A Tool on Web for Gene Regulatory Networks:
Toward Software Agent for Genome Information Analysis

Hiroshi Matsuno [1]
matsuno@sci.yamaguchi-u.ac.jp
Nobuaki Wada [1]
wada@webbies.sci.yamaguchi-u.ac.jp

Manabu Hori [1]
mhori@po.cc.yamaguchi-u.ac.jp
Miyako Tanaka [2]
miyako@ics.nara-wu.ac.jp

[1] Faculty of Science, Yamaguchi University
1677-1 Yoshida, Yamaguchi, 753, Japan

[2] Graduate School of Science, Nara Women's University
Kitauoyanishimachi, Nara, 630, Japan

1   Introduction

Saccharomyces cerevisiae is the first eukaryotic organism whose DNA sequences have been determined. Currently, it is considered that these DNA sequences encode 6,200 genes and only 43.3% of these are classified as 'functionally characterized' [4]. Now the main topic of researches on *S. cerevisiae* has shifted to the systematic functional analysis of the genes.

From July 1997, some parts of gene regulatory network (regulatory pathway) of *S. cerevisiae* are available in [3]. On the other hand, the project to identify the gene regulatory network of *S. cerevisiae* from experimental data obtained by gene disruptions and gene amplifications has been launched [5].

The aim of our research is to develop the system which automatically construct the gene regulatory network from biological papers. As a first step, we will present only the part of user-interface of the system to steal the knowledge of biologists.

2   A Tool for Biologist

To release biologists from the task of finding necessary information from the amount of papers, the system that extracts domain specific knowledge from human written biological papers was developed in [6].

We have constructed a tool on World Wide Web to be used by biologists who are intend to construct the gene regulatory network of *S. cerevisiae* from MEDLINE. The tool is used in the following manner.

1. A biologist specifies an arbitrary gene and enters it to the tool.

2. The tool collects the abstracts of papers which contain the information about the specified gene from MEDLINE.

3. For each abstract of the collected papers, the tool finds and displays the names of genes.

4. The biologist enters the relationship between the specified gene and the other gene (activate/inactivate/no decision) according to his wealth of knowledge.
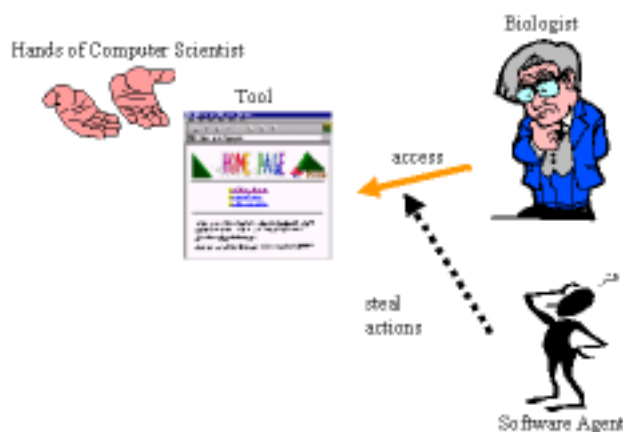
Figure 1: Software Agent steals actions of the biologist.

3   Future Works

Our aim is to develop a system which can automatically find the relationship between two genes from MEDLINE. We are having interests in Software Agent [2] as a technique to achieve the aim. While the biologist is using the tool, the software agent watches the actions of him as shown in Figure 1. When the biologist is free (maybe midnight), the software agent analyzes the stored actions and gets knowledge about gene relationships.

Acknowledgments

References

[1] Akutsu, T., Kuhara, S., Maruyama, O., and Miyano, S., "Identification of gene regulatory networks by strategic gene disruptions and gene amplifications," *Proc. Ninth Annual ACM-SIAM Symposium on Discrete Algorithms,* (to appear), 1998.

[2] Bradshaw, J. M., "Software Agents," *AAAI Press / The MIT Press*, 1997.

[3] http://www.genome.ad.jp/kegg/kegg2.html

[4] Mewes, H. W., Albermann, K., Bahr, M., Frishman, D., Gleissner, A., Hani, J., Heumann, K., Maierl, A., Oliver, S. G., Pfeiffer, F., and Zollner, A., "Overview of the yeast genome," *Nature*, 387(6632 Suppl.): 7–65, 1995.

[5] Miyano, S., "Knowledge discovery for genome information processing", *Technical report of Japanese Society of Artificial Intelligence,* SIG-FAI-9701-11(6/6), 63–68, 1997.

[6] Ohta, Y., Yamamoto, Y., Uchiyama, I., and Takagi, T., "Information finding from biological papers," *Proceedings of the Seventh Workshop on Genome Informatics*, 258–259, 1996.