**ActionMap: a web-based software that automates loci assignments to framework maps**

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**ABSTRACT**

Genetic linkage computation may be a repetitive and time consuming task, especially when numerous loci are assigned to a framework map. We thus developed ActionMap, a web-based software that automates genetic mapping on a fixed framework map without adding the new markers to the map. Using this tool, hundreds of loci may be automatically assigned to the framework in a single process. ActionMap was initially developed to map numerous ESTs with a small plant mapping population and is limited to inbred lines and backcrosses. ActionMap is highly configurable and consists of Perl and PHP scripts that automate command steps for the MapMaker program. A set of web forms were designed for data import and mapping settings. Results of automatic mapping can be displayed as tables or drawings of maps and may be exported. The user may create personal access-restricted projects to store raw data, settings and mapping results. All data may be edited, updated or deleted. ActionMap may be used either online or downloaded for free (http://moulon.inra.fr/~bioinfo/).

**INTRODUCTION**

Identification of genes involved in plant traits is a first step to understanding biological processes underlying these traits. Transcriptome and proteome studies, functional annotation and ultimately co-localization of a gene with a QTL must be taken into account to track candidate genes down. As only two complete plant genome sequences are available, large efforts are still required to genetically map genes in numerous other plant species. ESTs databases are a major source for new sequences to map. The throughput of genetic mapping does not allow systematic mapping of all these ESTs, but hundreds of cDNAs can still be mapped within a year by a single laboratory. For such projects, data storage and mapping computation need to be optimized. Automation of genetic linkage map computation may increase the throughput as well as the reliability of large-scale mapping projects.

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Figure 1. Mapping results display: (A) mapping results table; (B) results table optional fields; (C) graphical display of map. Loci of the framework are on the left side.
Users can access the database and mapping automation software via their usual web browsers (MacOS, Windows and Unix version of Explorer or Netscape). The web interface is used to input data, to set up the automatic process and to display and export the results. ActionMap was developed for Solaris platform with Perl 5.6.1, PHP 4.1.2 (Table 1) and Oracle 8i DBMS. It requires MapMaker 3 (http://www-genome.wi.mit.edu/ftp/distribution/software/).

### DATA MANAGEMENT AND SETTINGS

The new user must first choose a login and a password. Each user has access to only his or her own data. Before beginning to map, the user must create a ‘mapping project’ including data which describe the mapping population, the framework map and settings for the automatic mapping process. These settings include the minimal LOD of assignment, the maximum genetic distance, the mapping function, as well as decision criteria to stop or carry on mapping a marker when problems are encountered. The ActionMap documentation including a guide for first use of the software and sample data files is available (see Supplementary Material). Once a project is created, the user can submit new genotypic data to ActionMap. These data can be transferred into the database from a csv (comma separated values) file which may be produced by any spreadsheet program. The user is notified by email when the mapping job is completed and the results may then be viewed via a web link pointing to a table. The user can inspect the results for each new marker and choose to validate it or not. The results are then displayed as a table or map drawing (Fig. 1). Only validated loci will appear on the map drawing. A set of web pages are dedicated to browsing, updating, editing and deleting data. The user may delete data just for one locus or for a complete ‘mapping project’.

### MAPPING AUTOMATION

The ActionMap automatic mapping process consists of several scripts that automate MapMaker command steps (Fig. 2). The new markers are mapped one by one and the order in which they are processed is not important because each new locus is positioned on the same fixed framework map without being added to the map. ActionMap initially builds two files. The first one contains the segregation data of the framework map markers plus the new marker to be mapped and the second one contains parameters for MapMaker like the distance function and default linkage criteria, as well as the ordered list of markers for each linkage group. Data and user-defined settings are read from the ‘mapping project’ that is stored in the database (see before).

![Figure 2. Flowchart of the automatic mapping process.](image-url)
locus is linked to only one other locus of the linkage group. If not, the assignment is considered as reliable and the automatic process can carry on, but if the locus is linked to only one other locus, a segregation distortion test is computed (chi square) and the automatic process may be stopped depending on a user-defined threshold. If the marker is ‘Unassigned’, the minimal assignment LOD score value may be decreased to a user-defined minimal threshold. If the result remains ‘Unassigned’, the automatic mapping stops. If ‘Assign’ produces ‘conflicting data’ results, the new marker is ambiguously assigned to two linkage groups. Then, depending on a user-defined parameter, the process can select the assignment having the best LOD score, but only if the difference between LOD score values exceeds a user-defined threshold. If it does not, but one of the assignments is doubtful (distortion test) then the process selects the other one. When no choice is possible, the mapping process is stopped. In all cases, a warning indicates if the assignment has a low level of reliability.

After linkage group assignment, the next step is to find the flanking loci. This is achieved by the ‘Try’ function which uses the MapMaker try command. This command indicates the LOD score values associated with the assignments of the new marker to all possible intervals between adjacent loci in the linkage group. The ‘Try’ function can deal with co-localization cases or ambiguous position of the new marker and indicates the closest flanking loci corresponding to a given level of confidence of assignment.

The last step is performed by the ‘Map’ function. This function computes the distances between all adjacent loci of the linkage group. From this result, the ‘Map’ function computes the absolute position of the new marker in its linkage group.

The automatic mapping is then finished and all results are stored in the database.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at NAR Online.

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