SILESIAN UNIVERSITY OF TECHNOLOGY PUBLISHING HOUSE

SCIENTIFIC PAPERS OF SILESIAN UNIVERSITY OF TECHNOLOGY 2025
ORGANIZATION AND MANAGEMENT SERIES NO. 236

APPLICATION OF THE CHROMATOGRAPHIC DATA SEPARATION METHOD IN INDUSTRIAL IMAGE PROCESSING

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Purpose: The purpose of the paper is to present an innovative image processing method inspired by gas chromatography. The research aims to propose an alternative to classical segmentation and deep learning techniques by introducing a chromatographic data separation algorithm. This method enables efficient, selective analysis of images, particularly for industrial and medical (e.g., microscopic blood analysis) applications, through the transformation of images into chromatograms.

Design/methodology/approach: The research introduces a chromatographic approach to image processing by treating images as mixtures of "substances" (sub-images), each with a retention time determined by its affinity to a simulated stationary phase. The methodology involves dividing the image into sub-regions, calculating the retention time for each sub-image, creating chromatograms that reflect the distribution of these sub-images, and applying various image operations such as filtering, subtraction, removal of dominant peaks, dilation, and erosion. Additionally, algorithms modeled on chromatographic processes are used to analyze and transform images. The method's theoretical foundation is based on analogies with gas chromatography, enabling both qualitative and quantitative analysis of image content.

Finding: The proposed method effectively enables new operations in image processing, including the selective removal of dominant or unwanted elements, background elimination through chromatogram subtraction, skeletonization of objects (contour extraction), and morphological operations such as dilation and erosion within the chromatographic framework. These operations have proven useful in isolating features and enhancing image clarity. The results demonstrate the flexibility and selectivity of the approach, particularly in complex segmentation tasks.

Research limitations/implications: The method's performance is sensitive to parameter choices, especially the number of "shelves" (resolution levels) and the granularity of sub-image division. While the approach shows promise, further research is needed to optimize parameter selection and adapt the method to high-resolution color images and real-time systems. Future work could explore integration with existing deep learning techniques or its extension to 3D imaging.

Practical implications: The chromatographic approach to image analysis provides an alternative tool for industries and laboratories requiring robust image filtering and object recognition. Its ability to isolate and enhance image features may improve quality control processes, diagnostics, and object detection pipelines. Applications include microscopic imaging (e.g., blood analysis), product inspection, and environmental monitoring.

Originality/value: This paper introduces a novel paradigm in image processing that draws from chemical analysis techniques, specifically gas chromatography. Unlike traditional image analysis methods, this chromatographic data separation model provides a unique way to structure and process images. Its originality lies in merging chemical separation concepts with visual computing, offering a new pathway for segmentation, feature extraction, and morphological operations. It is valuable to researchers and practitioners in image analysis, industrial inspection, and medical diagnostics.
Keywords: chromatographic data separation, image processing, retention time, morphological operations, object segmentation.
Category of the paper: Research paper.

1. Introduction

In recent years, dynamic development of image processing methods has been observed, both in industrial and medical applications. Techniques enabling automatic analysis of images in real time, supporting diagnostic processes, quality control and classification of objects, are gaining particular importance. One of the key challenges in this area is the effective extraction of important information from the image and its further interpretation. The article proposes a new approach to image processing, inspired by the principles of gas chromatography.

The main motivation for undertaking the research was to find an alternative approach to image classification and segmentation that could compete with classical techniques and methods based on deep learning. The presented concept assumes treating the image as a mixture of substances, the elements of which can be separated and analyzed based on retention time – analogously to the chromatographic process. Thanks to this, it is possible to create the so-called image chromatogram, which reflects its structure in the form of a retention histogram.

The article presents a detailed description of the chromatographic data separation algorithm and the method of image representation using it. It also describes key image processing operations, such as filtration, selection, removal of dominant objects, skeletonization and morphological operations inspired by erosion and dilation. The authors show how the use of chromatograms allows performing complex analytical operations on images in an efficient and selective way.

The proposed method can be used in industry, biology, and especially in microscopic analysis of blood, where precise segmentation and classification of cells is crucial. The paper also includes examples of algorithms and visualizations of their effects. The aim of the paper is not only to present a new approach, but also to show its potential in practical image processing scenarios. Ultimately, this method can be an alternative or complement to existing techniques, opening new possibilities for visual analysis (Kristensen, Lützen, 2013).

2. Chromatographic data processing method

The chromatographic data separation method, which is inspired by the separation of substances by a gas chromatograph, is based on several assumptions. The first important assumption is that the vectors that are fed to the classification process are treated as a mixture – of substances. In the case of the presented algorithm, it was assumed that all vectors resulting from the division of the output vector are of the same length (Święcicki, 2024).

2.1. Principle of chromatographic image processing

Figure 1 presents the idea of the chromatographic data separation method. As you can see, the method consists of several phases. In the first phase, the processed vector is divided into smaller vectors and the affinity value for the stationary phase is calculated for each subvector. This value affects the speed of the vector migration through the chromatographic column, i.e. the retention time, i.e. the time a given vector spends in the column, will depend on this value. After leaving the "column", the vectors are counted. Where vectors with the same retention time are treated by the presented algorithm as the same vectors. As a result of the above-described process, we obtain a spectrum, i.e. the relationship between the number of vectors with the same retention time and the retention time (Hohrenk et al., 2020; Martens et al., 2017; Mondello et al., 2008; Stilo et al., 2021).

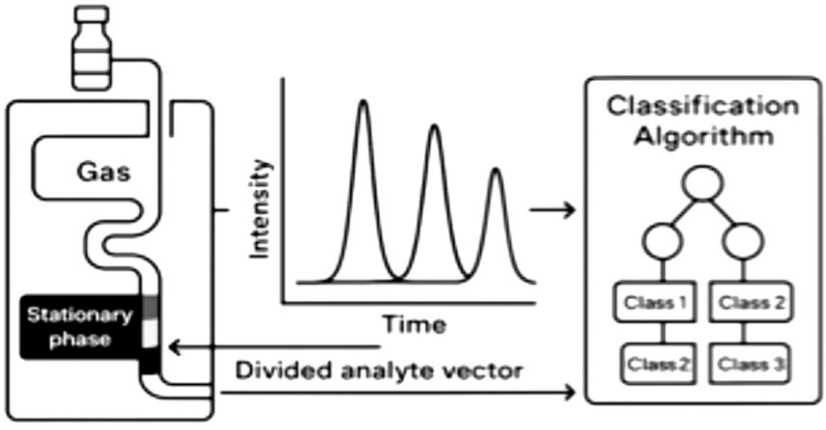

Figure 1. The idea of the chromatographic data separation method.

The chromatographic separation algorithm has been described in detail in the following works, therefore only those elements of the algorithm that are significantly related to the presented image processing methods will be presented in this article (Święcicki, 2024).

2.2. Representation of images

The image is represented as a two-dimensional array, the elements of which take values from 0 to 255 – in the case when the image is processed in grayscale. In accordance with the basic assumption of the chromatographic separation method of data. The array represents

a mixture of compounds that will be subject to the processing process, so the next step will be to divide the array into equal-sized sub-areas – sub-arrays that will be processed by the algorithm – for which the retention time will be calculated (Solomon, Breckon, n.d.).

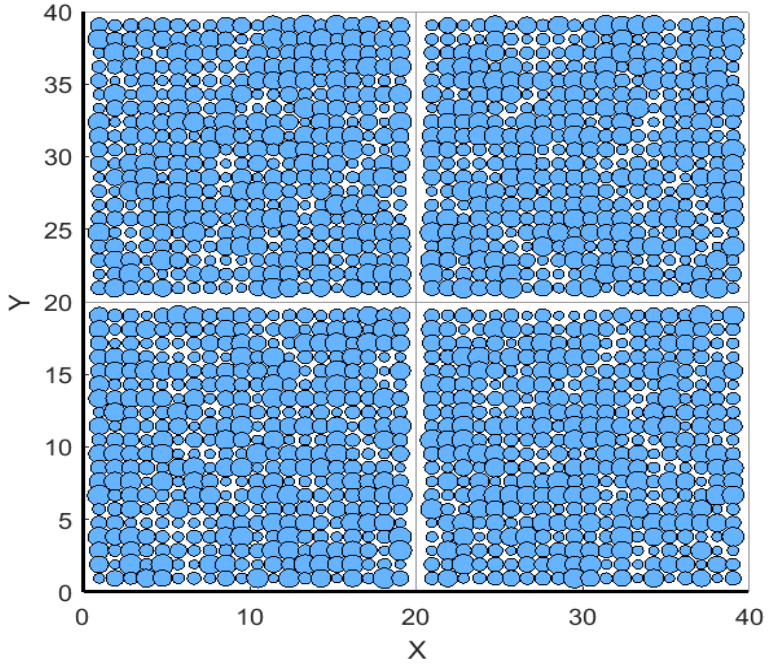

Figure 2. The division of the image, which constitutes a mixture, into four sub-regions, each treated as a separate "substance" for which the retention time will be calculated.

Figure 3 shows the process of converting an image to a chromatogram, which will be the basic structure in the further image processing. As it was shown, in this case the image, which was a mixture, was divided into one hundred sub-areas – substances for the chromatographic data separation algorithm for which the retention time will be calculated. It is obvious that the retention time value depends on the values of the elements that are in a given sub-area (Young et al., 1995).

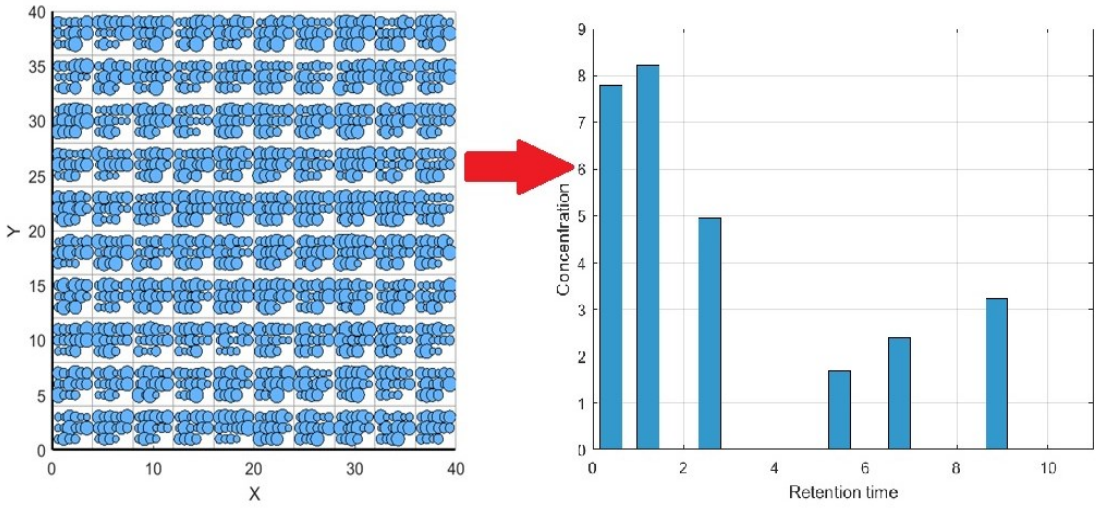

Figure 3. The process of converting an image into a chromatogram.

The result of the calculation for each retention time area and the grouping process is a chromatogram. The height of the individual bars – peaks in the chromatogram is determined by the number of sub-areas with the same retention time (Hohrenk et al., 2020; Pezzatti et al., 2020; Schmidt-Traub et al., 2020; Sparkman, 2005; Stilo et al., 2021).

2.3. Chromatographic data processing algorithm

Algorithm 1 presents an algorithm for chromatographic data separation, which is inspired by the gas chromatography method. As it results from the presented algorithm, the data for this algorithm is the processed image P, which in a special case can be a color image represented as an RGB table. The next parameters are the size N1 and M, which determine the size of the subimages into which the input image will be divided. The last input parameter for the presented algorithm is the parameter that is responsible for the resolution in the real chromatographic system, i.e. for the so-called number of shelves, which is determined by the length of the chromatographic column. The longer the chromatographic column, the higher the resolution of such a chromatograph. It is similar in the case of the presented algorithm.

Input : $P \subset \mathbb{R}^{M \times N}$: input image (mixture), K: number of non-overlapping subimages of size $M_1 \times N_1$, L: number of theoretical plates, $t_{\min}, t_{\max}$
Output: Ch: calculated chromatogram

Assumptions: Image P is divided into K subimages S_i $(i = 1..K)$. Subimages at borders may have smaller size if M_1, N_1 are not divisors of M, N. Retention time t_r is computed as $(t_{\max} - t_{\min})/L$ and rounded to nearest point. Affinity of substance to stationary phase is sum of subimage elements. Chromatogram Ch contains columns: retention time, frequency, subimages, positions. **End Assumptions**

Divide image P into subimages $S = \{S_1, ..., S_K\}$;
foreach *subimage* S_i *in* S **do**
    $\alpha_i \leftarrow \text{computeAffinity}(S_i)$;
    $\tau_i \leftarrow f(\alpha_i)$;
    $t_i \leftarrow \text{round}((\tau_i - t_{\min})/\Delta t) \cdot \Delta t$;
    $Ch[t_i] \leftarrow Ch[t_i] + 1$;
    Store S_i and its position in Ch at t_i;
end
return Ch;

Algorithm 1. The chromatographic data separation algorithm.

The chromatographic separation algorithm is based on concepts known from gas chromatography and is used to analyze an image containing a mixture of different substances. As an input, it takes an image of given dimensions, which is treated as a set of substances to be separated. This image is divided into smaller, non-overlapping sub-images, each of which represents a single substance. For each sub-image, the retention time is calculated, which determines its affinity for the stationary phase. The retention time values are discretized, i.e. rounded to the nearest points in a fixed time grid, the density of which depends on the number of plates and the minimum and maximum retention time.

Subimages with the same retention time are grouped and create common peaks in the chromatogram. The height of each peak corresponds to the number of subimages that belong to it. This process allows the input image to be transformed into a structure describing the composition of the mixture in the form of a chromatogram. The key part of the algorithm is the division of the image and the assignment of retention time based on specified rules. The algorithm allows for quantitative and qualitative analysis of the components contained in the image. The input parameters are the image, dimensions of subimages, the number of trays and the minimum and maximum retention time values. The output parameters are the structure of the chromatogram and a set of data grouped by retention time. This algorithm is the basis for further operations, such as the removal of selected substances or the reconstruction of the image without specific components. Thanks to its flexible structure, it can be used in various image processing applications inspired by chemical analysis.

3. Image operations

In this section, the operations on the image will be presented, which were implemented using the mechanisms and data provided by the chromatographic separation algorithm. The basis of all operations is the chromatogram, which will provide information about the structure of the processed image. It can be said that the central structure in the image processing process, which will be used in all the presented algorithms, is the chromatogram. It is thanks to the connection between a given peak in the chromatogram – and under the image, i.e. the substance that belongs to the mixture, i.e. the image, that it is possible to select individual images. It can be said that all operations on images will be related to the filtration operation – as it is in the case of a real chromatographic system (Babushok, 2015; Chromatography…, n.d.; Hage, 1999; Qi et al., 2018).

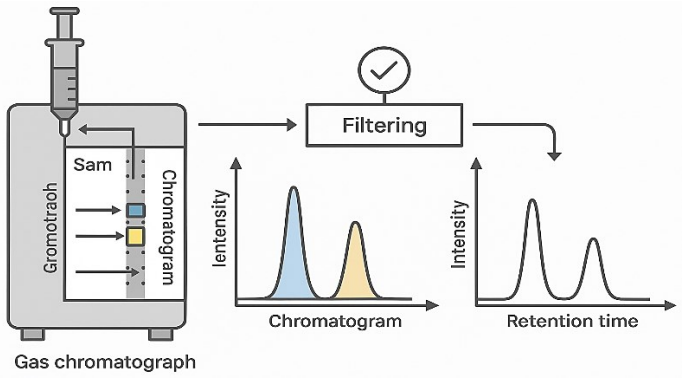

Figure 4. The idea of image processing corresponds to the filtration of individual peaks that belong to the chromatogram.

Figure 4 illustrate in a pictorial way the general concept of operations on images using a chromatographic data separation algorithm.

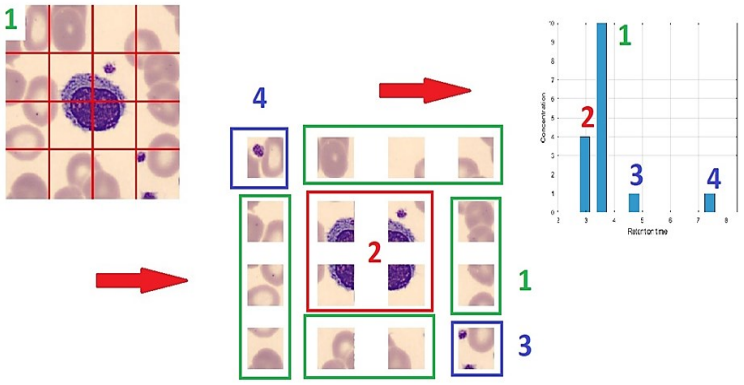

Figure 5. Phases of image processing using the chromatographic data separation algorithm.

Figure 5 shows the individual stages of image processing. As shown in the first phase, the image is divided into sub-images, for which the level of interaction with the stationary phase is calculated, resulting in the retention time value being determined. In the next phase, substances with the same retention time values are grouped. As can be seen from the presented figure, many images with the same retention time value can be assigned to one peak in the histogram. As can be seen from the figure, the peak marked.

3.1. Sub-image selection operation

The first operation that will be presented is the operation of filtering specific sub-images that are part of the processed image.

The algorithm is used to remove substances with a specific retention time from the image, using inspiration from the gas chromatography mechanism. The input image is treated as a mixture of substances, which is divided into sub-images, each of which represents a single substance. For each of these sub-images, the retention time is calculated based on their properties. The retention time determines the ability of a given substance to interact with the stationary phase. All calculated retention times are rounded to the nearest point values determined based on the number of plates and the specified minimum and maximum retention time values.

Then, a chromatogram is created that groups substances by common retention time. The height of each peak in the chromatogram corresponds to the number of substances at a given time. The algorithm analyzes this chromatogram and identifies substances that have a specified retention time to be removed. Sub-images corresponding to these substances are removed from the set. The remaining sub-images that do not meet the retention time criterion are retained.

Input : $P \subset \mathbb{R}^{M \times N}$: input image,
$\mathcal{S} = \{S_1, \ldots, S_K\}$: set of subimages,
$L \in \mathbb{N}$: number of theoretical plates,
$t_{\min}, t_{\max} \in \mathbb{R}$: min and max retention time,
$t^* \in \mathbb{R}$: retention time to remove

Output: $\mathcal{C}$: chromatogram,
$P' \subset P$: reconstructed image

Assumptions:
- $t_{\max} > t_{\min}$
- $\Delta t = \frac{t_{\max} - t_{\min}}{L}$
- $\mathcal{S}$ is a non-overlapping partition of P

End Assumptions

Initialize map $\mathcal{C} : \mathbb{R} \to \mathbb{N}_0$;
Initialize set $R = \emptyset$;
foreach $S_i \in \mathcal{S}$ **do**
  $\alpha_i \leftarrow \text{Affinity}(S_i)$;
  $\tau_i \leftarrow f(\alpha_i)$;
  $t_i \leftarrow \text{round}\left(\frac{\tau_i - t_{\min}}{\Delta t}\right) \cdot \Delta t$;
  $R \leftarrow R \cup \{(S_i, t_i)\}$;
  $\mathcal{C}[t_i] \leftarrow \mathcal{C}[t_i] + 1$;
end
Remove all $(S_i, t_i) \in R$ such that $t_i = t^*$;
Reconstruct P' from remaining subimages;
return $\mathcal{C}, P'$;

Algorithm 2. The algorithm for removing sub-images with a specific retention time from the image.

Based on the remaining sub-regions, the algorithm reconstructs a new output image. The final image no longer contains substances with unwanted retention time. The input parameters of the algorithm are the original image, the number of plates, the retention time range and the retention time to be removed. The algorithm operates on the chromatogram structure, which represents the frequency of occurrence of individual substances. As a result of the algorithm, we obtain a new chromatogram and a modified image from which specific substances have been eliminated. The key stages of the algorithm are: calculation of retention time, creation of the chromatogram, identification and removal of selected substances and reconstruction of the final image.

3.2. The operation of removing the peak, which corresponds to the substance with the highest concentration

Algorithm 3 presents the sequence of operations responsible for removing substances with the highest concentration from the chromatogram. As a result of this operation, sub-images, i.e. substances that occur most frequently, are removed from the mixture of substances – i.e. from the image. As can be seen from the presented algorithm, the input argument is the image that will be processed by the algorithm. The parameters also include parameters that determine the size of sub-images and the degree of generalization by the chromatographic data separation algorithm, i.e. the parameter defining the number of shelves.

Input : $P \subset \mathbb{R}^{M \times N}$: input image,
$\mathcal{S} = \{S_1, \ldots, S_K\}$: set of subimages,
$L \in \mathbb{N}$: number of theoretical plates,
$t_{\min}, t_{\max} \in \mathbb{R}$: min and max retention time
Output: $\mathcal{C}$: chromatogram,
$P' \subset P$: reconstructed image

Assumptions:
- $t_{\max} > t_{\min}$
- $\Delta t = \frac{t_{\max} - t_{\min}}{L}$
- Peak height equals number of subimages

End Assumptions

Initialize map $\mathcal{C} : \mathbb{R} \to \mathbb{N}_0$;
Initialize set $R = \emptyset$;
foreach $S_i \in \mathcal{S}$ **do**
  $\alpha_i \leftarrow \text{Affinity}(S_i)$;
  $\tau_i \leftarrow f(\alpha_i)$;
  $t_i \leftarrow \text{round}\left(\frac{\tau_i - t_{\min}}{\Delta t}\right) \cdot \Delta t$;
  $R \leftarrow R \cup \{(S_i, t_i)\}$;
  $\mathcal{C}[t_i] \leftarrow \mathcal{C}[t_i] + 1$;
end
$t_{\text{maxPeak}} \leftarrow \text{argmax}_{t \in \text{dom}(\mathcal{C})} \mathcal{C}[t]$;
Remove all $(S_i, t_i) \in R$ such that $t_i = t_{\text{maxPeak}}$;
Reconstruct P' from remaining subimages;
return $\mathcal{C}, P'$;

Algorithm 3. The algorithm for removing sub-images with the highest concentration from the image.

As Algorithm 3 shows, after removing the sub-images with the longest retention time, the image is reconstructed from the sub-images and the algorithm returns the image from which the fragments that occurred most frequently have been removed.

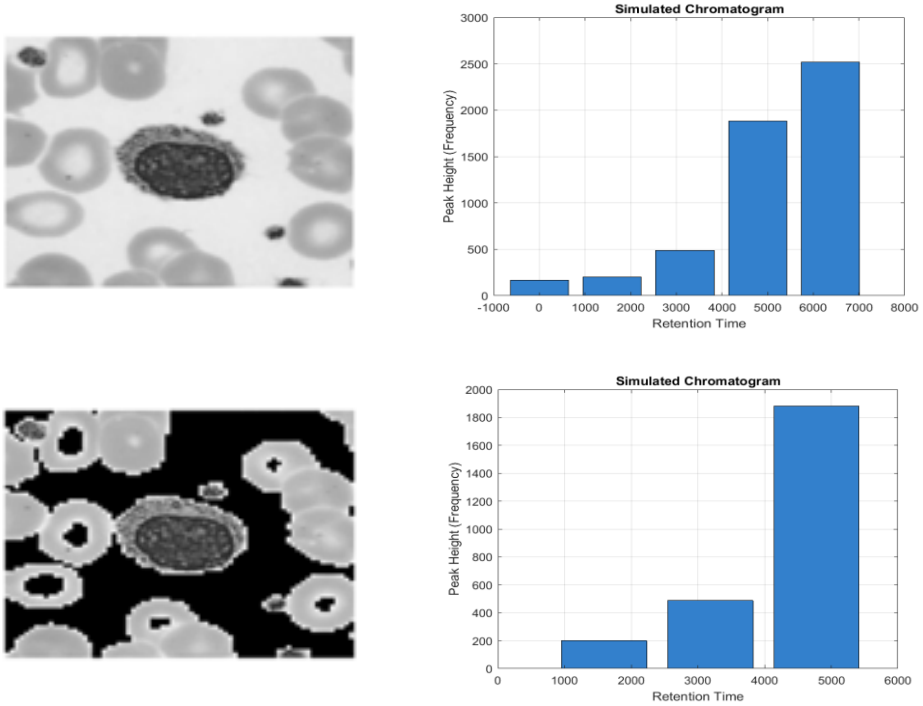

Figure 6. Image and chromatogram before and after removal of the dominant substance (Number of Poles = 4, Image dimensions 5x5).

Figure 6 the effect of the algorithm for removing the substances with the highest concentration was presented. As can be seen from the figure, the area that was the background of the image was removed from the lower part of the image. The second column contains chromatograms of the output image and the image that was created as a result of using the presented algorithm.

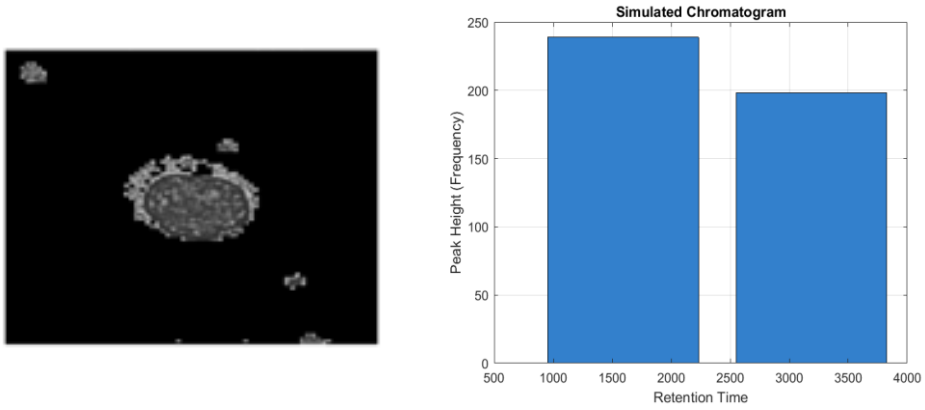

Figure 7. Image and chromatogram after removal of the dominant substance (Number of Poles = 4, Image dimensions 5x5), resulting from three iterations of the dominant peak removal operation on the original image.

Figure 7 shows the result of multiple application of the operation of removing the dominant peak from the image. As you can see, this process involves isolating an object from the image, which in a later stage can be another operation, which are related to recognizing a given object.

As it results from the presented chromatograms, the number of shelves used for the removal operation is 4. If the number of shelves increases, the generalization ability of the chromatographic algorithm will decrease – and the background removal process will require multiple applications of the presented algorithm.

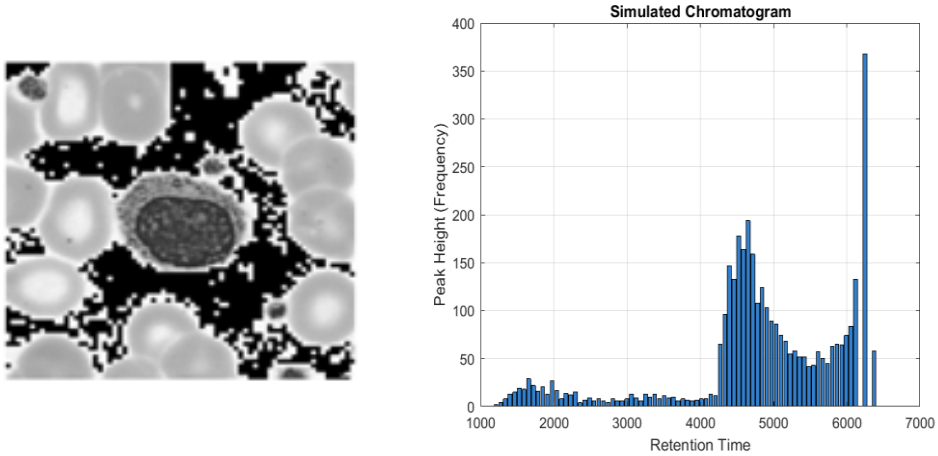

Figure 8. Image and chromatogram after removal of the dominant substance (Number of Poles = 100, Image dimensions 5x5), resulting from three iterations of the dominant peak removal operation on the original image.

Figure 8 the result of using the operation of removing the peak with the highest height to remove the background from the image was presented. As can be seen from the presented image, increasing the number of shelves in the algorithm caused the background removal

process to be longer, compared to the algorithm where the number of shelves was 4. On the other hand, it should be said that increasing the number of shelves in the algorithm causes the extraction process to be more selective (Solomon, Breckon, 2011; Young et al., 1995).

3.3. Algorithm for subtracting two chromatograms

Another operation on chromatograms that can be used in image processing is the operation of subtraction of two chromatograms. . **Algorithm 4** presents the sequence of operations related to the subtraction of two chromatograms. The input arguments of the presented algorithm are, among others, parameters that are responsible for the process of dividing the input image, and for the ability to generalize the chromatographic system, these parameters were discussed earlier. Another argument of the presented algorithm is the chromatogram, which will be subtracted from the chromatogram of the input image. The presented algorithm assumes that the input chromatogram was created by the chromatographic data separation algorithm with the same parameters that will be used to create the chromatogram of the image P, in particular the number of shelves, which is responsible for the resolution.

The algorithm is relatively simple, because the algorithm compares individual chromatogram peaks with each other, where the only criterion for comparison is the retention time. If the retention times of two peaks are the same, or the relative difference between the retention times is smaller than the value of the eps parameter, then such a peak, together with the images that belong to it, is removed from the chromatogram of the P image. Since the algorithm returns an image, as the algorithm states, the image is reconstructed based on the modified chromatogram.

The operation of subtracting chromatograms can be useful in the context of image processing in two categories of problems. The first category is the extraction of an object or objects from an image by removing the background, which often has a complex structure, then the use of **Algorithm 3** may not bring the desired results, especially when the extracted object or objects occupy a larger area than the background. The second category of problems, in which the presented algorithm can be used for skeletonization, i.e. representing an object in the form of a contour, which is an important issue in the image recognition process.

Input : $P \subset \mathbb{R}^{M \times N}$: input image (mixture),
$\mathcal{S} = \{S_1, \ldots, S_K\}$: set of non-overlapping subimages,
$ChSub$: subtracting chromatogram,
$L \in \mathbb{N}$: number of theoretical plates,
$t_{\min}, t_{\max} \in \mathbb{R}$: min and max retention time,
$\varepsilon \in [0, 1]$: retention time tolerance
Output: $\mathcal{C}_{out}$: resulting chromatogram,
$P' \subset P$: modified image after chromatogram subtraction

Assumptions:
- $t_{\max} > t_{\min}$
- $\Delta t = \frac{t_{\max} - t_{\min}}{L}$
- $\mathcal{S}$ is a non-overlapping partition of P
- $ChSub$ computed using same $L, t_{\min}, t_{\max}$
- $|\mathrm{dom}(ChSub)| \neq |\mathrm{dom}(\mathcal{C}_P)|$

End Assumptions

Initialize map $\mathcal{C}_P : \mathbb{R} \to \mathbb{N}_0$;
Initialize set $R = \emptyset$;
foreach $S_i \in \mathcal{S}$ **do**
  $\alpha_i \leftarrow \mathrm{Affinity}(S_i)$;
  $\tau_i \leftarrow f(\alpha_i)$;
  $t_i \leftarrow \mathrm{round}\left(\frac{\tau_i - t_{\min}}{\Delta t}\right) \cdot \Delta t$;
  $R \leftarrow R \cup \{(S_i, t_i)\}$;
  $\mathcal{C}_P[t_i] \leftarrow \mathcal{C}_P[t_i] + 1$;
end
Initialize map $\mathcal{C}_{out} \leftarrow \mathcal{C}_P$;
foreach $t_p \in \mathrm{dom}(\mathcal{C}_P)$ **do**
  foreach $t_s \in \mathrm{dom}(ChSub)$ **do**
    if $|t_p - t_s| \leq \varepsilon$ **then**
      Remove peak at t_p from $\mathcal{C}_{out}$;
      Remove all $(S_i, t_i) \in R$ such that $t_i = t_p$;
    end
  end
end
Reconstruct P' from remaining subimages in R;
return $\mathcal{C}_{out}, P'$;

Algorithm 4. Algorithm for subtracting two chromatograms.

Another important operation that plays a significant role in image processing is the skeletonization of a given object – that is, the presentation of a given object using contours, which allows in particular the identification of the object using shapes. In the case of using the chromatographic data separation method for image processing, this effect can be obtained with skillful processing of chromatograms.

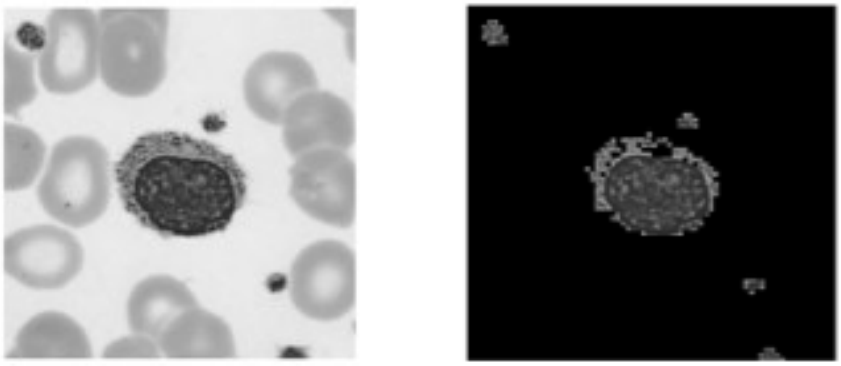

Figure 9. Background removal as a result of chromatogram subtraction operation.

Figure 9 shows the effect of the chromatogram subtraction operation. In this case, the chronogram that was subtracted was a chromatogram that was created based on an image containing graphic motifs related to the background. As can be seen in the figure on the right, the image has been stripped of its background, and in the center of the image there is an object that can be subjected to the recognition process.

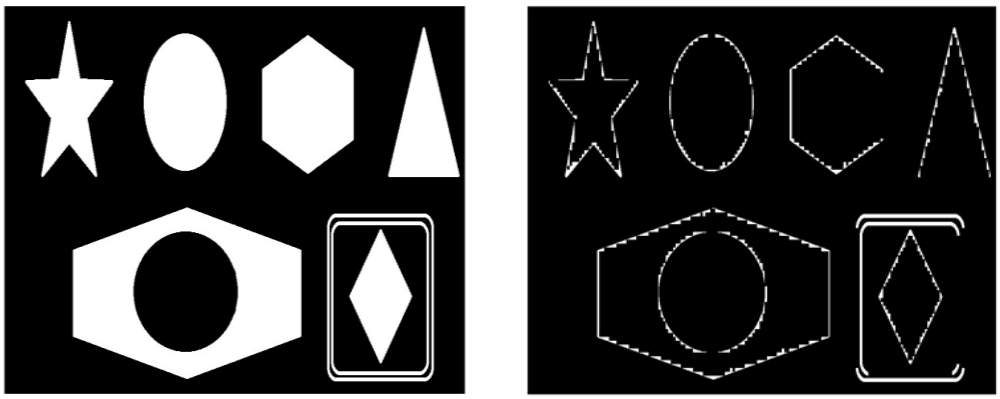

Figure 10. Skeletonization as a result of chromatogram subtraction operation.

Figure 10 shows the result of the chromatogram subtraction operation, in a situation where the subtracted chromatogram was created based on images that constitute the filling of objects that will be subjected to the skeletonization process. As shown in the figure on the left, the contours of objects were created. However, it should be noted that the appropriate selection of parameters also plays an important role, such as the number of shelves used by the chromatographic separation algorithm and the value of the eps parameter, which is responsible for the permissible value of the difference between individual chromatogram peaks Baxes, 1994; Mondello et al., 2008; Stilo et al., 2021).

3.4. Algorithm for removing common peaks between chromatograms

To obtain the effect of objects in the image being replaced by object contours, it is necessary to remove the common image fragments from the chromatogram containing the objects that we want to be represented by contours, which correspond to the filling of the images. This means that we must have at least two chromatograms, the first chromatogram was generated based on the image that is to contain the elements that we want to be removed from the second image. The remaining chromatograms were created based on the images that will undergo the skeletonization process.

Input : $\{P_i\}_{i=1}^N$: set of images, $\{S_i\}_{i=1}^N$: sets of subimages, $\{Ch_i\}_{i=1}^N$: chromatograms, $L \in \mathbb{N}$, $t_{\min}, t_{\max} \in \mathbb{R}$, $\varepsilon \in [0,1]$
Output: $\{Ch_i'\}_{i=1}^N$: modified chromatograms, $\{P_i'\}_{i=1}^N$: modified images, $\{S_i'\}_{i=1}^N$: modified subimage sets

Assumptions:
- $t_{\max} > t_{\min}$
- $\Delta t = \frac{t_{\max} - t_{\min}}{L}$
- $\forall i$, Ch_i computed with same $L, t_{\min}, t_{\max}$
- *Peakheightequalssubimagecount*

End Assumptions

$k \leftarrow \operatorname{argmin}_{i \in \{1,\ldots,N\}} |\mathrm{dom}(Ch_i)|$;
Reference chromatogram $Ch_{ref} \leftarrow Ch_k$;
foreach $i \in \{1,\ldots,N\}$, $i \neq k$ **do**
  foreach $t_r \in \mathrm{dom}(Ch_{ref})$ **do**
    foreach $t_i \in \mathrm{dom}(Ch_i)$ **do**
      if $|t_r - t_i| \leq \varepsilon$ **then**
        Remove peak at t_i from Ch_i;
        Remove all $(S,t) \in S_i$ such that $t = t_i$;
      end
    end
  end
end
foreach $i \in \{1,\ldots,N\}$ **do**
  Group peaks in Ch_i by identical retention times;
  Reconstruct P_i' from S_i';
end
return $\{Ch_i'\}, \{P_i'\}, \{S_i'\}$;

Algorithm 5. Algorithm for removing common peaks.

Algorithm 5 shows the sequence of operations, which aim to remove common peaks between chromatograms. The input arguments for the presented algorithm are chromatograms, which were created as a result of the chromatographic data separation algorithm, which is presented by **Algorithm 1**. The peaks between individual chromatograms are compared with respect to retention time. Peaks with the same retention time or with retention time where the difference between peaks is less than the value of the eps parameter, are removed from the chromatogram, which has a greater number of peaks. It is obvious that the chromatograms constituting the input arguments must have been created by **Algorithm 1** with the same parameters, and in particular with the same number of fields.

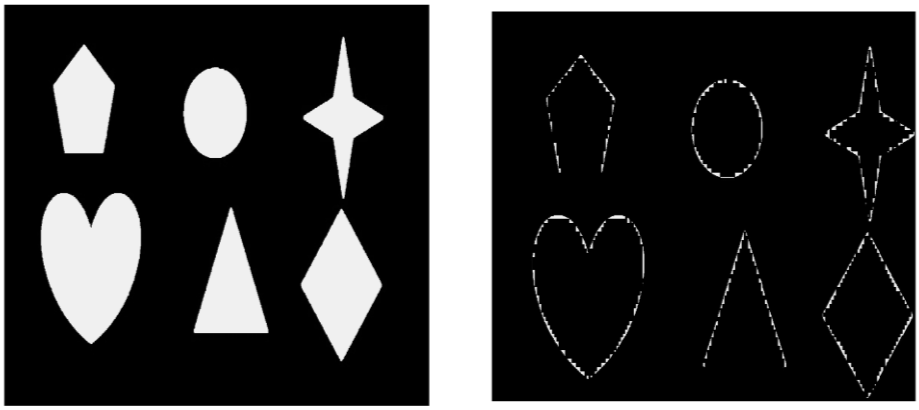

Figure 11. Input image and the image resulting from the application of the common peak removal algorithm (Algorithm 5).

Figure 9 shows the result of the operation, which consists in removing common peaks between chromatograms. As you can see, the result of this operation is the contours of the objects, which are on the left in the figure. Of course, the quality of the creation of the skeletons of individual objects is influenced by several parameters (Parker, 2010; Young et al., 1995).

3.5. Dilation algorithm

Dilation is one of the basic morphological operations in image processing, used mainly on binary images, but can also be extended to grayscale images. It consists in "expanding" objects contained in the image by adding pixels to their boundaries. In practice, dilation makes objects larger, and small gaps, cracks or irregularities in their structure are filled. Dilation is the opposite of erosion, which does the opposite – it reduces objects. Both of these operations are often used together, e.g. in morphological opening or closing, to clean images from interference**.**

In the case of representing images using chromatograms, it is also possible to define operations on the chromatograms that will ultimately correspond to the dilation operation.

Input : Ch_{in}: input chromatogram, L, $t_{\min}, t_{\max}$, M_1, N_1, M_2, N_2, L_2, $t_{\min 2}, t_{\max 2}$
Output: Ch_{out}: dilated chromatogram

Assumptions:
- Ch_{in} contains peaks with retention time, frequency, subimages, positions
- $t_{\max} > t_{\min}$
- $\Delta t = \frac{t_{\max} - t_{\min}}{L}$
- *Allimagesmayhavedifferentsizes*
- *split_chromatogramandreconstruct_imageareavailable*

End Assumptions

foreach *peak* p_i *in Peaks(*Ch_{in}*)* **do**
  if $t(p_i) > 0$ **then**
    foreach *subimage* S_{ij} *in SubImages(*p_i*)* **do**
      $Ch_{ij} \leftarrow$ split_chromatogram$(S_{ij}, M_2, N_2, L_2, t_{\min 2}, t_{\max 2})$;
    end
    $p_{max} \leftarrow \text{argmax}_{p \in \text{Peaks}(Ch_{ij})} (t(p), \text{freq}(p))$;
    foreach *peak* p_k *in Peaks(*Ch_{ij}*)* **do**
      if $p_k \neq p_{max}$ **then**
        Modify all subimages of p_k using representative subimage of p_{max};
      end
    end
    $S_i' \leftarrow$ reconstruct_image(SubImages(Ch_{ij}));
    Replace subimages of p_i in Ch_{in} by S_i';
  end
end
$P' \leftarrow$ reconstruct_image(AllSubImages(Ch_{in}));
$Ch_{out} \leftarrow$ split_chromatogram$(P', M_1, N_1, L, t_{\min}, t_{\max})$;
return Ch_{out};

Algorithm 6. Gas Chromatography-Inspired Dilation Algorithm.

The algorithm presented in the pseudocode performs the dilation operation inspired by the principles of gas chromatography. For each peak in the input chromatogram that has a non-zero retention time, a split of all its subimages is performed using the *split_chromatogram* function. From the obtained peaks, the one with the longest retention time and the highest frequency of occurrence is selected. Then, this selected subimage is used to modify the remaining subimages (including those belonging to peaks with zero retention time). The reconstructed subimages are inserted back into the original peak. After the operation is completed for all peaks, the entire image is reconstructed and split again – the final result is the reconstructed chromatogram after the dilation operation.

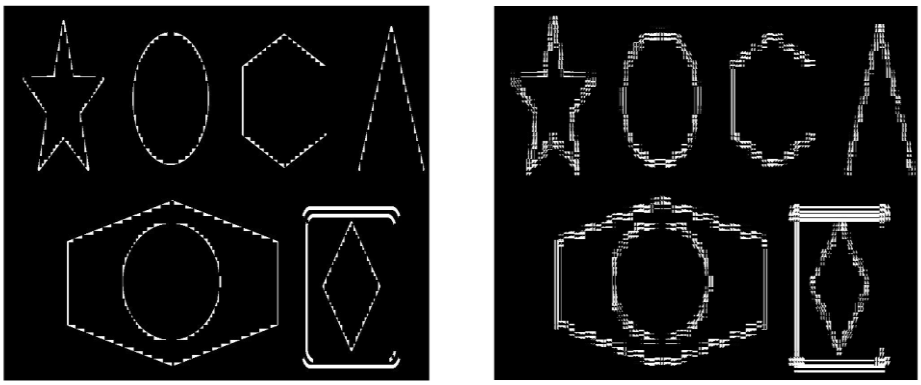

Figure 12. Input image and the image resulting from the application of the dilation algorithm (Algorithm 6).

Figure 12 shows the image before the dilation process – the image on the left. The image on the right was processed by the presented dilation algorithm. As you can see, the contours of individual objects have been thickened. However, the gaps that occurred in the outline of the objects have been filled in. It is obvious that the quality of the dilation process is influenced by the parameters that were described in the presented algorithm.

3.6 Erosion algorithm

Erosion is one of the basic morphological operations used in image processing, especially binary ones. It involves removing pixels from the edges of objects, thereby reducing their size. It works by moving a structural element across the image and leaving only those pixels that are completely within the object. As a result, erosion effectively eliminates small distortions and noise, which is useful in cleaning up the image before further analysis steps. As a result of this operation, fine structures and small details can disappear, allowing for better separation of closely located objects. The type of structural element used, e.g. circular, cross or square, affects the final effect of erosion. In the case of grayscale images, the operation involves assigning each pixel the minimum value of its neighbors defined by the structural element. Erosion is often used together with dilation, creating more complex operations such as morphological opening and closing. Despite its simplicity, it is an important tool in shape analysis, segmentation and recognition of objects in images. Its applications are found in many fields, from medicine to industry and vision systems (Young et al., 1995).

Input : Ch_{in}: input chromatogram, L, $t_{\min}, t_{\max}$, M_1, N_1, M_2, N_2, L_2, $t_{\min 2}, t_{\max 2}$, $ErosionThreshold \in [0,1]$
Output: Ch_{out}: eroded chromatogram, P': modified input image

1 **Assumptions:** All peaks in Ch_{in} contain retention time, frequency, subimages, positions. $t_{\max} > t_{\min}$. $\Delta t = \frac{t_{\max} - t_{\min}}{L}$. All images may have different sizes. Functions split_chromatogram() and reconstruct_image() are available. ErosionThreshold $\in [0,1]$ defines activation level of erosion. **End Assumptions**
2 **foreach** *peak* p_i *in Peaks*(Ch_{in}) **do**
3 **if** $t(p_i) > 0$ **then**
4 **foreach** *subimage* S_{ij} *in SubImages*(p_i) **do**
5 $Ch_{ij} \leftarrow$ split_chromatogram$(S_{ij}, M_2, N_2, L_2, t_{\min 2}, t_{\max 2})$;
6 **if** *exists peak* p_0 *in Peaks*(Ch_{ij}) *with* $t(p_0) = 0$ *and* $height(p_0) > ErosionThreshold * M_2 * N_2$ **then**
7 Replace all subimages in Ch_{ij} with subimage corresponding to p_0;
8 **end**
9 **end**
10 $S'_i \leftarrow$ reconstruct_image(SubImages(Ch_{ij}));
11 Replace subimages of p_i in Ch_{in} by S'_i;
12 **end**
13 **end**
14 $P' \leftarrow$ reconstruct_image(AllSubImages(Ch_{in}));
15 $Ch_{out} \leftarrow$ split_chromatogram$(P', M_1, N_1, L, t_{\min}, t_{\max})$;
16 **return** Ch_{out}, P';

Algorithm 7. Gas Chromatography-Inspired Erosion algorithm.

The algorithm performs the erosion operation in the context of processing chromatographic data representing images of chemical substances. The input is a chromatogram containing peaks, each of which consists of sub-images and an assigned retention time. It is assumed that the retention time is rounded to values consistent with the formula based on the number of shelves and the retention range. Additionally, all images can have different sizes, and the erosion threshold (ErosionThreshold) is in the range [0, 1]. The algorithm uses the split_chromatogram function, which separates sub-images based on the given parameters. For each peak with a retention time different from zero, a separation is performed, and in the case of detecting a dominant peak with zero retention time exceeding the threshold, all sub-images are replaced with this one. Then, the sub-images are reconstructed using the reconstruct_image function, which leads to their update. After completing all transformations, the algorithm rebuilds the entire chromatogram and performs its final segmentation. The algorithm outputs an updated chromatogram and a reconstructed image containing erosion results. The goal of the algorithm is to eliminate weak signals by applying erosive image reduction, which leads to a simplification of the input data structure.

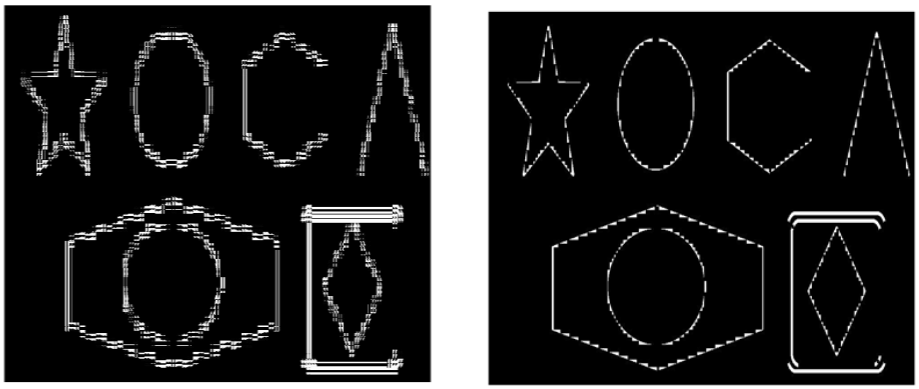

Figure 13. Input image and the image resulting from the application of the erosion algorithm (Algorithm 7).

Figure 12 shows the image before the erosion process – the image on the left. The image on the right was processed by the presented erosion algorithm. As you can see, the contours of individual objects have been eroded – they are thinner.

4. Summary

The text describes an innovative approach to image processing, based on the chromatographic data separation method, inspired by gas chromatography. Image processing is crucial in the automation of quality control and diagnostics, including in industry and hematology. Classical image analysis methods use segmentation, feature extraction and classification using algorithms such as SVM or neural networks. The proposed method treats the image as a mixture of substances, where individual fragments (subimages) correspond to "substances" subjected to the chromatographic process. Subimages are assessed in terms of affinity to the stationary phase, which affects their retention time in the "chromatographic column".

The process produces a chromatogram, i.e. a distribution of sub-image retention times, which reflects the image structure. The algorithm divides the image into sub-areas, calculates the retention time for them, and creates a histogram grouping sub-images with similar times. This approach allows for performing various operations on the image, such as selection, removing dominant fragments (e.g. background) or extracting objects.

An important element is the ability to remove subimages with the highest concentration from the image, which allows for the isolation of important elements and reduction of interference. Additionally, the algorithm allows for the subtraction of chromatograms, which allows for the removal of the background or skeletonization of objects, i.e. the creation of contours useful for shape recognition. As a result, you can obtain an image without a background or extract its contour structures.

This method allows for image filtering in a manner similar to chromatographic filtration, which is a unique approach in the field of image analysis. The advantage of the algorithm is the ability to adjust the resolution (number of shelves), which affects the selectivity and generalization of the process. It was emphasized that the appropriate selection of parameters is crucial for the quality of the results.

The operations of removing common peaks between chromatograms are also presented, which allows further processing and extraction of information from images. The method can be used in various applications, from product quality control to medical diagnostics, especially hematology.

Classical image processing techniques, such as segmentation, feature extraction, and classification, have long been the foundation of many applications in industry and medicine. These methods typically rely on algorithms like edge detection (e.g., Canny or Sobel operators), thresholding, region growing, and machine learning models, including Support Vector Machines (SVM) and neural networks. Although these techniques have proven useful in various tasks, they often encounter issues related to sensitivity to noise, complexity of feature extraction, and difficulty in handling highly variable image data without significant pre-processing.

The chromatographic data separation method, in contrast to traditional approaches, proposes a unique technique by treating the image as a mixture of substances, similar to chemical processes in chromatography. This enables selective analysis of the image's components based on their "affinity" to a simulated stationary phase, offering a new way to segment and manipulate image data. The process of converting an image into a chromatogram allows not only for effective feature isolation but also for performing operations that enable selective enhancement or removal of specific image elements (e.g., background or unwanted disturbances).

The chromatographic method allows for precise adjustment of image processing resolution (through the number of chromatographic shelves), which increases the accuracy of feature extraction. This is particularly beneficial when working with images that are highly complex or noisy, where traditional segmentation may fail. Since this method allows for various operations, such as removing dominant elements, selectively adjusting the background, or extracting contours, it is useful in analyses that require precise object separation, such as in medical applications (e.g., microscopic blood analysis) or industrial quality control.

Another significant advantage is the reduced sensitivity to background noise. By focusing on the retention time of individual sub-images, the method enables more precise removal of the background and irrelevant parts of the image, ultimately increasing the accuracy of object detection and image filtering. This approach also stands out due to its innovative combination of chemical analysis principles with image processing, opening new possibilities in fields such as environmental monitoring and medical diagnostics, where classical methods may have limitations.

One of the main challenges of the chromatographic method is its sensitivity to parameter selection, such as the number of shelves or the granularity of sub-image division. Incorrectly choosing these parameters can lead to inefficient image segmentation or excessive loss of relevant information. Therefore, it is necessary to carefully adjust these settings to achieve the optimal result.

In summary, the chromatographic data separation algorithm is a novel tool for image analysis and processing, offering the possibility of selection, filtering and extraction of objects based on the chromatographic model, which opens new directions in image automation and recognition.

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