Mobile Agent System for Animal Genome Database

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1 Introduction

It is important to develop the genome database for searching the genetic regions or genes responsible for economic traits. We have developed an animal genome database and its search system (http://ws4.niai.affrc.go.jp/) [2] and a client-server system name gRanch [3] in order to query the animal genome database and to analyse the genetic linkage. However, there are some restrictions of WWW with client software and client machine is limited to the UNIX machine as for gRanch. In the present study, we have developed a mobile agent system for animal genome database in order to solve these problems. The system is written by Java language and the client program is translated to the binary program for Microsoft Windows95. This system has the function to predict corresponding chromosome in other animals' genomes, correspondence between the linkage and cytogenetic map [4] and viewer for DNA sequences.

2 System overview

The client connects with the certification server when it is invoked and user ID, password and IP address of the client are checked. Then, the menu agent is downloaded from the agent server to the client. All agents are stored in the agent server and are written by Java language. The agent is transferred if necessary between the agent server and the client, the query is retrieved on the server side, and the results is graphically displayed on the client side (Fig. 1). Since the agent including program and data is compressed when moving through the network, the communication time is shortened compared with the system based on Java applet. The time which hangs to the start and the display of graphic images in the client is also reduced using the translated binary program. The agents who belong to the same user communicate with each other on the client, exchange information, draw the intention of the user, and adjust the display of the results.

3 Prediction of chromosome in other animal's genome

We consider two genes on the same chromosome of d CM or less in the linkage map of MGD database. The probability($p(d)$) that the two genes exist on the same chromosome of another species is estimated using information of the comparative mapping. The posterior probability that interesting gene exists in i chromosome of another species is estimated using the following formula,

$$P(i|d_1, d_2,\ j_1, j_2) = \frac{p(d_1)^{\delta_{i,j_1}}(1-p(d_1))^{1-\delta_{i,j_1}}p(d_2)^{\delta_{i,j_2}}(1-p(d_2))^{1-\delta_{i,j_2}}}{\sum_{k=1}^{M} p(d_1)^{\delta_{k,j_1}}(1-p(d_1))^{1-\delta_{k,j_1}}p(d_2)^{\delta_{k,j_2}}(1-p(d_2))^{1-\delta_{k,j_2}}}$$

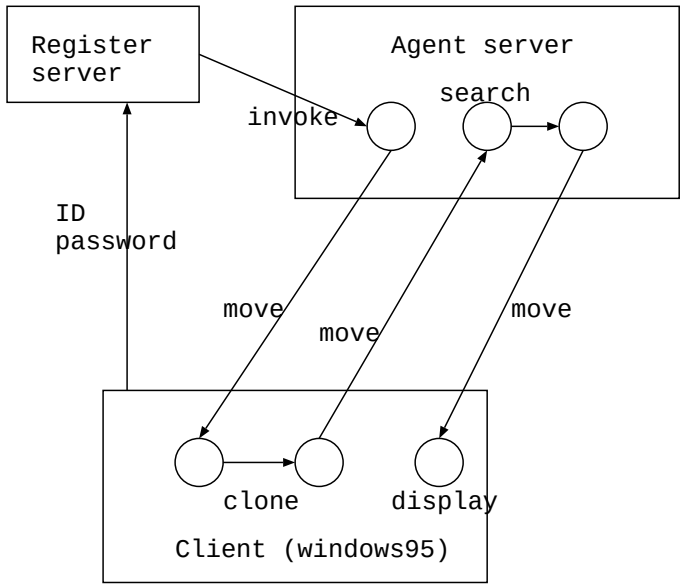

Figure 1: System overview.

where d_1 (d_2) is the distance between the interesting gene and the two nearest genes on the mouse chromosome, j_1 (j_2) is the chromosome in which the two genes exist on the genome of another species.

4 Viewer for DNA sequences

User can also search an entry of DNA database and display the DNA sequences and their related information of some mammals in this system. One dimension structure of the DNA sequence named exon or intron is classified and displayed by a different color.

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References

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