

An analysis system of 2-D gel electrophoresis images for genomic scanning - DNAinsight -

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1 Introduction

RLGS(restriction landmark genomic scanning) method developed by Hayashizaki et al.[1] is one of the most powerful experimental procedures which can be applied to high-speed genome mapping. Through the method, restriction enzyme sites on genomic DNA are used as landmarks, being guideposts on the genome. These landmark information can be scanned over the whole genome by employing direct end-labeling of genomic DNA fragments and high-resolutonal two-dimensional gel electrophoresis. Such landmarks can be detected as several thousands of spots on an autoradiogram image of two-dimensional gel electrophoresis. Since each variant spot segregates as an independent genetic locus, simultaneous mapping of a large number of loci can be achieved by recognizing the spot locations and intensities.

It is impossible, however, either to separate all of several thousands of spots or to determine their intensities by visual inspection. It is also difficult by hand to compare two or more images, in order to perceive the translocation, amplification and deletion of spots. Such difficulties on RLGS analysis make the high-speed multiplex genome scanning impractical. To overcome these problems, we have developed a powerful image processing system, **DNAinsight**[2], dealing with two-dimensional electrophoretograms of genomic DNA. Here, we demonstrate this system with a mobile DOS/V computer.

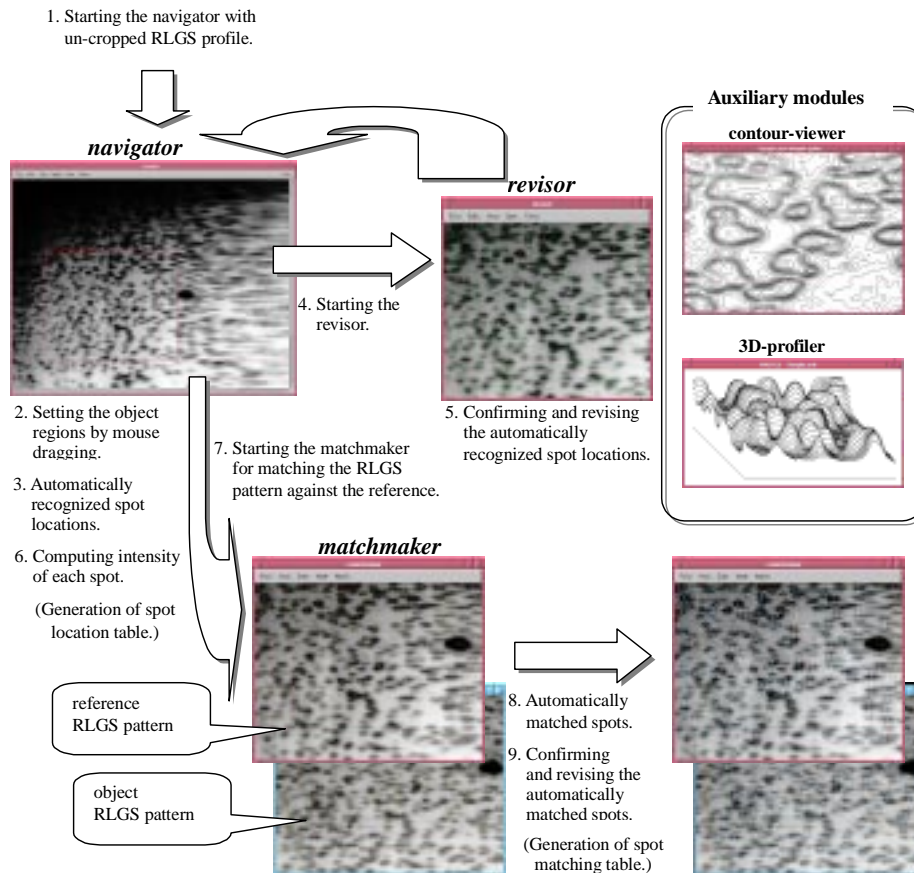
2 System design and implementaion

An RLGS pattern analysis with **DNAinsight** can be performed by choosing an item from the pull-down menu, simple mouse operation and with a little keyboard input. **DNAinsight** is very effective and very powerful, since it performs automated detection of RLGS spots and matching of several RLGS patterns, such as those from tumor-cell and normal-cell. It also provides utility modules for confirming and revising the automatically recognized spots or matched pairs of spots together with auxiliary utility modules, such as contour-viewer, 3D-profiler and spotdomain-viewer, so that any user without expert knowledge can make use of interactive operation.

Our system is implemented on a DOS/V computer compatible to PC running with Linux, and can be implemented on any computers running with UNIX, on which X-window and Motif are available, from personal computers to engineering workstations.

3 Analysis procedure

A typical analysis procedure with **DNAinsight** is shown as follows, after digitizing an X-ray film with an image scanner.



4 Summary

We have developed a powerful image processing system, **DNAinsight**, which deals with autoradiogram images obtained with two-dimensional electrophoresis of genomic DNA. **DNAinsight** provides a rapid and objective way to analyze several thousands of landmark spots found on a large sized RLGS profiles and also to extract matched, appeared or disappeared spots from the related RLGS profiles. Actually, it takes about ten minutes to detect all spots on a RLGS profile and compare them with those on a reference RLGS profile even with cheaper DOS/V computer running with Linux, while it takes about two or three hours by visual inspection.

References

- [1] Y. Hayashizaki, et al. "Restriction landmark genomic scanning method and its various application," *Electrophoresis*, 14, pp. 251-258, 1993.
- [2] K.Takahashi, M.Nakazawa and Y.Watanabe, "DNAinsight: An Image Processing System for 2-D Gel Electrophoresis of Genomic DNA," *Proc. of the 8th Workshop on Genome Informatics*, 1997.