DDGEL/DDCHIP: Web-Based Systems for Analysis of 2-D Gel Electrophoresis Images and DNA Macro/Micro Array Images

Kyotetsu Kanaya 1	Akira Ohyama 1
kanaya@hydra.mki.co.jp	akr@hydra.mki.co.jp
Tatsuya Akutsu ²	Asao Fujiyama 3
takutsu@ims.u-tokyo.ac.jp	afujiyam@lab.nig.ac.jp

¹ Department of Bioscience Systems, Mitsui Knowledge Industry Co., Ltd., 2-7-14 Higashinakano, Nakano-ku, Tokyo 164-8555, Japan

² Human Genome Center, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

³ National Institute of Genetics, 1111 Yata, Mishima-city, Shizuoka 411-8540, Japan

1 Introduction

We have been developing a web-based software tool named **DDGEL** [3] for analysis of two-dimensional (2-D) gel electrophoresis image data obtained by the RLGS (Restriction Landmark Genomic Scanning) method. The RLGS method has been developed in order to detect and analyze the genetic alterations by observing the entire genomic DNA after separating DNA fragments in a single 2-D slab gel [2]. DDGEL has the following functions: (1) User identification/registration, (2) Spot detection, (3) Modification of spot data, (4) Database of reference gel image/spot data, (5) Addition and modification of comments on image/spot data, (6) Spot matching (under construction).

Recently, we began to develop a web-based software tool for analyzing image data obtained from DNA macro arrays and/or DNA micro arrays. This tool is named **DDCHIP**. In this short article, we briefly report a recent improvement on DDGEL and an overview of DDCHIP.

2 Recent Improvement on DDGEL

The most important improvement is that a new spot matching algorithm was implemented. Before developing a matching algorithm, we made a theoretical study and we proved that spot matching is a computationally hard problem (NP-hard) [1]. This result justifies the development of heuristic algorithms. Since it seems that previously developed heuristic algorithms [4, 5] are not sufficient, we developed a new heuristic spot matching algorithm based on dynamic programming and least-squares fitting, where details are described in [1]. Improvement of spot detection is being done too. The α -version of DDGEL on web is available via http://bonsai.ims.u-tokyo.ac.jp/cgi-bin/ddtop/cgi-bin/index.cgi.

3 Overview of DDCHIP

Since DNA micro arrays are becoming popular, a lot of image data will be produced from DNA micro arrays. The last author of this article is currently developing a system for detection and analysis of genetic alterations using DNA macro arrays. Since functions required for analysis of DNA macro/micro array images are similar to those for analysis of 2-D gel electrophoresis images, we began to develop the DDCHIP system by modifying the DDGEL system. Although the same algorithms as in DDGEL are currently used for spot detection and spot matching, they will be replaced by new ones specialized for DNA macro/micro array images in the near future. A snapshot of DDCHIP is shown in Fig. 1.



Figure 1: Snapshot of the web interface of DDCHIP.

Acknowledgment

This work is supported in part by a Grant-in-Aid "Genome Science" for Scientific Research on Priority Areas from the Ministry of Education, Science, Sports and Culture in Japan.

References

- Akutsu, T., Kanaya, K., Ohyama, A., and Fujiyama, A., Matching of spots in 2D electrophoresis images. Point matching under non-uniform distortions, *Lecture Notes in Computer Science*, 1645:212–222, 1999.
- [2] Hatada, I. et al., A genomic scanning method for higher order organisms using restriction sites as landmarks, Proc. Natl. Acad. Sci. USA., 88:9523–9527, 1991.
- [3] Kanaya, K., Ohyama, A., Akutsu, T., and Fujiyama, A., Development of web interface of image analysis system DDGEL for 2D gel electrophoresis, *Genome Informatics 1998*, Universal Academy Press, 336–337, 1998.
- [4] Sugahara, Y., Hayashizaki, Y., and Tanihata, I., An automatic image analysis system for RLGS films, *Genome Informatics 1997*, Universal Academy Press, 340–341, 1997.
- [5] Takahashi, K., Nakazawa, M., and Watanabe, Y., DNAinsight: an image processing system for 2-D gel electrophoresis of genomic DNA, *Genome Informatics 1997*, Universal Academy Press, 135–146, 1997.