$$

where Y_{ij} , M_{ij} , and Z_{ij} are the entries of \boldsymbol{Y} , \boldsymbol{M} , and \boldsymbol{Z} , respectively showing the measurement, desired low-rank, and noise matrices, all with $N \times l$ dimensions. Also, Ω represents the measurement set and, without loss of generality, we assume that N < l. To estimate \boldsymbol{M} , the following minimization has been proposed [1].

$$\min_{\boldsymbol{X}} \|\boldsymbol{X}\|_{*} \quad \text{s.t.} \quad \|P_{\Omega}(\boldsymbol{X} - \boldsymbol{Y})\|_{F} \le \delta$$
(2)

in which $[P_{\Omega}(\mathbf{A})]_{ij} = A_{ij}$ for $(i, j) \in \Omega$ and zero, otherwise. Also, $\|\cdot\|_F$ and $\|\cdot\|_*$ denote the Frobenius and the nuclear norms, respectively.

Here, we consider the haplotype reconstruction problem, a.k.a haplotype assembly problem [3, 5] in which the quality of each measurement is defined by Q_{ij} . Then, the error probability of the $(i, j)^{th}$ measurement; which is exploited to estimate the haplotypes more accurately, is given by $P_{ij} = 10^{-Q_{ij}/10}$ [4].

Here, we first propose a new weighted optimization scheme in which each measurement is utilized based on its Q_{ij} and the corresponding error bound is derived. Accordingly, the weights are optimized using Q_{ij} 's. At last, an algorithm is developed to estimate haplotypes.

3 Proposed optimization

In order to cope with diverse quality of data, we introduce the following optimization problem called the Nuclear norm minimization with a Weighted Constraint (NuWeC):

$$\min_{\mathbf{X}} \|\mathbf{X}\|_{*} \quad \text{s.t.} \ \|\mathbf{W} \odot P_{\Omega}(\mathbf{X} - \mathbf{Y})\|_{F} \le \delta,$$
(3)

where \odot is the Hadamard product and \boldsymbol{W} is the weight matrix which will be introduced in the next sections. The geometric interpretation of proposed optimization in (3) is illustrated in Fig. 1 in which the ellipsoid is the feasible set intersecting the smallest nuclear norm ball at $\hat{\boldsymbol{M}}$ showing the optimal point. The error bound of the NuWeC is derived in Theorem 1.



Figure 1: Geometric interpretation of the proposed nuclear norm minimization with weighted constraint.

Theorem 1. Consider \hat{M} as the optimal point of the optimization problem (3). Then, we obtain

$$\|\hat{\boldsymbol{M}} - \boldsymbol{M}\|_{F} \le 2\delta \sqrt{\frac{p+2}{p} \frac{N}{(1-\alpha)^{2}} + 1} \left\{ \sum_{ij} \frac{1}{W_{ij}^{2}} \right\}^{1/2}$$
(4)

in which $p = \frac{|\Omega|}{Nl}$ is the sampling rate and $0 < \alpha < 1$ is a numerical constant. **Proof:** By denoting $\boldsymbol{H} \triangleq \hat{\boldsymbol{M}} - \boldsymbol{M}$, we intend to bound $\|\boldsymbol{H}\|_F^2 = \|\boldsymbol{H}_{\Omega}\|_F^2 + \|\boldsymbol{H}_{\Omega^c}\|_F^2$, where $\boldsymbol{H}_{\Omega} = P_{\Omega}(\boldsymbol{H}), \, \boldsymbol{H}_{\Omega^c} = P_{\Omega^c}(\boldsymbol{H})$, and P_{Ω^c} is the complement operator of P_{Ω} . One can easily see that the following inequality holds,

$$\|\boldsymbol{H}_{\Omega}\|_{F} \leq \|P_{\Omega}(\hat{\boldsymbol{M}} - \boldsymbol{Y})\|_{F} + \|P_{\Omega}(\boldsymbol{M} - \boldsymbol{Y})\|_{F}.$$
(5)

To bound the term $||P_{\Omega}(\hat{M} - Y)||_{F}$, we first note that for a give matrix A, using the Holder inequality and $||a||_{2} \leq ||a||_{1}$, we can derive

$$\|\boldsymbol{A}\|_{F} \leq \left\{ \sum_{ij} \frac{1}{W_{ij}^{2}} \right\}^{1/2} \left\{ \sum_{ij} W_{ij}^{2} A_{ij}^{4} \right\}^{1/2} \\ \leq \left\{ \sum_{ij} \frac{1}{W_{ij}^{2}} \right\}^{1/2} \sum_{ij} W_{ij} A_{ij}^{2}.$$
(6)

Then, for the feasibile point $\hat{\boldsymbol{M}}$ in (3) which satisfies the constraint $\|\boldsymbol{W} \odot P_{\Omega}(\hat{\boldsymbol{M}} - \boldsymbol{Y})\|_{F} \leq \delta$ and defining $\boldsymbol{A} = P_{\Omega}(\hat{\boldsymbol{M}} - \boldsymbol{Y})$, we obtain from (6)

$$\|P_{\Omega}(\hat{\boldsymbol{M}} - \boldsymbol{Y})\|_{F} \leq \left\{\sum_{(i,j)\in\Omega} \frac{1}{W_{ij}^{2}}\right\}^{1/2} \delta.$$
(7)

Now, we show the feasibility of M in (3) to conclude that (7) also holds for M similar to \hat{M} . To do so, we can write

$$\|\boldsymbol{W} \odot P_{\Omega}(\boldsymbol{M} - \boldsymbol{Y})\|_{F}^{2} = \sum_{(i,j)\in\Omega} W_{ij}^{2} (M_{ij} - Y_{ij})^{2}$$
$$= \sum_{(i,j)\in\Omega} W_{ij}^{2} Z_{ij}^{2} \le \|\boldsymbol{W}\|_{\infty}^{2} \|\boldsymbol{Z}\|_{F}^{2} < \delta^{2},$$
(8)

where $\|\boldsymbol{W}\|_{\infty} = \max \boldsymbol{W}_{ij}$. This result shows that \boldsymbol{M} is feasible for $\delta > \|\boldsymbol{W}\|_{\infty} \|\boldsymbol{Z}\|_{F}$ and thus the last term of (5) is bounded. Using these results in (5) leads to

$$\|\boldsymbol{H}_{\Omega}\|_{F} \leq 2\delta \left\{ \sum_{(i,j)\in\Omega} \frac{1}{W_{ij}^{2}} \right\}^{1/2}.$$
(9)

On the other hand, based on [1], with a high probability, H_{Ω^c} obeys

$$\|\boldsymbol{H}_{\Omega^{c}}\|_{F}^{2} \leq (1+\frac{2}{p})\frac{N}{(1-\alpha)^{2}}\|\boldsymbol{H}_{\Omega}\|_{F}^{2},$$
(10)

in which $0 < \alpha < 1$ can be taken equal to $\frac{1}{2}$. From (9) and (10), the bound given by (4) in Theorem 1 is proved.

4 Optimization of weights

We now consider the bound derived in Theorem 1 as an objective function to optimize W as follows:

$$\min_{\mathbf{W}} 2\delta \sqrt{\frac{p+2}{p} \frac{N}{(1-\alpha)^2} + 1} \left\{ \sum_{ij} \frac{1}{W_{ij}^2} \right\}^{1/2} \text{ s.t. } \|P_{\Omega}(\mathbf{W})\|_{\infty} = 1.$$
(11)

Furthermore, in order to exploit the error probabilities, we suggest the following relationship:

$$W_{ij} = a \log_2\left(\frac{1}{P_{ij}}\right) + b \quad (i,j) \in \Omega,$$
(12)

in which an entry with a lower error probability will be more effective on the penalty term of (3), *i.e.*, $\sum W_{ij}^2 (M_{ij} - Y_{ij})^2$. Making use of the logarithmic function enables us to incorporate all the measurements while restricting the large variation of error values. Then, by substituting (12) in (11), we get the following optimization problem:

$$\min_{a,b} \sum \frac{1}{(a \log_2\left(\frac{1}{P_{ij}}\right) + b)^2} \quad \text{s.t.} \ \max\{a \log_2\left(\frac{1}{P_{ij}}\right) + b\} = 1.$$
(13)

Using $b = 1 + a \log_2 P_{\min}$ in (13), the corresponding unconstrained non-convex optimization problem may be solved by a grid search.

5 Proposed algorithm for haplotype reconstruction

For the haplotype reconstruction problem, $\mathbf{Y} \in \{0, \pm 1\}^{N \times l}$, $\mathbf{M} \in \{\pm 1\}^{N \times l}$, and $\mathbf{Z} \in \{0, \pm 2\}^{N \times l}$ described by (1) are the read, haplotype, and the noise matrices, respectively [3]. For diploids, \mathbf{M} consists of two different rows \mathbf{h}_1 and \mathbf{h}_2 and thus its rank is 2. The goal of haplotype reconstruction is to estimate two rows of \mathbf{M} using the read matrix. By exploiting the NuWec optimization problem given by (3), we develop the "Haplotype reconstruction using nuclear norm minimization with Weighted Constraint (HapWeC)" algorithm as below.

Algorithm 1: Haplotype reconstruction using nuclear norm minimization with Weighted Constraint (HapWeC)

Input : N reads and quality scores Q_{ij} **Output:** Haplotypes

- 1 Construct the read matrix \boldsymbol{M} $(N \times l)$.
- **2** Calculate the error probability using $P_{ij} = 10^{-Q_{ij}/10}$.
- **3** Find the weights based on (13).
- 4 Find \hat{M} using convex optimization problem (3).
- **5** Compute the SVD of $\hat{\boldsymbol{M}} = \sum_{i=1}^{r} \sigma_i x_i y_i^T$.
- 6 Truncate the SVD by setting all singular values to zero except the two largest ones: $T(\hat{M}) = \sum_{k=1}^{2} -\pi e^{T}$
 - $T_2(\hat{\boldsymbol{M}}) = \sum_{i=1}^2 \sigma_i x_i y_i^T.$
- 7 Obtain haplotypes \hat{h}_1 and \hat{h}_2 by extracting the independent rows of $T_2(\hat{M})$.
- **s** Round the haplotypes h_1 and h_2 to ± 1 .

It can be shown that by truncating the Singular Values Decomposition (SVD) of \hat{M} , the error bound is changed by a factor of $k = 1 + \sqrt{\operatorname{rank}(\hat{M}) + 1}$, *i.e.*, $\|T_2(\hat{M}) - M\|_F^2 \leq k \|\hat{M} - M\|_F^2$.

6 Simulation results

First, we evaluate the NuWeC using a synthetic dataset. To do so, a rank-two random matrix $M \in \{\pm 1\}^{40 \times 40}$ is generated whose 10% of entries are contaminated with noise. We consider both nuclear minimization problem and the NuWeC defined by (2) and (3), respectively. The Normalized Reconstruction Error (NRE) is defined as

$$NRE = \frac{1}{n} \sum_{i=1}^{n} \frac{\|\hat{\boldsymbol{M}}^{(i)} - \boldsymbol{M}\|_{F}}{\|\boldsymbol{M}\|_{F}},$$
(14)

where $\hat{\boldsymbol{M}}^{(i)}$ shows the estimated desired matrix in the i^{th} experiment and n = 20 is the number of independent Monte Carlo experiments. The NREs are shown as a function of the sampling percentage in Fig. 2. As seen, the NREs of NuWeC decreases about 2dB which is effectively due to incorporation of the quality scores.

In the second scenario, we consider the read database of [2]. The number of reads and the haplotype length are selected as N = 86 and l = 100, respectively. Also, the sampling percentage is



Figure 2: NREs of NuWeC and nuclear minimization problems vs. the sampling percentage for the synthetic data.

p = 7% and the coverage per column is 6. The results in Fig. 3 show the superiority of the NuWeC compared to the nuclear minimization by reducing the NREs. Now, we compare the proposed



Figure 3: NREs vs. the percentage of noisy entries for the NuWeC and nuclear minimization problems based on the dataset addressed in [2].

HapWeC with the nuclear minimization, NuWeC, and alternating minimization algorithm [6] for haplotype reconstruction. To inspect the estimated and actual haplotypes, the reconstruction rate (rr) is defined as [2]

$$rr = 1 - \frac{1}{4nl} \sum_{i=1}^{n} \|\hat{\boldsymbol{h}}_{1}^{(i)} - \boldsymbol{h}_{1}\|_{1} + \|\hat{\boldsymbol{h}}_{2}^{(i)} - \boldsymbol{h}_{2}\|_{1},$$
(15)

where $\hat{h}_{2}^{(i)}$ and $\hat{h}_{1}^{(i)}$ are the estimated haplotypes of the i^{th} experiment. Decrease of the reconstruction rates shown in Fig. 4 reveal the outperformance of the developed HapWeC.



Figure 4: Comparison of reconstruction rate vs. the percentage of noisy entries for different algorithms based on the dataset addressed in [2].

7 Conclusion

The NuWec, a new weighted optimization algorithm was developed for matrix completion by exploiting the quality of measurements and the corresponding error bound was derived. Computer simulations showed about 2dB reduction in the resulting estimation error compared to that of the nuclear norm minimization technique. The NuWeC was then used to design the new HapWeC algorithm for haplotype estimation. This algorithm increased the reconstruction rate about 10% in camparison to some recent methods.

Mohammad Hossein Kahaei, (School of Electerical Engineering, Iran University of Science & Technology, Tehran, Iran.)

E-mail: kahaei@iust.ac.ir

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