How to Color a Checkerboard with a Given Distribution – Matrix Rounding Achieving Low 2×2-Discrepancy

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Abstract

Motivated by a digital halftoning application to convert a continuous-tone image into a binary image, we discusses how to round a $[0,1]$-valued matrix into a $\{0,1\}$ binary matrix achieving low discrepancy with respect to the family of all 2×2 square submatrices (or regions). A trivial upper bound of the discrepancy is 2 and the known lower bound is 1. In this paper we shall show how to achieve a new upper bound $5/3$ using a new proof technique based on modified graph matching.

1 Introduction

Rounding real numbers into discrete values frequently occur in practice. In this paper we are interested in rounding a two-dimensional matrix of real entries in the interval $[0,1]$ into a binary (i.e., $\{0,1\}$-valued) matrix. To measure the discrepancy between an input real matrix and the resulting binary matrix, we introduce a family $\mathcal{F}$ of regions (submatrices) over the matrix and define the discrepancy by the maximum difference between the sums of entries in all regions in the family. It is known [5] that we can bound the discrepancy by 1 when the family consists of all rows and all columns.

Little is known for a family consisting of small-sized two-dimensional regions. The authors proved that the problem to find an optimal binary matrix minimizing the discrepancy with an input real matrix is NP-hard even for a family of all 2×2 regions [2, 3]. On the other hand, if we have two different partitions of a matrix into 2×2 square regions, we can find an optimal rounding into a binary matrix and also we can show that the discrepancy is always strictly less than 1 for the family of 2×2 regions in these two partitions.

For the family $\mathcal{F}_2$ of all 2×2 regions, based on an odd cycle argument, we can show that there is a $[0,1]$-valued matrix such that the discrepancy of an optimal rounding is exactly 1 for the family of all 2×2 regions. On the other hand, it is quite easy to give a rounding with discrepancy 2 by rounding each entry independently to its nearer integer. Since the error generated from each entry is at most $1/2$, the error amounts to 2 for a 2×2 region. However, it is nontrivial to improve these upper bound and lower bound. Previously, the authors claimed
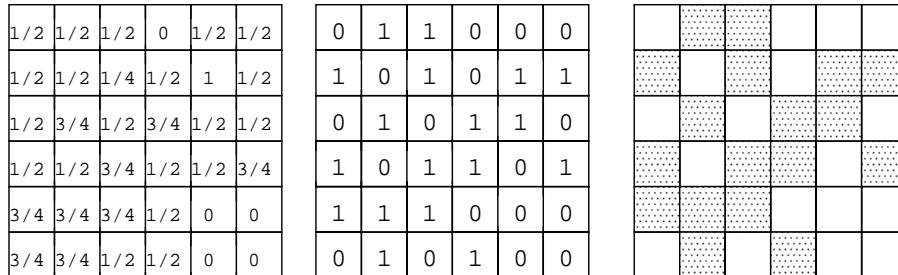
1/2	1/2	1/2	0	1/2	1/2
1/2	1/2	1/4	1/2	1	1/2
1/2	3/4	1/2	3/4	1/2	1/2
1/2	1/2	3/4	1/2	1/2	3/4
3/4	3/4	3/4	1/2	0	0
3/4	3/4	1/2	1/2	0	0

0	1	1	0	0	0
1	0	1	0	1	1
0	1	0	1	1	0
1	0	1	1	0	1
1	1	1	0	0	0
0	1	0	1	0	0

Figure 1: A rounding and its corresponding (generalized) checkerboard

a 7/4 upper bound in a conference paper [2]; Unfortunately, the proof has not been published yet formally, since it is based on complicated case analysis.

In this paper, we give an improved upper bound 5/3 for the family $\mathcal{F}_2$ of all 2×2 regions. We give a systematic argument as well as the improved bound. A key idea is to apply a recursive rounding procedure after discretizing input real values into several distinct values. Also, we apply a variation of matching in a graph to give the construction.

If each entry of the original matrix has a value 0.5, it is obvious that the parity-rounding (rounding an entry into 1 if and only if the sum of its row index and its column index is even) gives a perfect (zero-error) rounding. If we consider the rounded matrix as a square $n \times n$ array on a playing board, and color a cell black (resp. white) if it corresponds to a 1-valued (resp. 0-valued) entry, the parity rounding gives the checkerboard pattern. Thus, what we are aiming at is a combinatorial problem to design a checkerboard pattern approximating a given general $[0, 1]$-valued distribution instead of the special uniform distribution. We remind that the discrepancy theory (with respect to a wider class of region families) on a uniform distribution is a major topic in combinatorics and Monte-Carlo simulation [6]. Fig. 1 gives an example of rounding (its rounding error for $\mathcal{F}_2$ is 0.5) and its corresponding checkerboard pattern.

Besides its combinatorial charm, this work is motivated by an application to digital halftoning, which is an important technique to generate a binary image that looks similar to an input continuous-tone image. This kind of technique is indispensable to print an image on an output device that produces black dots only, such as facsimiles and laser printers. Up to now, a large number of methods and algorithms for digital halftoning have been proposed (see, e.g., [9, 8, 4, 10, 11, 12]). A common criterion for the quality of output binary image is FWMSE (Frequency Weighted Mean Square Error). Simply speaking, it is to minimize the sum of all squared errors for a family of all $k \times k$ regions where error in a region is given by difference of the weighted sums in the input and output images. This criterion corresponds to L_2 distance. Our criterion based on the discrepancy is the L_∞ distance version of the problem for $k = 2$. We omit proofs of several lemmas in this version because of space limitation.

2   Matrix Rounding Problem with Related Works

Given a real number α, its *rounding* is either $\lfloor \alpha \rfloor$ or $\lceil \alpha \rceil$. Given an $n \times n$ matrix $A = (a_{ij})_{1 \leq i,j \leq n}$ of real numbers, its rounding is an integral matrix $B = (b_{ij})_{1 \leq i,j \leq n}$ such that each entry b_{ij} is a rounding of a_{ij}. There are 2^{n^2} possible roundings of a given A, and we would like to find an optimal rounding with respect to a given criterion. This is called the *matrix rounding problem*. In this paper we are interested in the case in which each entry of A is in the closed interval

$[0, 1]$ and each entry is rounded to either 0 or 1. It is a special case of discrepancy problems [7].

In order to give a criterion to determine the quality of roundings, we define a distance in the space $\mathcal{A}$ of all $[0, 1]$-valued matrices. We introduce a family $\mathcal{F}$ of regions over the $n \times n$ integer grid. Let R be a region in $\mathcal{F}$. For an element $A \in \mathcal{A}$, let $A(R)$ be the sum of entries of A located in the region R. The l_∞ distance between two elements A and A' in $\mathcal{A}$ with respect to $\mathcal{F}$ is defined by

$$Dist_\infty^{\mathcal{F}}(A, A') = \max_{R \in \mathcal{F}} |A(R) - A'(R)|.$$

Although analogously defined l_1 and l_2 distances are also popular, we are concerned with the l_∞ distance in this paper.

Once we define a distance in $\mathcal{A}$, the optimal rounding B of a given $[0, 1]$-valued matrix A is a binary matrix in $\mathcal{A}$ that is closest to A in the sense of the above-defined distance. Such a binary matrix B is called the *optimal rounding* of A, and the distance between A and B is referred to as the *optimal rounding error*.

The supremum of the optimal rounding error $\sup_{A \in \mathcal{A}} \min_{B \in \{0,1\}^d} Dist_\infty^{\mathcal{F}}(A, B)$ is called the *inhomogeneous discrepancy* of $\mathcal{A}$ with respect to the family $\mathcal{F}$ [7]. We consider the following problem:

> Discrepancy Problem: For a given region family $\mathcal{F}$, give combinatorial upper and lower bounds of the inhomogeneous discrepancy with respect to $\mathcal{F}$.

The difficulty of the above problem depends on geometric property of the family $\mathcal{F}$ of regions. We could consider the one-dimensional version of the problem, which is referred to as the sequence rounding problem. The inhomogeneous discrepancy with respect to $Dist_\infty^{\mathcal{F}}$ is less than 1 for any family $\mathcal{F}$ of intervals. On the other hand, it can be infinitesimally near to 1 even if we consider the family of all intervals of length 2. Therefore, the discrepancy problem is easily settled. Moreover, the authors showed in [2] that the optimal rounding of a sequence can be computed in $O(\sqrt{n}|\mathcal{F}| \log^2 n)$ time with respect to any given family $\mathcal{F}$ of intervals. A basic idea was a procedure to detect a negative cycle in a network.

For the matrix rounding problem, the inhomogeneous discrepancy depends on the choice of the family $\mathcal{F}$ of regions: If $\mathcal{F}$ is the set of all orthogonal regions, an $O(\log^3 n)$ upper bound and $\Omega(\log n)$ lower bound are known [7]. On the other hand, Baranyai [5] showed that the inhomogeneous discrepancy is less than 1 if $\mathcal{F}$ consists of $2n + 1$ regions corresponding to all rows, columns and the whole matrix. Baranyai's result is applied to problems in operations research ([1] pp.171–172).

Motivated from an application in *digital halftoning*, we would like to consider the family $\mathcal{F}_k$ consisting of all $k \times k$ square regions for a small k. An $O(\log^3 k)$ upper bound and an $\Omega(\log k)$ lower bound of the inhomogeneous discrepancy can be obtained straightforwardly from the above mentioned known results.

However, it is combinatorially attractive to give better bounds for a small fixed constant k, and the problem seems to be highly nontrivial even for $k = 2$. Thus, we focus on the family $\mathcal{F}_2$ in this paper, and give a nontrivial $5/3$ upper bound for the inhomogeneous discrepancy.

3 Low Discrepancy Theorem for $\mathcal{F}_2$

Let $A = (a_{i,j})$ be an $n \times n$ matrix whose entries are real numbers in the interval $[0, 1]$. We denote the sum of entries $a_{i,j}, a_{i+1,j}, a_{i,j+1}, a_{i+1,j+1}$ by $A^{(2)}(i, j)$ for $1 \leq i, j \leq n - 1$. Given a $\{0, 1\}$-valued matrix B, the 2×2 discrepancy between A and B is $\max_{1 \leq i,j \leq n-1} |A^{(2)}(i, j) - B^{(2)}(i, j)|$. We prove the following theorem:

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Theorem 3.1 *For an arbitrary* $[0, 1]$*-valued matrix* A *there exists a* $\{0, 1\}$*-valued matrix* B *such that* 2×2 *discrepancy between* A *and* B *is at most* $5/3$.

The following is a key lemma:

Lemma 3.2 *If each entry of* A *is among* $0, 1/4, 1/2, 3/4$, *and* 1, *then there exists a* $\{0, 1\}$*-valued matrix* B *such that* $|A(R) - B(R)| \leq 5/4$ *holds for every* 2×2 *region* R.

We first derive the theorem assuming the lemma is true. Let α is an upper bound of the discrepancy. Given A, we construct the matrix $C = (c_{i,j})$ where

$$c_{i,j} = a_{i,j} - \frac{1}{4} \lfloor 4 a_{i,j} \rfloor.$$

Thus, $4C$ is a $[0, 1]$-valued matrix. We have a rounding D of $4C$ with discrepancy less than α. Consider the matrix $H = A - C + (D/4)$. It is easy to observe that each entry of H is among $0, 1/4, 1/2, 3/4, 1$. Hence, we have a rounding B of H such that 2×2 discrepancy between B and H is at most $5/4$. Thus, the discrepancy between B and A is less than $(5 + \alpha)/4$. We continue this argument to have a recursion $\alpha \leq (5 + \alpha)/4$, and hence $\alpha \leq 5/3$.

3.1 Basic Observations

Let $A = (a_{i,j})$ be a matrix in which each entry has a discrete value among $0, 1/4, 1/2, 3/4$ and 1. An entry is called *large* (*small*, respectively) if its value is $3/4$ or 1 ($1/4$ or 0, respectively). The entries with the values $1/2$ are called *medium* entries. A entry is indicated by a symbol L (S, respectively) if its value is $3/4$ ($1/4$, respectively). A medium entry $a_{i,j}$ is indicated by either m or M according to its parity, that is, m if $i + j$ is even, and M otherwise. Thus, two m entries are arranged diagonally or offdiagonally but never be aligned horizontally or vertically. We often indicate an integral entry (0 or 1) of A by I.

A rounding B of A is called a *tame rounding* if it satisfies the following conditions:
(1) Every large entry is rounded to 1. (2) Every small entry is rounded to 0.

We basically consider tame roundings. Thus, our control is just rounding medium entries. Indeed, this is a little cheating, since we will flip some S or L entries in the final stage of the construction. However, until then, we only consider tame roundings. Given a rounding B, a 2×2 region (rigid submatrix) R is called a *violating region* if $|B(R) - A(R)| > 5/4$. Otherwise, it is called a *safe region*. The following lemmas are elementary:

Lemma 3.3 *Let* R *be a* 2×2 *region in a given matrix. Then,* R *is a safe region for any tame rounding if (i)* R *has at most one medium entry, or (ii)* R *has both a large entry and a small entry.*

Lemma 3.4 *If a* 2×2 *region* R *has at least one medium entry and at least one* S *(*L*, resp.) entry, then* R *is safe as far as the medium entry is rounded to* 1 *(*0*, resp.).*

Lemma 3.5 *If a* 2×2 *region* R *has two medium entries, then* R *is safe as far as the two medium entries are rounded to different binary values, one to* 0 *and the other to* 1.

Lemma 3.6 *If three entries characterized as SmS or SMS (LmL or LML, resp.) are aligned horizontally or vertically in order, any* 2×2 *region containing two of them is safe as far as the middle medium entry is rounded to* 1 *(*0*, resp.).*

We call a medium element a *sandwiched element* if it is between two S or two L elements on a row or a column as in the above lemma.

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3.2   Proof of Lemma 3.2

We are now ready to prove our main lemma 3.2 which guarantees that we can always round a matrix A consisting of $0, 1/4, 1/2, 3/4$ and 1 into a binary matrix so that the rounding error is between $-5/4$ and $5/4$ for any 2×2 region in the matrix.

We first round all the sandwiched elements so that those between two S elements are turned into 1, and those between two L elements are turned into 0. It may happen that an element is sandwiched by both two S elements and two L elements (vertically and horizontally), where we flip the element into 0. We finalize the rounded values of sandwiched elements as above. For simplicity, the finalized sandwiched elements are denoted by F. From Lemma 3.6, no region containing an F element can become a violating region.

We next apply *parity rounding*, which rounds m to 0 and M to 1 for the rest of medium elements. Table 1 summarizes the error caused by pairs of elements in the parity rounding. We omit pairs containing F elements, since every region containing an F element is safe.

error $= \pm 1$	$\pm 3/4$	$\pm 1/2$	$\pm 1/4$	0
mm, MM	Sm, LM	$0m, 1m, SS, 1M, 0M, LL$	$0S, 1S, SM, Lm, 0L, 1L$	$00, mM, SL, 11$

Table 1. Error caused by pairs in the parity rounding.

Neither the pattern mm nor MM can occur vertically or horizontally in a 2×2 region. Thus, from the above table, violating regions are characterized by $\{S, m, S, m\}$ and $\{L, M, L, M\}$ where two medium entries are arranged diagonally or offdiagonally. If there is no such region, then the parity rounding gives us a rounding with discrepancy bounded by $5/4$.

The parity rounding is an intermediate stage. In the subsequent process, if we flip m to 1, we denote it by m^*, and if we flip M to 0, we denote it by M^*. We consider a violating region R consisting of S and m entries. We can symmetrically treat a region consisting of L and M entries.

R is either $\begin{pmatrix} S & m \\ m & S \end{pmatrix}$ or its rotated pattern $\begin{pmatrix} m & S \\ S & m \end{pmatrix}$ because of the parity condition. We flip at least one of the two m entries to make it safe. Such a flipped entry is denoted by m^*.

We consider the first case where two S entries are in the main diagonal position. It is easy to adapt the following argument to the second case above. Suppose we flip the m-entry in the first row. This flipping may cause side-effect. From Lemma 3.4, any 2×2 region containing the S entry and flipped medium entry m^* is always safe. Thus, we have to worry about only the region R_1 which intersects $R = R_0$ only at the flipped entry m^*. If the region R_1 is safe for the new rounding, then we stop any further flipping. We call R_1 the *sink region* of the flipping sequence and the region R the *source region*.

Note that there are many violating regions in the parity rounding, and this safe region might become violating again due to side-effect if we try to resolve other violating regions. We ignore such interaction for the time being. If a region is always safe once the flipping is done, it is called a *guarded region*.

Observation 3.7 *A region containing m^*M^*, Sm^* or LM^* is a guarded region, whereas a region containing a row or column of Im^* or IM^* is safe but not guarded, where I is an integral entry.*

$$\begin{array}{cc} & M \quad \hat{L} \\ S & m^* \quad M^* \\ m & S \end{array} \qquad \begin{array}{cc} & M^* \quad \hat{L} \\ S & m^* \quad M \\ m & S \end{array} \qquad \begin{array}{cc} & L \quad L \\ S & m^* \quad M^* \\ m & S \end{array} \qquad \begin{array}{cc} & M^* \quad L \\ S & m^* \quad L \\ m & S \end{array}$$

Figure 2: Possible situations after flipping an entry of R_1 to remove side-effect.

We note that the source region is guarded because of the above observation. If R_1 is not safe, we have to continue flipping one of medium entries in R_1. Here note that if R_1 has no other medium entry then Lemma 3.3 guarantees that R_1 is safe for any tame rounding. The region R_1 contains the flipped entry m^* at its lower left corner.

We can observe that R_1 is violating only if it is one of the following patterns: $\begin{pmatrix} M & \hat{L} \\ m^* & M \end{pmatrix}$, $\begin{pmatrix} L & L \\ m^* & M \end{pmatrix}$ and $\begin{pmatrix} M & L \\ m^* & L \end{pmatrix}$, where $\hat{L}$ is $0, 1$, or L. In the first case we have two M entries which can be flipped into M^* (flipping one of them suffices to make R_1 safe but flipping both of them still makes R_1 safe). Thus, we have two possible flipping sequences branched from a flipping from R_1. In the remaining two cases we have only one M entry to flip it into M^*. Possible situations are shown in Fig. 2.

The flipping(s) in R_1 may cause another side-effect, that is, a safe region may become violating by the flip. Such a region R_2 is characterized again by the one intersecting only at the flipped M^* entry in R_1.

Without loss of generality, we consider the case where R_1 has an M^* entry at its lower-right corner, and R_2 intersects R_1 at the entry. Due to a similar argument, the region R_2 must be $\begin{pmatrix} M^* & m \\ m & \hat{S} \end{pmatrix}$ or $\begin{pmatrix} M^* & S \\ m & S \end{pmatrix}$ or $\begin{pmatrix} M^* & m \\ S & S \end{pmatrix}$, where $\hat{S}$ is $0, 1$ or S. We can observe that the second case cannot happen; indeed, the m entry below M^* is sandwiched by two S entries, since if we write down both R and R_2, we have $\begin{pmatrix} S & m^* & M^* & S \\ m & S & m & S \end{pmatrix}$. Thus, it should be $\begin{pmatrix} S & m^* & M^* & S \\ m & S & F & S \end{pmatrix}$ in truth, and R_2 is safe.

In the first case, if $\hat{S} = S$, we can similarly see that the m entry left to the S entry must be an F entry. Thus, we assume that the $\hat{S}$ is an integral element. We can stop this flipping operation by just flipping the m entry below the M^* entry. In this case, the sequence bends, and we call the sequence has a bending end. (Otherwise, we call it has a straight end). Then, we have a pair $(m^*, \hat{S})$ with the S entry in R, and thus after the flip any 2×2 region containing the last flipped entry is safe, since m^* element is sandwiched by $\hat{S}$ and S, and the rounding error of $(\hat{S}, m^*)$ is 0.5. Thus, no region containing the m^* element is violated in the current rounding, since neither MM nor mm appears as a row in a 2×2 region of the parity rounding. We remark that the region (we also call it the sink region of the flipping sequence) containing $(\hat{S}, m^*)$ and other two entries below them might become a violated region due to side-effect caused by resolving other violated region.

For the third case, the flipping operations may continue only when the new region contains exactly two medium entries guarded by S and L from both sides. Fig. 3 depicts a typical situation where consecutive flipping operations are forced.

Lemma 3.8 *Whenever we are forced to flip medium entries consecutively, they are aligned horizontally or vertically without any bend except at the last flip.*

$$
\begin{array}{ccccccc}
 & M & \hat{L} & L & L & L & \\
S & m^* & M^* & m^* & M^* & m^* & \cdots \\
m & S & S & S & S & S &
\end{array}
\qquad\qquad
\begin{array}{ccccccc}
 & M & \hat{L} & L & L & & \\
S & m^* & M^* & m^* & M^* & b & \\
m & S & S & S & a & S &
\end{array}
$$

Figure 3: Forced consecutive flipping operations (left), and its tail region (right).

Proof We have already seen that forced consecutive flipping sequence can proceed straight horizontally or vertically. So, it suffices to show that it never bends (except the last flip). Without loss of generality we consider the situation shown in the right pattern in Fig. 3. Let R_i be the 2×2 region intersecting only at the last flipped entry. Then, by the similar argument, the diagonal entry of R_i must be S. To change the flipping direction, the entry a just below M^* must be a medium entry m. What happens when we flip the m entry into m^*? The region we have to worry about is the one containing S and m^* in its upper row. Since the lower row of the region cannot be MM, Mm^*, or m^*m^* because of the parity condition and our assumption that there is no other flipping sequence. This means the rounding error for the lower row never exceeds $-3/4$ and thus the region is safe. Therefore, we can stop the flipping sequence here at the position a in the fight pattern of Fig. 3. □

So far we have considered each violating region independently. Next we shall consider interaction among flipping sequences from different violating regions. Let us examine the safe but unguarded regions caused by a flipping sequence.

Lemma 3.9 *If a safe region is unguarded, it can become unsafe because of side-effect by other flipping sequences if it contains an I entry and three medium entries.*

Proof From Observation 3.7, we have a flipped medium entry and an I in a column. Thus, the only possibility that it becomes unsafe is that it has three medium entries and they are flipped into a same binary value. □

Usually, only the sink region is the (possible) unguarded region containing a flipped element. Unfortunately, there are some exceptional cases, where the sequence stops as one of the patterns in Fig. 4. In each of the cases, the entries **I** and **M*** in the bold letters cause a problem. Indeed, the pair I and M^* has error 0.5, and it is adjacent to m, M. Thus, it becomes violated if the M entry is flipped as a side effect of another flipping sequence; thus, it is an unguarded region that is not the sink region. If the original sink region itself is guarded, we regard the unguarded region as the sink region of the sequence; otherwise, we call the region a *subsink*, and a flipping sequence containing a subsink is called a *two-headed flipping sequence*. Patterns in Fig. 4 and their transformed analogues (i.e, figures obtained by rotating or reflecting, and/or exchanging every M with m and S with L) exhaust patterns of two-headed flipping sequences. We sometimes call *single-headed flipping sequences* for other sequences. For simplifying the subsequent argument, if the two-headed flipping sequence is ended with a bending end, and can flip the other medium entry (if exists) in the straight direction to have a single-headed flipping sequence, we take that choice instead of the two-headed flipping sequence.

An important fact is that for each case, the flipped entry in the new tempolary-safe regin is in the diagonal (resp. off-diagonal) position if the one in the orinignal sink region is in the off-diagonal (resp. diagonal) position.

Lemma 3.10 *There are either at least two single-headed flipping sequences or at least two two-headed flipping sequences from a given source region.*

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$$
\begin{array}{ccc}
 & M & \mathbf{I} & M \\
S & m^* & \mathbf{M}^* & m \\
m & S & & M
\end{array}
\qquad
\begin{array}{cccc}
 & M & m & M \\
M & \mathbf{I} & \mathbf{M}^* & I \\
S & m^* & M^* & m^* \\
m & S & S & S
\end{array}
\qquad
\begin{array}{ccc}
 & M & \mathbf{I} & M \\
S & m^* & \mathbf{M}^* & m \\
m & S & m^* & I \\
 & & M & m
\end{array}
$$

Figure 4: Patterns causing two-headed flipping sequences

Proof As seen in Fig. 4, a two-headed flipping sequence branches from
$$
\begin{array}{cc}
M & I \\
S \quad m^* & M^* \\
m & S
\end{array}
$$
and hence there are other paths which flip M in the top row or flip m in the bottom row. Thus, we have at least three paths, and hence the lemma holds. □

Lemma 3.11 *If both of subsink and sink regions are violated in a two-headed flipping sequence because of side-effect caused by other sequences, we can give flipping of some entries to resolve both of violated regions without influencing other regions.*

Proof We remark that we may destroy the tame condition here, and we emphasize that these operations are done in the final stage of the construction. Thus, we give the proof of this lemma later in Appendix I. □

Definition 3.12 (Negative interaction of sequences) *We define that a pair of flipping sequences (originated from different source region) has negative interaction if they share an unguarded sink (or subsink) region but they have different flipped entries located in the diagonal or off-diagonal position to make the region violated.*

Lemma 3.13 *If we have a set of flipping sequences without negative interaction, the "union" of them creates no violating regions, where we mean "union" for the configuration obtained by flipping every medium entry that is flipped in at least one of the sequences.*

Proof A flipping sequence proceeds straight along a sequence of medium entries which are guarded by S and L from both sides, and all interior entries are flipped. We need not care a region containing a pair of entries with error at most 0.25, since our rounding is tame. Also, in the source region, we can flip both of the medium entries keeping it safe. Hence, we only worry about the region which is a sink region shared by more than one flipping sequences. Of course, if its only one entry is flipped, we have no problem. It is fine if two medium entries in a row or a column are simultaneously flipped, since these two have total error 0. Thus, there are diagonal or orthogonal flipped pair, and hence we have a negative interaction by definition. □

Definition 3.14 (covering by flipping sequences) *A set $\mathcal{C}$ of flipping sequences is called a good covering of the matrix if its sequences are classified into* **active sequences** *and* **normal sequences** *satisfying the following conditions: (1): An active sequence must be a two-headed flipping sequence, (2) every violated region in the parity rounding becomes a source region of at least one sequence in $\mathcal{C}$, (3) each active sequence has negative interaction with normal sequences at both its sink and subsink, (4) each normal sequence can have negative interaction with only active sequences.*

Lemma 3.15 *If there exists a good covering, there exists a rounding whose discrepancy is at most 1.25.*

Proof Consider the union of the flipping sequences. If there is no active sequence, there is no negative interaction, and we have no problem because of Lemma 3.13.

An active sequence corresponds to a two-headed flipping sequence that has negative interactions at both of their sinks and subsinks. However, Lemma3.11 assures that we can resolve sinks and subsinks in active sequences without influencing other regions.

If a flipping sequence shares its sink and/or subsink region(s) only with active sequences, we do not need to worry about the region, since it has been resolved within the active sequence. Thus, the lemma holds. □

Hence, it suffices to find a good covering. We select (in an arbitrary manner) exactly either a pair of single-headed flipping sequences or a pair of two-headed flipping sequences for each source node. This is called *trimming operation*, and always possible because of Lemma 3.10. We will find a good covering as a subset of this trimmed set by translating the problem into a graph theoretic problem.

We prepare an easy graph theoretical fact:

Lemma 3.16 *In a bipartite graph G, between node sets X and Y, if each node degree of X is at least two and each node degree of Y is at most two, G has a matching of size $|X|$.*

Proof For any subset Z of X, the size of its neighbor is at least $|Z|$ from the degree condition. Thus, we have a matching of size $|X|$ because of Hall's SDR theorem. □

We construct a graph $G = (U \cup V, E \cup J)$ from our set of flipping sequences (after applying the trimming operation) as follows: The nodes in U are called *source nodes* while the nodes in V are called *sink nodes*, although G is not a bipartite graph in general. The edges in E are called *regular edges*, while those in J are called *joint edges*. For each source region R of a single-headed flipping sequence, we construct a source node $v(R)$. For each 2×2 region R, we define two sink nodes $v(R, +)$ and $v(R, -)$ in V. If there is a single-headed flipping sequence with a source region R and a sink region R' containing the final flipped entry in its diagonal (resp. off-diagonal) position, we define a regular edge e in E between $u(R)$ and $v(R', +)$ (resp. $v(R', -)$).

Next, consider a source region R of two-headed flipping sequences (by our trimming operation, we have exactly two such sequences). For a two-headed flipping sequence with a source region R with a sink region R_1 and a subsink region R_2, we define a joint edge between two sink nodes $v(R_1, \epsilon_1)$ and $v(R_2, \epsilon_2)$, where ϵ_i are determined from the position of the flipped entry in the same manner as the case of regular edges.

Let $\mathcal{R}$ be the set of all source regions of two-headed flipping sequences. In the construction of G we do not define source nodes for a region R in $\mathcal{R}$; however, corresponding joint edges are labeled by the source region R. In other words, for each region R in $\mathcal{R}$, we have a subset $\pi(R)$ of E consisting of two edges labeled by R.

We indeed consider the graph G together with $\mathcal{R}$ and the labeling function π (from $\mathcal{R}$ to the set of doubletons in E). We denote $[G, \mathcal{R}, \pi]$ for the triple.

Lemma 3.17 *In the graph G, the node degree of a source node is two, and the node degree of a sink node is at most two.*

Proof The first statement follows from definition. The proof of the second statement is omitted in this version. □

Consider a three coloring (into red, blue, and white) of P, where the blue color is only used for some joint edges. Intuitively, blue edges correspond to active flipping sequences, and red edges correspond to normal flipping sequences in a good covering.

Definition 3.18 *A coloring of G is a good coloring if (1) each source node is adjacent to at least one red or blue edge, (2) at most one red edge is incident to a sink node, and each blue (joint) edge is adjacent to two red edges.*

Definition 3.19 (covering coloring) *A covering coloring of $[G, \mathcal{R}, \pi]$ is a good coloring of G satisfying that at least one edge of $\pi(R)$ is colored either red or blue for each $R \in \mathcal{R}$.*

To get intuition, if there is no joint edge, G is a bipartite graph, and containing a matching of size $|U|$ because of Hall's SDR theorem and Lemma 3.17. Thus, we have a good coloring (automatically a covering coloring if there is no joint edge) by coloring matching edges into red. We want to extend this fact to the general case, since we have the following lemma:

Lemma 3.20 *If G has a covering coloring, we have a good covering of the matrix by flipping sequences.*

Proof We consider the flipping sequences associated with the red edges and blue edges in the coloring. Since each source node is covered by such an edge, every source region that has one-headed flipping sequences is covered. Since at least one edge in $\pi(R)$ for a souce node R having two-headed flipping sequence is colored into red or blue, such an R is also covered. The good coloring condition assures that the set of flipping sequences is a good covering. □

Lemma 3.21 *The triple $[G, \mathcal{R}, \pi]$ has a covering coloring.*

Proof Let P be a connected component of G. Since the maximum node degree of G is two, P is either a cycle or a path. If it is a path, its end vertices must be in V, since node degree of a vertex in U must be two. The *critical edges* of P are (1) none if it has at most one joint edge, (2) the leftmost joint edge and the rightmost joint edge if P is a path with two or more joint edges, (3) all joint edges if P is a cycle with two or more joint edges.

We claim that if we fix any one of critical edges for each P, there exisits a good coloring that colors all the joint edges except the fixed edges red or blue. This claim can be constructively proved by using a greedy method. We omit details since it is routine.

Now, we consider a new bipartite graph $H = (\mathcal{R}, \mathcal{P}, F)$ where $\mathcal{P}$ corresponds to the connected components of G that are paths containing at least two joint edges. We have an arc from $R \in \mathcal{R}$ to $P \in \mathcal{P}$ if (at least) one of edges in $\pi(R)$ is in P as its critical edge. It is easy to see that the graph H has a matching of size $|\mathcal{P}|$. From the claim we have shown above, we can color all joint edges in G into red or blue except those corresponding to the arcs in the matching of H. Since at most one edge of $\pi(R)$ is selected in the matching for each $R \in \mathcal{R}$, at least one of them is red or blue. Thus, the coloring is a covering coloring. □

Thus, from Lemma 3.20 and Lemma 3.15, we can conclude that there exists a rounding whose maximum error is bounded by 1.25 if each entry of the input matrix is an integral multiple of 0.25.

4   Concluding Remarks

In this paper we have discussed how to achieve low discrepancy with respect to 2×2 square regions when we round a $[0, 1]$-valued matrix into a binary one. Our new upper bound is $5/3 \simeq 1.67$. There still exists a large gap between the lower bound ($= 1$) and the upper bound. Thus, a simple but interesting open question is to tighten the gap; indeed the authors are curious whether we can construct an example forcing the optimal rounding error to be 1.25 if the input matrix consists of entries of integral multiples of 0.25 (it is easy to make an example in which the rounding error is forced to be 1). Another direction is to extend the region size from 2×2 to k-by-k regions for $k \geq 3$. Even for the case $k = 3$, we have neither a nontrivial upper bound nor a lower bound.

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Appendix

Appendix 1: Proof of Lemma 3.11

One important observation is that a two-headed sequence is always very short. Indeed, the subsink and sink are intersecting or adjacent to each other, and this enables to resolve the violated region. If both of sink and source regions are violated, the situation are those given in Fig. 5.

	M	$\mathbf{I}$	M^*				M^*	m	M^*				M	$\mathbf{I}$	M^*
S	m^*	$\mathbf{M^*}$	m			M	$\mathbf{I}$	$\mathbf{M^*}$	I		S	m^*	$\mathbf{M^*}$	m
m	S		M^*		S	m^*	M^*	m^*			m	S	m^*	I
					m	S	S	S					M	m^*

Figure 5: When both of sink and subsink are violated

In the first two cases, we flip the m entry sandwiched by two M^* (on the third column for the first case, on the first row for the second case). Since the pair m^*, M^* has error zero, it will give no side effect and similtaneously resolve both violated regions. The third case is troublesome. If we can flip the m in the first column, we have no problem. Hence the problem occurs when we cannot flip it. Here, instead we flip the S entry in the second column to obtain the following configuration:

	M	$\mathbf{I}$	M^*
S	m	M	m
m	S^*	m	I
	M	m^*	

The error of m, S^* is 0.25, and hence it causes no side-effect since all the m entries around it are rounded to 0. We note that this destroys the tame condition. It might happen that the M entry in the top row and second column is flipped due to some side effect. In that case, we apply the following flipping configuration.

	M^*	$\mathbf{I}$	M^*
S	m^*	M	m
m	S^*	m	I
	M	m^*	

Appendix 2: Proof of Lemma 3.17

To prove that the degree of sink is at most two, we consider a sink region R which contains two medium entries in either diagonal or off-diagonal positions. Let p be one of medium entries in such a region R, and consider flipping sequences with the sink region R and having p as the last flipped element. Because of symmetry, we assume that p is an M^* node, and p is located at the upper-left corner of R. There are at most seven patterns of flipping sequences which have such an R as a sink region and flip p as the last flipped entry. In precise, Fig. 6 shows all the possible seven patterns of a sink region (bold-bounded region) R where p is the M^* entry located at the center.

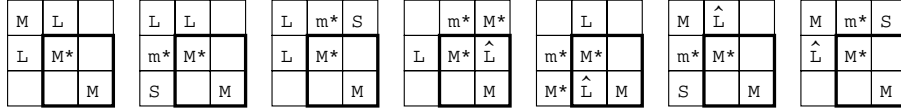| M	L			L	L			L	m*	S			m*	M*				L			M	$\hat{\mathrm{L}}$			M	m*	S
L	M*			m*	M*			L	M*			L	M*	$\hat{\mathrm{L}}$			m*	M*			m*	M*			$\hat{\mathrm{L}}$	M*	
		M		S		M				M				M			M*	$\hat{\mathrm{L}}$	M		S		M				M

Figure 6: Possible patterns for a sink

Indeed, at least four of the eight neighbors of p are determined in each pattern, and it can be observed that no two of such patterns can simultaneously exist around p. Thus, if the sink region has two diagonal (resp. off-diagonal) medium entries, the node degree of $w(R, +)$ (resp. $w(R, -)$) is at most two.

Also, we can see that a sink and a subsink cannot be similtaneously exist around p; Here, we may worry about the following pattern

$$
\begin{array}{ccccccc}
 & & M & m & M & & \\
 & M & I & M^* & I & M & \\
S & m^* & M^* & m^* & M^* & m^* & S \\
m & S & S & S & S & S & m
\end{array}
$$

where the subsink from the two-headed sequence originated from the leftmost region is the sink from the two-headed sequence originated from the rightmost region, and they share an M^*. However, since we have adopted a rule that we choose a single-headed flipping sequence at a bending end of a two-headed sequence if possible, that kind of pair of two-headed sequences cannot occur, and the real figure is the following one.

$$
\begin{array}{ccccccc}
 & & M & m & M & & \\
 & M & I & M & I & M & \\
S & m^* & M^* & m^* & M^* & m^* & S \\
m & S & S & S & S & S & m
\end{array}
$$

It is easier to handle the case to show that $w(R, +)$ (resp. $w(R, -)$) has degree at most two if R has only one medium entry in the diagonal (resp. off-diagonal) position[1].

---

[1] This case is indeed irrelevant since it is not related to a negative interaction.