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Reconstruction, Enumeration, and Examination of Binary Images with Prior Information

Summary of the PhD Dissertation

by

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1 Introduction

The main task of tomography is to reconstruct images representing two-dimensional cross-sections of three-dimensional objects from their projections. Undoubtedly, the main applications of tomography arise from the field of medicine, but it is a very useful imaging tool also in physics, chemistry, biology, industry, and so on. An important subfield is binary tomography [24], which aims to reconstruct binary images. In the most common applications of this field usually just few projections of the object can be measured, since the acquisition of the projection data can be expensive or damage the object. Moreover, the physical limitations of the imaging devices make it sometimes impossible to take projections from numerous angles. Owing to the small number of projections the binary reconstruction can be extremely ambiguous. A common way to reduce the number of solutions of the reconstruction task is to assume that the image to be reconstructed satisfies certain geometrical properties.

In many applications of binary tomography the image itself is naturally not known in advance. However, when one thinks of encoding binary images by their projections for data security or image compression reasons, it is clear that the original image is available. Then, in the decoding phase it becomes important to know whether the image, possibly with some additional prior information, can be uniquely revealed from the projection data [25]. Therefore, analysis of binary patterns plays a vital role in binary tomography.

In the field of binary tomography an important substructure of a binary matrix is the so-called switching component, which also plays a significant role in data analysis, biogeography, and binary matrices describing the relationship between datasets.

This thesis is a summary of the Author's research in the field of binary tomography and binary matrices. The central concept of this work was to examine additional prior information for the reconstruction task from at most two projections, expand the theoretical background for switching components and the complexity of the reconstruction, determine the number of solutions for certain classes of binary images, and develop new algorithms connected to the field of binary tomography.

2 The Binary Reconstruction Problem

In binary tomography the task is to reconstruct a two-dimensional binary image from a set of projections. The image can be represented by a binary matrix $A = (a_{ij})$, or can be defined as a finite subset of $\mathbb{Z}^2$ (definition is up to translation), where the size of the image is defined by the size of its minimal bounding discrete rectangle. In binary tomography, usually only a few number of projections are given. In case of only two projections, the horizontal and vertical projection of a binary image can be defined as the vector of the row and column sums, respectively, of the image matrix. The task is to reconstruct the binary image A from its horizontal and vertical projections. The related questions to the problems are the complexity of the algorithms, the number of solutions, and what prior information could reduce the number of solutions.

3 Eliminating Switching Components in Binary Matrices

Binary matrices can describe the connection between the data represented in rows and the data represented in columns; they can contain binary patterns in a natural way; or can represent a whole digital image. Analyzing binary matrices is an important task of intelligent data analysis [4], data mining [32], low-level image processing [14], and machine learning [29]. One

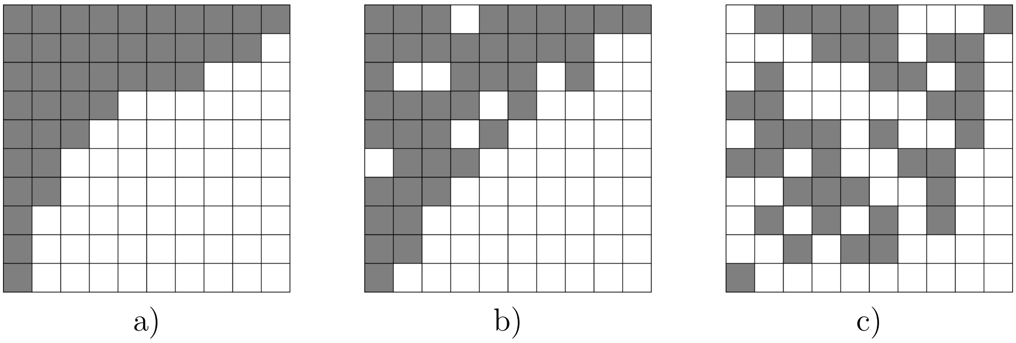

a) b) c)

Figure 1: Three matrices with rearranged columns and rows to form a triangluar (nested) shape as close as possible. a) A fully nested (switching component free) matrix; b) a nearly fully nested matrix with low number of flips; c) a uniform random matrix.

commonly performed task is to localize and enumerate special subpatterns in the binary matrix. Such a basic and essential subpattern of a binary matrix is the so-called switching component, which is a 2×2 submatrix with exactly two 1-s in the diagonal and two 0-s in the antidiagonal (or vice versa). The absence of these subpatterns is a necessary and sufficient condition for the unique reconstruction of the matrix from the vectors of its row and column sums [30]. Even if the matrix contains switching components, there is still a chance to reconstruct the matrix uniquely, if properly chosen elements of the original matrix are stored as well [10], using them as prior information. One can store, e.g., the positions of 0-s which need to be inverted to 1-s (by so-called 0-1 flips) in order to make the matrix switching component free. The aim is then to find the minimal number of 0-1 flips needed to achieve uniqueness.

Apart from image reconstrucion, the number and the position of switching components play also important roles in the field of biogeography and ecology. In those cases, binary matrices can represent the presence or absence of certain species (rows) on certain locations (columns), which is also strongly connected to the theory of 0-1 flips [27]. Here, the so-called nestedness is a relevant measure of the matrix, which describes how strongly the species depend on each other and their locations. If the matrix is not fully nested, but close to be one, then the number of switching components, and thus the number of flips in order to make the matrix fully nested, is low (see Fig. 1 for example).

Unfortunately, as it was proven in [27], determining the minimal number of 0-1 flips to achieve uniqueness is generally an NP-hard problem. In the thesis we showed that the minimal number of 0-1 flips can be found by determining the proper ordering of the columns of the matrix according to a certain filling function, instead of searching through matrix elements and switching components. Based on theoretical results, we developed two deterministic, polynomial-time heuristics to find the minimal number of 0-1 flips. We compared those methods to another well-known methods in the literature, on a wide set of random binary matrices, and also a real life dataset of presence-absence matrices. Finally, we showed how to use these algorithms in a simple way for general binary image compression.

3.1 Problem Setting

The Minimum Flip Augmentation Problem (Mfa) is the following: given a binary matrix, what is the minimum number of 0-1 flips to make the binary matrix switching component free. First we define the canonical expansion. The canonical expansion of the binary matrix A is a binary matrix ψA of the same size as A, with elements defined by

$$\psi a_{ij} = \begin{cases} 0 & \text{if } a_{ij'} = 0 \text{ for every } j' \geq j, \\ 1 & \text{otherwise.} \end{cases}$$

We proved the following theorem:

Theorem 1 *Let A be a binary matrix of size $m \times n$, and let A^* denote a solution of* MFA*(A). Then there is a column permutation π of order n such that $\pi^{-1}\psi\pi A = A^*$.*

Thus, to find a solution of the MFA(A) problem, it is sufficient to search for the corresponding column permutation π.

3.2 Heuristics and Results

We describe four different heuristics for the MFA problem. Algorithms SWITCH and COLUMNS are taken from [27] for comparison. The first one is a switching component searching algorithm, while the second one is a naive but fast approach for column permutations. Our own methods COLPERM1 (Algorithm 1) and COLPERM2 (Algorithm 2) are based on the previous theorem.

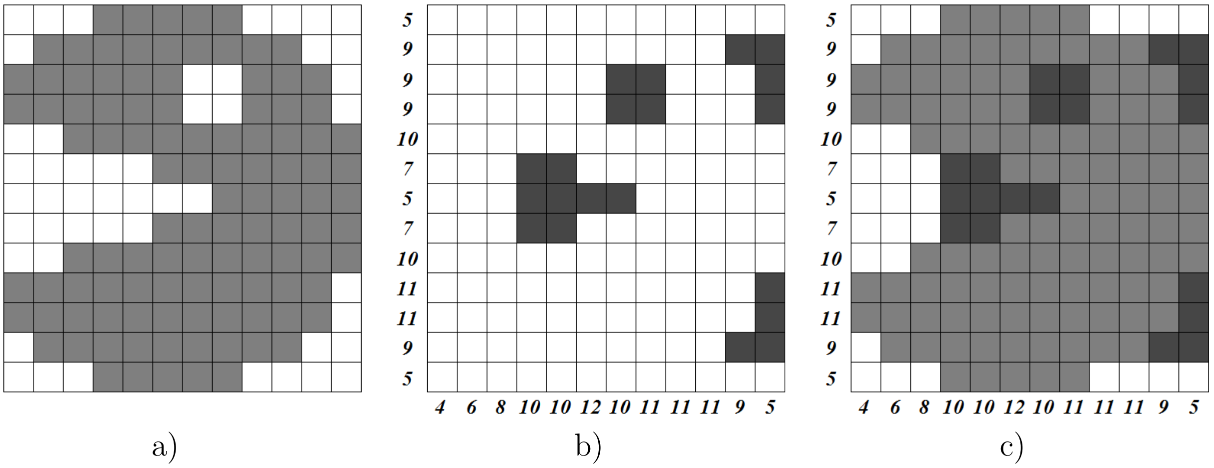
Algorithm 1 COLPERM1

```
Let $\pi$ be the identical permutation
for each column index $i$ do
    Let $j > i$ be the column index for which the column permutation $\pi_{ij}$ yields the biggest decrease in the number of 0-1 flips when applying the operator $\psi$
    Swap columns $i$ and $j$ by $\pi_{ij}$
    $\pi \leftarrow \pi \cdot \pi_{ij}$
end for
return $A' \leftarrow \pi^{-1}\psi\pi A$
```

Algorithm 2 COLPERM2

```
while true do
    Let $i$ and $j$ be column indices for which the column permutation $\pi_{ij}$ yields the biggest decrease in the number of 0-1 flips when applying the operator $\psi$
    if there are such $i$ and $j$ indices then
        Swap columns $i$ and $j$ by $\pi_{ij}$
        $\pi \leftarrow \pi \cdot \pi_{ij}$
    else
        Break loop
    end if
end while
return $A' \leftarrow \pi^{-1}\psi\pi A$
```

We studied the performance of the heuristics on random binary matrices and on an existing database containing real life data. Our test set contained matrices of size 20×20, 40×40, 60×60, 80×80, and 100×100 and with exactly 10%, 20%, …, 90% number of 1-s related to the total number of the matrix entries, thus providing matrices of different densities. With each size and



a) b) c)

Figure 2: An example of image compression. a) Original image; b) the stored data of the projections and the forbidden positions (0-1 flips); c) the unique solution of the reconstruction using Chang's algorithm.

density we generated 50 binary matrices from uniform random distribution. Thus, our test set contained a total of 2250 matrices.

We deduce that searching through column permutations yields a result much faster than searching through switching components, as Switch does. Furthermore, ColPerm2 gave better results for the number of 0-1 flips, especially when the matrix was big and sparse. We also deduce that Switch performs better if the number of switching components is small, which occurs if the matrix is small and/or dense.

We also tested our algorithms on a real life dataset [27]. The majority of the dataset were assembled for a meta-analysis of nested subset distribution patterns and the metrics used to evaluate them. The dataset contains binary matrices describing 150 archipelagos, to identify poorly represented taxa (many invertebrate groups), life-zones (especially aquatic and marine systems), or geographic locations (e.g., tropical systems). The database contains 289 matrices overall. We classified the matrices into 9 groups according to their density. We compared the algorithms by the number of flips, and counted how many times they provided the best or the worst result out of four. The results of the real dataset are highy correlated to the results of the artificial dataset, namely, ColPerm2 provided usually the best results (most wins and least losses), while Switch gave usually good results, especially on dense matrices. ColPerm2 was moderate in the number of flips, and Columns was usually the worst, however, the last two heuristics was much faster than the first two. ColPerm2 and Switch took several seconds on large matrices, while ColPerm1 and Columns always gave an answer within a fraction of a second.

If we store the positions of the 0-1 flips, we can use Chang's algorithm [10], a polyominal-time algorithm for reconstructing binary images from the horizontal and vertical projections, and the positions of the flips. Figure 2 shows an example of such a reconstruction. The proposed method can be comparable with current lossless image compression methods, which a future plan of the authors.

The findings of this reasearch have been published in a conference proceeding [18] and accepted for publication in a journal [17].

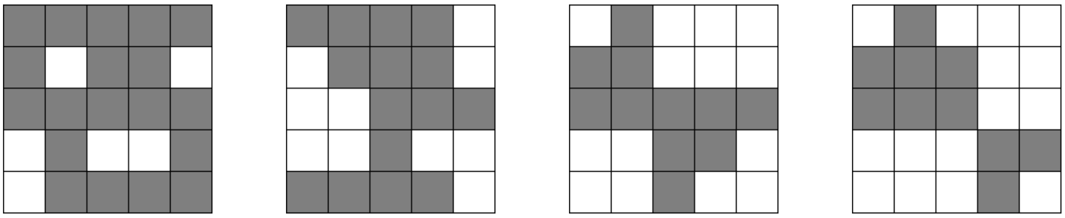


Figure 3: Binary images of size 5 × 5 with different properties: (a) a general polyomino with holes; (b) an h-convex but not v-convex polyomino; (c) an hv-convex polyomino; (d) an hv-convex 8-connected but not 4-connected binary image. Note that the last one is not a polyomino.

4 Reconstruction and Random Generation of *hv*-Convex Images from the Horizontal Projection

Many of the subclasses of binary images had been studied, where the image to be reconstructed has to meet some certain properties. One of the most frequently studied classes of binary images is that of hv-convex polyominoes, where each rows and columns are convex, and the binary image is 4-connected. See Fig. 3 for examples of binary images with different properties.

Although the reconstruction of hv-convex polyominoes from the horizontal and vertical projections along with the identification of the number of possible solutions have been extensively studied [2, 3, 8, 11, 12, 13], those problems have been surprisingly not yet investigated if just one projection is given. We filled this gap by describing a linear-time reconstruction algorithm and providing formulas for the number of solutions with minimal and with any given number of columns. Also, we extended the above results by giving an elementary enumeration algorithm which provides a method for generating hv-convex polyominoes with given horizontal projection from a uniform random distribution, in quadratic time. We also had similar results for canonical hv-convex images and their subclass of hv-convex 8-connected but not 4-connected images. We showed that reconstructing an hv-convex canonical image with minimal width from the horizontal projection is always possible in time linear in the length of the horizontal projection.

4.1 Reconstructing *hv*-Convex Polyominoes

Let $H = (h_1, \ldots, h_m) \in \mathbb{N}^m$ be a vector of size m. We give an algorithm called *GreedyRec* which constructs an A hv-convex polyomino with m rows and the minimal possible number of columns. Algorithm 3 gives the pseudo code. In the followings, we call the consecutive 1-s in the i-th row of an hv-convex polyomino as the i-th strip.

Theorem 2 *GreedyRec constructs an hv-convex polyomino satisfying the horizontal projection with minimal number of columns, in $O(m)$ time.*

One can easily modify the output of *GreedyRec* to expand it to have a predefined number of columns (if possible) by moving the k-th, $(k+1)$-st, …, m-th strips further to the right, if the previous strip allows it (i.e., when the image remains hv-convex and 4-connected). The smallest possible number of columns (provided by *GreedyRec*) is $N_{\min} = N_m$, where

$$N_i = \begin{cases} h_i & \text{if } i = 1\ , \\ N_{i-1} & \text{if } h_i \le h_{i-1}\ , \\ N_{i-1} + h_i - h_{i-1} & \text{if } h_i > h_{i-1}\ . \end{cases} \tag{1}$$

Algorithm 3 *GreedyRec*

```
$s_1 \leftarrow 1$
for $i = 2 \rightarrow m$ do
    if $h_i = h_{i-1}$ then
        Let the $i$-th strip be just below the $(i-1)$-th strip
    end if
    if $h_i < h_{i-1}$ then
        Let the $i$-th strip be aligned to the right of the $(i-1)$-th strip
    end if
    if $h_i > h_{i-1}$ then
        Let the $i$-th strip be aligned to the left of the $(i-1)$-th strip
    end if
end for
return $s_1, \ldots, s_m$ trip positions
```

This formula can be easily derived from the steps of the algorithm *GreedyRec*. The biggest possible number of columns is

$$N_{\max} = \sum_{i=1}^{m} h_i - m + 1 \ , \tag{2}$$

where every strip is connected with the previous and the next strips through only one element. The modified *GreedyRec* can construct any solution between $N_{\min}$ and $N_{\max}$ in linear time.

4.2 Enumerating *hv*-Convex Polyominoes

We give a formula to calculate the number of *hv*-convex polyominoes with a given horizontal projection $H = (h_1, \ldots, h_m)$, if there is no restriction on the number of colums of the resulted image. We use the definitions of upper stack polyomines, lower stack polyominoes, parallelogram polyominoes, smallest left anchor position k, smallest possible left anchor position K, greatest right anchor position l, and greatest possible right anchor position L.

If $\overline{S}_k(H)$, $\underline{S}_l(H)$ and $P_{k,l}(H)$ denote the number of upper stack, lower stack, and parallelogram polyominoes for fixed anchor positions, respectively, then the number of solutions are (assuming $K < L$):

$$\overline{S}_1(H) = 1, \quad \overline{S}_k(H) = \prod_{i=2}^{k} (h_i - h_{i-1} + 1) \ (k \geq 2) \ , \tag{3}$$

$$\underline{S}_m(H) = 1, \quad \underline{S}_l(H) = \prod_{i=l}^{m-1} (h_i - h_{i+1} + 1) \ (l < m) \ , \tag{4}$$

$$P_{k,l}(H) = \prod_{i=k}^{l-1} \min\{h_i, h_{i+1}\} \ . \tag{5}$$

The number of *hv*-convex polyominoes with the horizontal projection H is

$$P_{K<L}(H) = 2 \cdot \sum_{k=1}^{K} \sum_{l=L}^{m} \Big(\overline{S}_{k-1}(H) \cdot (h_k - h_{k-1}) \cdot P_{k,l}(H) \cdot (h_l - h_{l+1}) \cdot \underline{S}_{l+1}(H) \Big) \ . \tag{6}$$

If $K \geq L$, then the number of solutions is

$$P_{K \geq L}(H) = P_{K<L}(H) - \overline{S}_L(H) \cdot \underline{S}_K(H) \ . \tag{7}$$

We also give a recursive formula to calculate the number $P_n(H)$ of *hv*-convex polyominoes having the horizontal projection $H = (h_1, \ldots, h_m)$, when the number of columns is fixed to n. First, assume again that $K < L$. Let $r \geq 1$ and $P(p_1, \ldots, p_r, n)$ denote the number of parallelogram polyominoes with n columns, having the horizontal projection $(p_1, \ldots, p_r)$. Trivially, $P(p_1, n) = 1$ if $p_1 = n$, and $P(p_1, n) = 0$ if $p_1 \neq n$. Furthermore, for $r > 1$ we have the following recursion:

$$P(p_1, \ldots, p_r, n) = \begin{cases} \sum_{i=1}^{p_1} P(p_2, \ldots, p_r, n - i + 1) & \text{if } p_1 \leq p_2 \ , \\ \sum_{i=1}^{p_2} P(p_2, \ldots, p_r, n - (p_1 - p_2) - i + 1) & \text{if } p_1 > p_2 \ . \end{cases} \tag{8}$$

The number of solutions for a fixed n is

$$P_n(H) = 2 \cdot \sum_{k=1}^{K} \sum_{l=L}^{m} \Big(\overline{S}_{k-1}(H) \cdot (h_k - h_{k-1}) \cdot P(h_k, \ldots, h_l, n) \cdot (h_l - h_{l+1}) \cdot \underline{S}_{l+1}(H) \Big) \ , \tag{9}$$

where $P(h_k, \ldots, h_l, n) = 0$ if $k > l$.

Based on these results, a random generation of *hv*-convex polyominoes satisfying a given horizontal projection is possible for either fixed or arbitrary number of columns. The algorithm we described in the thesis has a running time of $O(m^2)$ for arbitrary number of columns.

4.3 Reconstructing Canonical *hv*-Convex Images

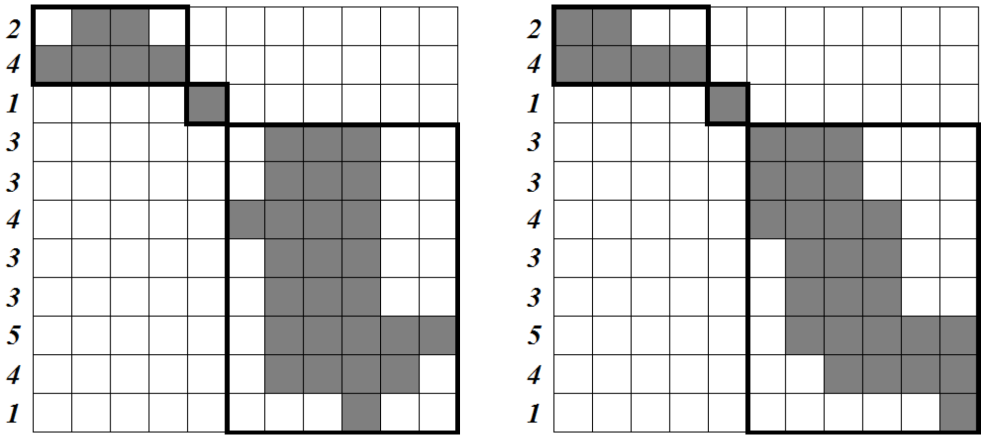
An *hv*-convex image is called canonical [1], if it consists of a single 4-connected component or the smallest containing rectangles of the 4-connected components are 8-connected to each other with their bottom-right and upper left corners. The task is given a horizontal projection and an integer, construct a canonical *hv*-convex image such that the result satisfies the horizontal projection and contains exactly the given number of 4-connected components, where the size of the binary image is minimal. Figure 4 shows an example of such a reconstructed image.

The algorithm *CanonicalRec* (see Algorithm 4) gives an 8-connected solution of the reconstruction problem in $O(m)$ time. The definition of breakpoints can be found in the thesis. One can also modify the *CanonicalRec* algorithm in a way that the obtained image has n number of columns, where n can be any value between the minimal value provided by *CanonicalRec* and the maximal value of $\left(\sum_{i=1}^{m} h_i \right) - m + k$, where k is the number of 4-connected components.

Algorithm 4 *CanonicalRec*

```
1) Find $c_1, c_2, \ldots, c_{k-1}$ ($1 \leq c_i < m$, and $c_i \neq c_j$ if $i \neq j$) such that $\sum_{c_i} \min\{h_{c_i}, h_{c_i+1}\}$ is minimal
2) Create image $G$ with GreedyRec from $H$
3) Create image $F^*$ by using the series of $c_i$ as breakpoints in $G$
return $F^*$
```

The findings of this reasearch have been published in two conference proceedings [15, 20], and one journal paper [19].



a) b)

Figure 4: (a) A minimal width canonical *hv*-convex image; (b) the result of the proposed algorithm *CanonicalRec*. Both images contains 11 columns. Note that the second image is 8-connected.

5 Morphological Skeleton as Additional Information for the Reconstruction

We studied the reconstruction from an additional shape descriptor, the so-called morphological skeleton [14, 31]. The morphological skeleton of a discrete binary image can be expressed via morphological operations, such as the iterative morphological dilation ($\oplus_k$), and the iterative morphological erosion ($\ominus_k$). We omit the lower right index for $k = 1$. The morphological skeleton $\mathcal{S}(F, Y)$ of a binary image F determined by a structuring element $Y \subset \mathbb{Z}^2$ is defined by

$$\mathcal{S}(F,Y) = \bigcup_{k=0}^{K} \mathcal{S}_k(F,Y), \tag{10}$$

where

$$\mathcal{S}_k(F,Y) = (F \ominus_k Y) \setminus \left[(F \ominus_{k+1} Y) \oplus Y\right] , \tag{11}$$

and K is the radius of the largest inscribed disk. A point $p \in F$ is called a skeletal point if $p \in \mathcal{S}(F, Y)$ for a fixed structuring element Y.

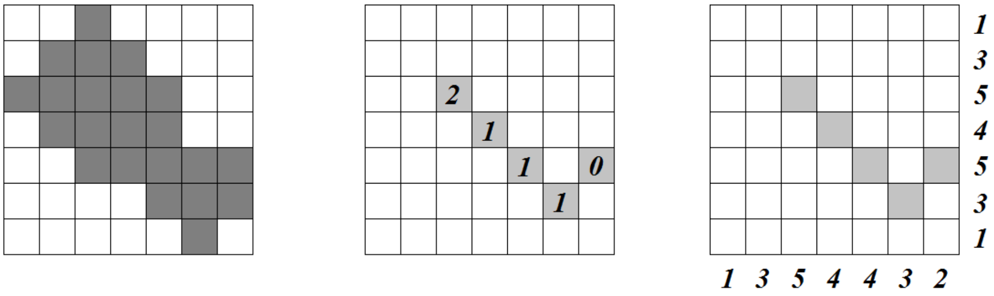
An important property of the morphological skeleton is that the image F can be exactly reconstructed from the skeletal subsets and the structuring element:

$$F = \bigcup_{k=0}^{K} \left[\mathcal{S}_k(F,Y) \oplus_k Y\right] = \bigcup_{p \in \mathcal{S}(F,Y)} \left(p \oplus_{\kappa_p} Y\right), \tag{12}$$

where κ_p denotes the skeletal label of p such that $p \in S_{\kappa_p}(F, Y)$. Since the skeletal subsets are disjoint, the labels are unique and well-defined. We assume that the structuring element Y corresponds to the 4-neighbors of the origin and the origin itself:

$$Y = \{\ (-1,0),\ (0,-1),\ (0,0),\ (0,1),\ (1,0)\ \} . \tag{13}$$

Our task is to reconstruct a binary image from its two projections and the morphological skeleton. Figure 5 gives an example of the reconstruction problem. We managed to prove the following theorems:



a) b) c)

Figure 5: (a) The image F to be reconstruced; (b) if the skeletal label is known for each $p \in \mathcal{S}(F,Y)$, F is uniquely reconstructable; (c) the considered problem is to reconstruct F from $\mathcal{S}(F,Y)$ and the two projections.

Theorem 3 *The reconstruction of polyominoes from two projections and the morphological skeleton is NP-complete. The reconstruction of general binary images from two projections and the morphological skeleton is NP-complete. The reconstruction of general binary images from one projection and the morphological skeleton is NP-complete.*

5.1 Reconstruction as Optimization Problem

Although the reconstruction from two projections and morphological skeleton is generally NP-hard, under some circumstances an acceptable image quality can be achieved. We transform the problem into an energy minimization (or function minimization) task, where finding a minimum of the given function is equivalent to finding an optimal solution to the reconstruction problem. We chose Simulated Annealing (SA) [9, 26, 28] as the optimization method for our problem because its simplicity, robustness, and flexibility in the control parameters.

We need to define our reconstruction problem as an energy function. Let $H \in \mathbb{N}_0^n$ and $V \in \mathbb{N}_0^n$ be two vectors, and $S \subset \mathbb{Z}^2$ be a finite set of points. Our task is to reconstruct an image F for which $\mathcal{S}(F,Y) = S$, and which (at least approximately) satisfies $\mathcal{H}(F) = H$ and $\mathcal{V}(F) = V$. For each point $p \in \mathcal{S}(F,Y)$ there is a unique skeletal label κ_p, thus, the image F can be uniquely represented by a vector $K(\mathcal{S}(F,Y)) = (\kappa_{p_1}, \kappa_{p_2}, \ldots, \kappa_{p_{|\mathcal{S}(F,Y)|}}) \in \mathbb{Z}^{|\mathcal{S}(F,Y)|}$. Now our goal is to find a $K^*(S) = (\kappa^*_{p_1}, \kappa^*_{p_2}, \ldots, \kappa^*_{p_{|S|}})$ which corresponds to the image F^* generated by (12), such that $f(\mathbf{x}^*) = ||\mathbf{A}\mathbf{x}^* - \mathbf{b}||_2^2$ is minimal. Here, $\mathbf{x}^*$ is the column vector representing F^*; $\mathbf{b}$ is a vector containing the projections, and $\mathbf{A}$ is binary matrix describing the connection between the pixels and the projection values. An adjusted version of SA is described in Algorithm 5.

We empirically established the parameters. We developed three different strategies for the reconstruction. In two strategies the following property of the skeletal labels was used, which we proved in the thesis:

Lemma 1 *For every skeletal point p and q with the previously given structuring element Y, it holds that $d(p,q) > |\kappa_p - \kappa_q|$, where $d(p,q)$ denotes the Manhattan-distance of p and q.*

We want to enforce that the difference on 8-adjacent skeletal labels are 1 at most.

1. *No Skeletal Constraint* (NSC): In the SA modification step, we choose a $kappa_p$ randomly, and change it randomly between its bounds.

Algorithm 5 Simulated Annealing on the Introduced Problem

```
$K(S) \leftarrow K_0(S)$ initial skeletal labels
$t \leftarrow 0$
repeat
  $K'(S) \leftarrow \text{MODIFY}(K(S))$
  Calculate $\mathbf{x}'$ and $\mathbf{x}$ from $K'(S)$ and $K(S)$, respectively
  if $f(\mathbf{x}') < f(\mathbf{x})$ or RAND $< \exp\left(\frac{f(\mathbf{x})-f(\mathbf{x}')}{T(t)}\right)$ then
    $K(S) \leftarrow K'(S)$
  end if
  $t \leftarrow t+1$
until the termination criterion is satisfied
return $K(S)$ skeletal labels
```

2. *Dynamic Skeletal Constraint* (DSC$_C$): In each step, we modify a randomly chosen κ_p by defining its new value such that $|\kappa_p - \kappa_q| \leq C$ holds for each q 8-adjacent to p. If $C = 1$, we allow only 1 as a difference for 8-adjacent skeletal points. Because it also means slow convergence during iterations, we allow higher C values in the beginning of the reconstruction, and decrease C through time.

3. *Combined Energy Function* (CEF$_\alpha$): We incorporate restriction on the skeletal labels by using an extended energy function:

$$f(\mathbf{x}) = \alpha||\mathbf{A}\mathbf{x} - \mathbf{b}||_2^2 + (1-\alpha)g(\mathbf{x}),$$

where α is a weighting parameter ($0 \leq \alpha \leq 1$),

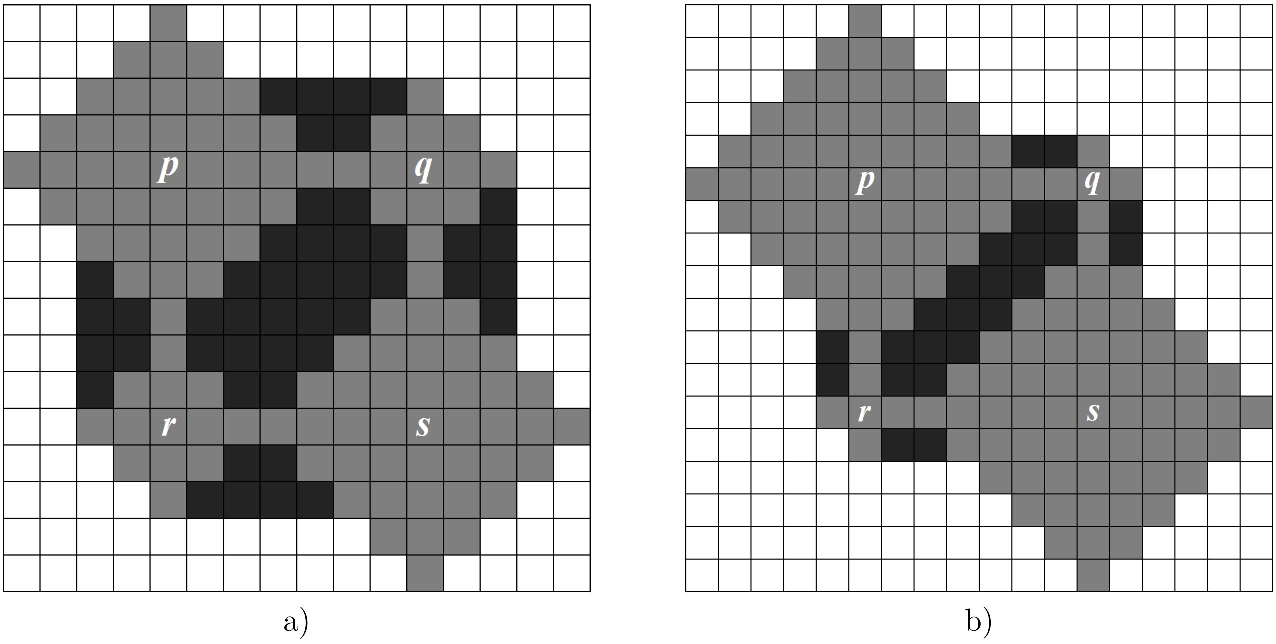
$$g(\mathbf{x}) = \sum_{0<d_1(p,q)\leq 2} h(\kappa_p, \kappa_q) \quad \big(\ p, q \in S,\ \ \kappa_p, \kappa_q \in K(S)\ \big),$$

and

$$h(\kappa_p, \kappa_q) = \begin{cases} 0 & \text{if } |\kappa_p - \kappa_q| \leq 1 \\ |\kappa_p - \kappa_q|/2 & \text{otherwise.} \end{cases}$$

We tested our algorithm on 50 artificial images. Six of our test samples have one point thin morphological skeleton consisting of few 8-connected components. However, we also tested on many other images which have more complex skeletons. All of the test images have the size of 256 × 256. We performed each test 10 times and measured the mean CPU time and errors of the reconstruction. For the numerical evaluation of the quality of the reconstructed images, we calculated the relative mean error of the resulted images.

We found that without assuming the properties of Lemma 1, a rough reconstruction is always possible in a short time and a small number of iterations. With additional restrictions the result will be smoother, although the convergency of the method becomes slower. The NSC variant provides overall satisfactory results, but it contained a lot of error around the edges. The DSC creates smoother results in most cases, but needs more iterations to converge. The CEF variant is just slightly worse than the NSC, but much slower. Beside that, in all the three considered variants we found that the result is much more dependent on the number of the skeletal points, rather than on the size of the image. We also tested our algorithms if only one projection and the morphological skeleton was given; the results were slightly worse, but overall the algorithms performed similarly.



a) b)

Figure 6: Example images of $B_{k,l}$: (a) the $B_{4,2}$ image; (b) the $B_{5,1}$ image. Grey and black pixels indicate the corresponding subset G and H, respectively. From the horizontal and vertical projections and the morphological skeleton the reconstruction of $B_{4,2}$ is non-unique, $B_{5,1}$ is uniquely reconstructable.

5.2 A Uniqueness Result for Reconstructing hv-Convex Polyominoes

Uniqueness of certain type of binary images is a related issue to the reconstruction. We studied the uniqueness of the reconstruction of certain type of 4-connected hv-convex images, using two projections and the morphological skeleton. We showed that the uniqueness of a certain parametric subclass of hv-convex binary images is strongly connected to its parameters. For given $k, l \in \mathbb{N}_0$, let $G_{k,l}$ be the binary image

$$G_{k,l} = (p \oplus_k Y) \cup (q \oplus_l Y) \cup (r \oplus_l Y) \cup (s \oplus_k Y), \tag{14}$$

where $p = (i, j)$, $q = (i,\ j + k + l + 1)$, $r = (i + k + l + 1,\ j)$, $s = (i + k + l + 1,\ j + k + l + 1)$. Furthermore, let $H_{k,l} \subset \mathbb{Z}^2$ be constructed from $G = G_{k,l}$ by

$$\begin{aligned} H_{k,l} \;=\; & \big\{(u, v) \mid \exists(u_1, u_2)\;\; u_1 < u < u_2, \\ & (u_1, v) \in G, (u_2, v) \in G, (u, v) \notin G\big\} \\ \bigcup\; & \big\{(u, v) \mid \exists(v_1, v_2)\;\; v_1 < v < v_2, \\ & (u, v_1) \in G, (u, v_2) \in G, (u, v) \notin G\big\}. \end{aligned}$$

Finally, let $B_{k,l} = G_{k,l} \dot\cup H_{k,l}$, where $\dot\cup$ denotes the disjoint union. Figure 6 shows examples with $k = 4$, $l = 2$, and $k = 5$, $l = 1$.

We found the following relation between k, l and the uniqueness of the reconstruction of the image $B_{k,l}$.

Theorem 4 *Let $B = B_{k,l}$ for arbitrary fixed $k \geq l$. Then the reconstruction of B is non-unique if and only if*

$$\left\lfloor \frac{k + l}{2} \right\rfloor \leq 2l. \tag{15}$$

The findings of this reasearch have been published in two conference proceedings [16, 22], and two journal papers [23, 21]. Finally, up to date, there have been four independent references to the findings of the results [5, 6, 7, 33].

Summary of the author's contributions

The findings of the research can be divided into three thesis groups. Table 1 gives the connection between the results and the publications of the Author.

In the first thesis group, I examined the methods for eliminating switching components in binary matrices with possibly low number of 0-1 flips. The results were published in a conference proceeding [18] and accepted for publication in a journal [17].

I/1. I provided a proof to reduce the search space drastically while the optimal solutions still can be found in the reduced search space. I managed to give two heuristics that outperform the previous methods in the number of 0-1 flips to make a binary image switching component free.

In the second thesis group I examined the binary reconstruction of *hv*-convex polyominoes and *hv*-convex canonical images where only the horizontal projection is given. The results were published in two conference proceedings [15, 20], and one journal paper [19].

II/1. I managed to give an algorithm to reconstruct *hv*-convex polyominoes with running time linear in the size of the horizontal projection. I proved that the algorithm always gives a result with minimal number of columns. Moreover, the algorithm can be easily modified to provide an image with a given size. Furthermore, I provided a formula for the exact number of solutions with arbitrary number of columns according to a given horizontal projection, and a recursive formula with fixed number of columns.

II/2. I provided an algorithm for the uniform random generation of *hv*-convex polyominoes, according to a given horizontal projection. The worst case running time of the algorithm is $O(m^2)$, where m is the size of the projection. The algorithm can be modified to generate polyominoes with fixed number of columns.

II/3. I showed how to reconstruct *hv*-convex canonical images from one projection. I provided an algorithm which always gives an 8-connected result minimal in size.

In the third thesis group, I examined the reconstruction problem of binary images if the morphological skeleton with a certain structuring element is also provided. The results were published in two conference proceedings [16, 22], and two journal papers [23, 21].

III/1. I proved that the reconstruction of polyominoes from two projections and the morphological skeleton (considering a certain structuring element) is NP-complete. Furthermore, without the restriction of the 4-connectedness the problem is still NP-complete. If only the horizontal projection is given with the morphological skeleton, finding a solution is, again, NP-complete.

III/2. I redefined the problem as an energy minimization problem, and used simulated annealing to solve the reconstruction of general binary images. I studied three variants of a parametric SA, and showed that a rough reconstruction is usually possible in a short time and a small number of iterations.

III/3. I defined a certain parametric subclass of *hv*-convex polyominoes, and showed that the uniqueness of the reconstruction from two projections and the morphological skeleton is determined by the parameters.

	[15]	[16]	[17]	[18]	[19]	[20]	[21]	[22]	[23]
I/1.			●	●					
II/1.						●			
II/2.					●				
II/3.	●								
III/1.							●		●
III/2.								●	●
III/3.		●							

Table 1: The connection between the thesis points and the Author's publications.

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