An Image Analysis System for Two-Dimensional Gel Electrophoresis

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1 Introduction

A method called RLGS(Restriction Landmark Genomic Scanning) has recently been developed in order to detect and analyze the genetic alterations by observing the entire genomic DNA after separating DNA fragments in a single two-dimensional slab gel. To analyze gel images obtained by the RLGS method, a lot tasks must be done: thousands of spots must be detected where each spot corresponds to a gene; correspondences of spots between two images must be detected; links between spots and genetic information must be classified and stored in a database. We have been developing a software tool so that such tasks can be done automatically or semi-automatically.

2 System and Functions

The software is written in C and runs on a Unix workstation with SunOS 4.1.2, Solaris 2.3, or an upper-compatible operating system. OSF/Motif 1.2 is also required.

The following functions are implemented in the current version: image data format conversion and transfer; spot detection; spot classification and spot matching between two different images. Basic image analysis functions such as background noise reduction, image rotation and inversion, edge detection and direct cut-and-paste function of images are also implemented.

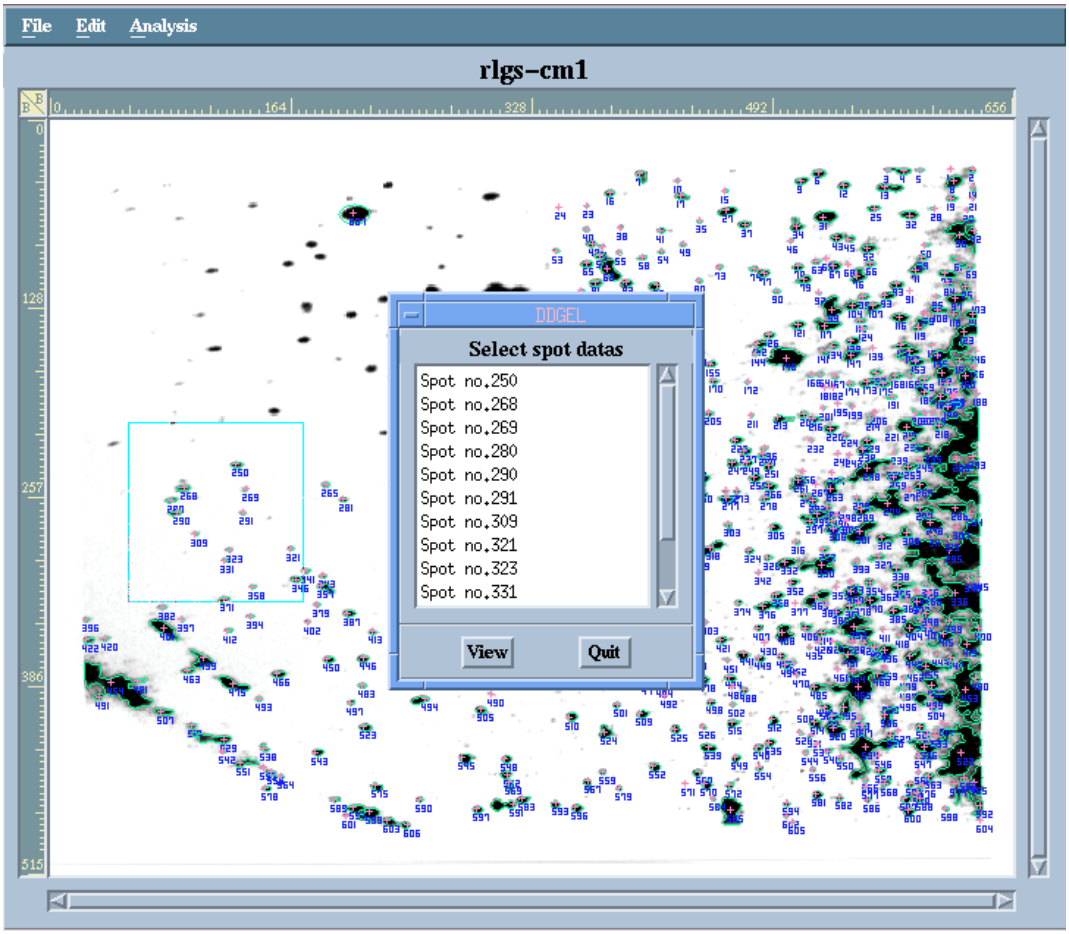

Figure 1: Spots detected from the gel image of Human Chromosome 1.

3 Result

A result of spot detection applied to Human Chromosome 1 is shown in Figure.1. Although the number of spots detected by the software heavily depends on the quality of the gel image, there was a little difference between the spots detected by the system and those detected by a human expert. Since the system sometimes fails to detect low-intensity and large size spots, we are developing an improved method.

References

[1] A. Ohyama, T. Akutsu and A. Fujiyama, "A Software Tool for Mapping Human Genome by Chromosome-specific Two- Dimensional Electrophoresis Method," *Proc. Genome Informatics Workshop 1995*, pp. 144-145, 1995.