An Image Enhancement Method for TGGE Images for Genenome Profiling

Khoa Pho (JAIST)・ Misato Baba (KyotoU)・ Yutaro Narukawa (KyotoU)・ Yuto Tsutsumi (KyotoU)・ Kiyoshi Yasukawa (KyotoU)・ Atsuo Yoshitaka (JAIST)

1 Introduction

Genome Profiling (GP) [1] is a wide-range-applicable method which has potential for analyzing the gene information of individual cells or species. GP helps to understand why people react in different ways to the same drugs and to develop suitable diagnoses and treatments. In GP, DNA is PCR-amplified with a random primer. Temperature gradient gel electrophoresis (TGGE) is performed. DNA fragments in TGGE profiles are visualized as images of trajectories.

In this paper, an image enhancement method for the is proposed to toward automatic TGGE analysis process. The intensities of pixels of a trajectory are not constants. Within a trajectory, the intensities are lower around the bottom and higher around the top of the image. The thinner trajectories have lower intensities than the thicker trajectories. Global normalization, which change the all the pixels into the same range of intensity values, may remove the thin trajectories. Therefore, the image is divided into multiple patches to be treated locally. Local equalization is applied to emphasize the trajectories.

2 Proposed Method

The binary thresholding method is applied to remove surrounding noise pixels of the target trajectories. Morphological operators are applied to remove lower intensity regions between two trajectories. Erosion operator is applied to erode the thin trajectories and small regions. This operator is also helpful for separating the trajectories that are closed to each others. Dilation operator is applied to refill the trajectories. However, dilation operator also fills in the region between trajectories and edges of the patch. It creates vertical and horizontal stripes in the result image when combining all the resulting patches (Output1). Therefore, the edges of the resulting patch is removed (Output2).

An iterative updating process is proposed to emphasize the pixels of the lines over the pixels of isolated regions. At the initial stage, pixels are set to 1 if its intensity value higher than a threshold and to 0 vice versa. The values are then updated iteratively. In each iteration, only the pixels, which are initialized as 1, are updated. The value of the pixel is updated by the sum of its value and its neighbors in a kernel of 3x3. The values of pixels that have more connections increase faster than the pixels that have fewer connections. In the next iterations, pixels in large regions spread their high values therefore increase faster than pixels in isolated small regions. After a certain number of iterations, the values of pixels in large regions are much higher than pixels in isolated regions. A threshold is applied to remove the isolated regions.

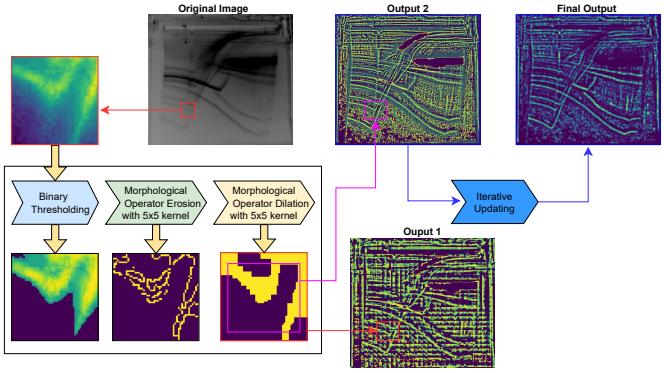

図 1: Our proposed image enhancement process.

3 Experiment

We evaluate our enhancement method on EME, AME, and SDME metric. Higher values denote more contrast and clarity of information. We evaluate on our dataset of Bacillus coli and NIH.

	EM	AME	SDME
Original	4.21	0.06	-80.58
HE	16.63	0.14	-68.39
CLAHE	12.32	0.17	-64.62
Proposed	24.86	0.33	-40.76

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参考文献

[1] Koichi Nishigaki, Norihiko Amano, and Tsutomu Takasawa, “Dna profiling. an approach of systemic characterization, classification, and comparison of genomic dnas,” *Chemistry Letters*, vol. 20, no. 7, pp. 1097–1100, 1991.