Assistant Software for Linkage Analysis

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Abstract

We have developed a new system for assistance of linkage analysis using the Java language and the HORB, which is an object broker for the Java language. This system includes an automatic correction of allele types, display of alleles transmission in families, normal distribution test of traits data.

Introduction

We are currently mapping the porcine genetic markers for linkage analysis to elucidate genes or genetic regions responsible for phenotypes under the collaboration of the National Institute of Animal Industry, National Institute of Animal Health and STAFF institute. For this analysis, the online linkage analysis system have been developed[5]. We have also developed a gene mapping workbench named gRanch[6] for data registration and computing lod scores. However, the gRanch can not be used on personal computers and it is difficult for collaboration of multiple CPUs on these systems. Therefore, a new system has been developed for assistance of linkage analysis using the Java language[3] and the HORB[2], which is an object broker for the Java language.

System overview

Our system has been written by the Java language based on the JDK1.1. With the appletviewer of the JDK1.1.x, users can access the applet of our system (http://genome.niai.affrc.go.jp/linkagent/). However, the present version of Netscape and Internet Explorer can not perform the applet based on the JDK1.1. Users can handle the data for linkage analysis and check the mistakes of allele typing in the applet. The system has a connection to CRI-MAP 2.4[1] for computing lod scores between two markers. Following its instruction, the users can invokes Java's remote objects in the HORB server from the applet. These objects access the relational database and process data as request from users, and the results of the processing are returned to the applet and displayed graphically. For recognition of the user and their project, the applet checks the user ID, password and the IP address of the client computer. The log of all commands is written to the relational database. In night time, the agent program is programmed to run in the HORB server to check the problems of the system and the database.

Automatic correction of allele types

We observed allele type errors at an frequency in our system using GeneScan 672 and Genotyper. Since the allele type is based on the size of fragments produced in each locus, the size was sometimes estimated differently even though a same sample was used for the analysis. Therefore, in order to perform the genotyping accurately, tolerance values were introduced into the determination of size of the fragments.

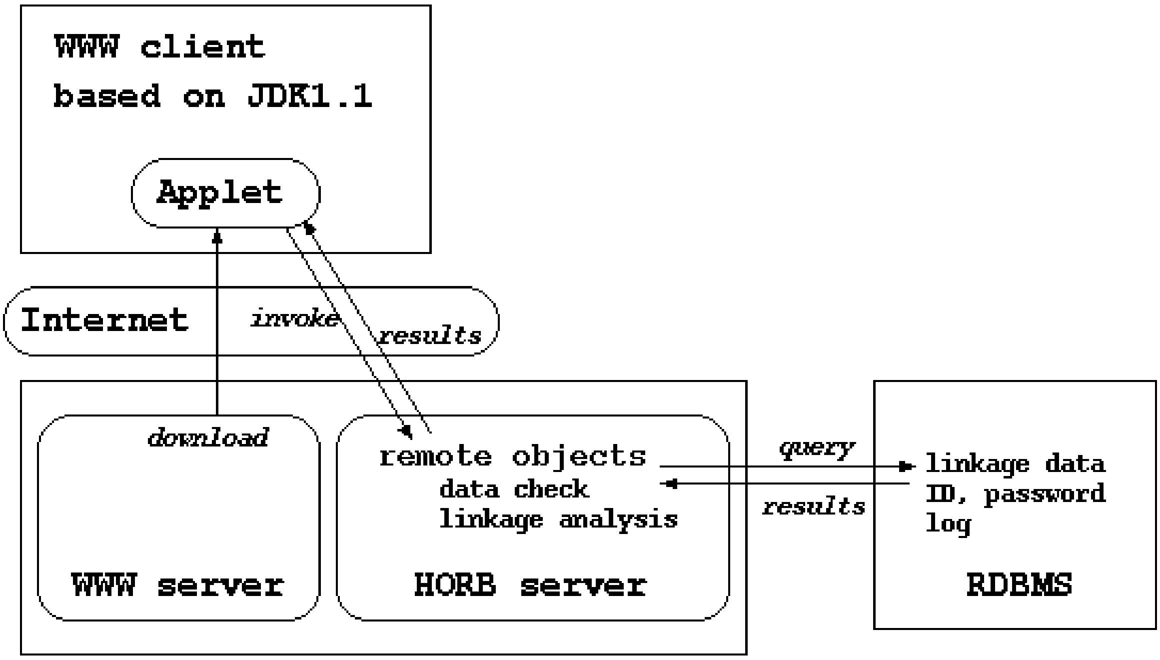

Figure 1: System overview of assistant software for linkage analysis

Display of allele transmission in the families

In order to facilitate the finding of mistakes in allele typing, allele transmission in the families are displayed graphically in the applet.

Future works

We have developed an animal genome database for network users[4]. In order to provide an useful software agent for linkage analysts, we will develop an interface connecting the animal genome database and the system for linkage analysis.

References

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