Genetics and population analysis

CMap3D: a 3D visualization tool for comparative genetic maps

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ABSTRACT

Summary: Genetic linkage mapping enables the study of genome organization and the association of heritable traits with regions of sequenced genomes. Comparative genetic mapping is particularly powerful as it allows translation of information between related genomes and gives an insight into genome evolution. A common tool for the storage, comparison and visualization of genetic maps is CMap. However, current visualization in CMap is limited to the comparison of adjacent aligned maps. To overcome this limitation, we have developed CMap3D, a tool to compare multiple genetic maps in three-dimensional space. CMap3D is based on a client/server model ensuring operability with current CMap data repositories. This tool can be applied to any species where genetic map information is available and enables rapid, direct comparison between multiple aligned maps.

Availability and Implementation: The software is a stand-alone application written in Processing and Java. Binaries are available for Windows, OSX and Linux, and require Sun Microsystems Java Runtime Environment 1.6 or later. The software is freely available for non-commercial use from http://flora.acpfg.com.au/

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1 INTRODUCTION

Advances in DNA marker technology not only permit the rapid generation of high-resolution genetic linkage maps but also facilitate detailed comparisons among and between species. Genetic maps provide an insight into the genomic organization of an organism and may be used to study the evolution of species, synteny between related species and rearrangement across taxa (Choi *et al.*, 2007). The genetic mapping of complementary or common molecular genetic markers across related species permits the alignment of chromosomes of those species. Comparative genetic mapping helps researchers translate information from one map to another, and enables information to be transferred from map-rich to map-poor species. Furthermore, comparative mapping allows the comparison of non-model species with sequenced model species (Chao *et al.*, 1989; Moore *et al.*, 1995).

Integrating data from studies in genetics, genomics, proteomics, phenomics and other related fields allow researchers to link

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sequenced genome data with observed traits, bridging the genome to phenome divide (Edwards and Batley, 2004). This linking of genomic data to traits is a pressing issue in bioinformatics, and comparative genetic maps that have been annotated with phenotypic and genomic data allow researchers to identify correlations between features and across genomes.

CMap (Youens-Clark *et al.*, 2009) is a popular and powerful tool for the comparison of genetic maps and sequenced genomes. CMap has been successfully applied for intra- and inter-species comparison within and between a variety of species including sheep, cattle, pig and wallaby (Liao *et al.*, 2007), honeybee, grasses and cereals (Carollo *et al.*, 2005; Jaiswal *et al.*, 2006; Somers *et al.*, 2004), *Brassica* (Lim *et al.*, 2007), peanut (Jesubatham and Burow, 2006), Rosaceae (Jung *et al.*, 2008) and legumes (Gonzales *et al.*, 2005). CMap displays lines of correspondence between markers on adjacent maps in two-dimensional space, drawing maps in a side-by-side arrangement, allowing users to view relationships between adjacent maps. However, the restriction to two-dimensional space limits direct comparison to a maximum of two maps at a time. Another limitation of CMap is that whenever a view is modified, for example during map reorientation or hiding/revealing of features, a reload and redraw of the map are required. To overcome these limitations we have developed CMap3D, a tool to visualize new and existing CMap data in three-dimensional space.

2 METHOD AND APPLICATION

CMap3D has been developed using a client/server approach to ensure compatibility with current CMap databases. The client-side is a stand-alone, cross-platform application that connects to designated servers or repositories. The server-side is a plugin interface for the CMap API that has been developed for integration with existing CMap installations. This plugin is packaged with CMap versions 1.01 and higher. The CMap3D client first connects to a central repository listing server, which provides the client with a list of available and compatible CMap repositories and their details. The client then communicates directly with the repository server using the HTTP protocol to request and retrieve the required data. The client software uses the HTTP protocol for data transfer to minimize institution network security conflicts.

The CMap3D module in CMap acts as a go-between for the CMap3D viewer and the underlying CMap relational database. Communication between the viewer and the scripts uses XML. The module (as well as the CMap application) is written in perl, and essentially functions as a translation service, translating data from a relation database format, into XML.
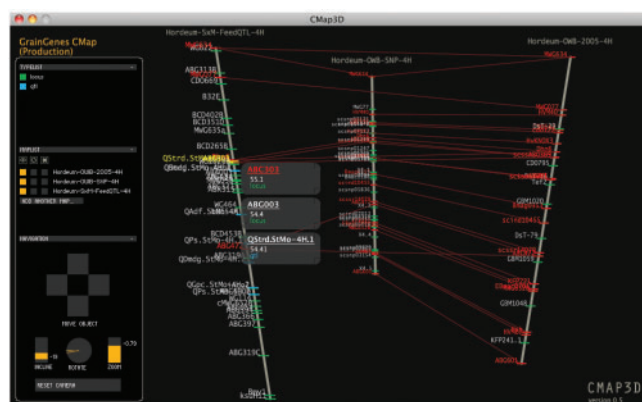
Fig. 1. A screenshot of CMap3D, showing three barley linkage groups (grey vertical bars) with a variety of correspondences. Features are marked as notches on the maps and are colour coded to their class. The red lines/features represent features of correspondence between maps. Controls on the left allow users to: move around the viewing space; flip, hide or remove maps; or hide/display features at a class level.

The CMap3D viewer is a stand-alone client written in Processing (http://www.processing.org) and is available for Windows, OSX and Linux. The viewer takes XML comparative mapping data as input, and displays the maps in three-dimensional space (Fig. 1). As with the original CMap viewer, features are colour coded according to type, and are represented as points or a range on the map. Features with correspondence are highlighted in red, and red lines are drawn between related features. By clicking on a feature in the viewing space a browser window will launch, providing the relevant web page results.

Once connected to a repository, the user may add genetic maps to the three-dimensional viewing space and view correspondence between the selected maps. When a set of maps is loaded, the user can interact with the viewing space by manipulating the object and camera positions.

Map orientation may be reversed in relation to the other maps to improve the alignment of correspondences or removed from the viewing window altogether. CMap3D also has the ability to temporarily hide maps from view. When a map is hidden, it is still in the current map selection list, and corresponding features on remaining maps will continue to be highlighted.

Any feature/marker for a map has an associated type. These can relate to information such as the class of marker, for example, amplified fragment length polymorphism, simple sequence repeat or single nucleotide polymorphism; or about the class of annotation, such as predicted gene or quantitative trait loci. CMap3D has the ability to hide classes of feature types without needing to redraw the maps. This provides viewing flexibility and visualization suited to each project.

3 RESULTS

CMap3D is a tool developed for the visualization and comparison of multiple genetic maps. Based on the powerful CMap tool, CMap3D allows users to compare multiple maps in three-dimensional space, an essential requirement as the number of genetic and physical maps continues to increase. Maps can be moved around, zoom levels can be changed and features/map can be shown or hidden without requiring a redrawing of the viewing space. CMap3D is currently being applied to view genetic maps in the Gramene (Jaiswal *et al.*, 2006), GrainGenes (Carollo *et al.*, 2005) and the *Brassica* CMap repositories.

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