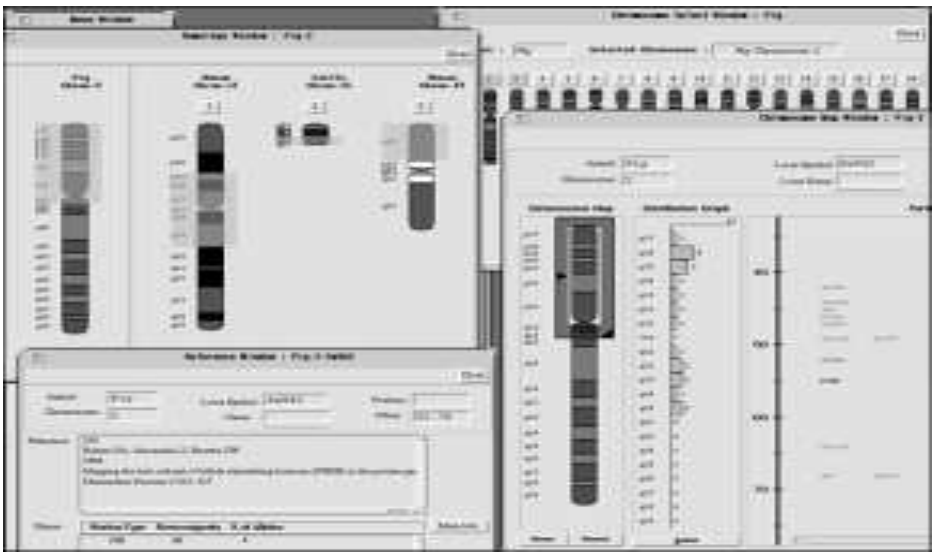

Figure 1: The sample image of the usage of gRanch

In the linkage analysis, the users can select the correct pedigree code or allele code in the code list when they input, modify and delete these data. The new or modified data are put in the database for the linkage analysis. Lod scores and recombination frequencies are able to compute using by CRI-MAP[2].

As for animal genome database, the gRanch display the gene map which integrate the physical map and the linkage map, two kinds of homology map between species, references and the information of PCR primer. One of the homology map display the homology areas of each species. The other homology map display the homology of the chromosome between species.

3 Future Works

The aim of the gRanch is to perform genetic linkage analysis and to assist to construction gene map. The function of construction a linkage map will be implemented. The linkage analysis need many computational power, however, super computer is high price. We are planning to implement a new linkage analysis program using by the parallel computing technique.

References

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gRanch: Gene Mapping Workbench

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Abstract

We have been developing a gene mapping workbench named gRanch. This system display the integrated gene map and two kinds of homology map between species. The functions of input pedigree or allele data and analysis the linkage map are implemented in the gRanch.

1 Introduction

Our research group developed the animal genome database and its query system for network users(http://ws4.niai.affrc.go.jp) last year[1]. This query system have been accepted more than 5000 requests per month. We have been developing a new client-server system named gRanch in order to analyze the genetic linkage and to query the animal genome database effectively. The gRanch display the gene map which are integrated the linkage map and the physical map, and two kinds of homology map between species.

2 System Overview

The two databases are constructed in the server system. One is the database which include the pedigree data and the allele data for the linkage analysis. These data are separated into each mapping project and open to persons involved the project. The system recognize the persons using by the userid and the password. The other is the animal genome database which include the linkage map, physical map, references, information of PCR primers and homology between species.

The client program is written by Tcl/Tk language. The server-client communication is based on HTTP. The client program have local data files and get the new mapping data from the server and put the new pedigree or allele data, if necessary.

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