Advances in DNA marker technology not only permit the rapid genetic mapping of complementary or common molecular related species and rearrangement across taxa (Choi and may be used to study the evolution of species, synteny between provide an insight into the genomic organization of an organism detailed comparisons among and between species. Genetic maps 1989; Moore species. Furthermore, comparative mapping allows the comparison enables information to be transferred from map-rich to map-poor 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 sequenced genome data with observed traits, bridging the genome to phenotype 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 (Jesubathith 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.

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.

© The Author 2009. Published by Oxford University Press. All rights reserved. For Permissions, please email: journals.permissions@oxfordjournals.org
The viewer takes XML comparative mapping data as input, and displays the multiple genetic maps. Based on the powerful CMap tool, CMap3D visualization suited to each project. Without needing to redraw the maps. This provides viewing flexibility and quantitative trait loci. CMap3D has the ability to hide classes of feature types polymorphism; or about the class of annotation, such as predicted gene or fragment length polymorphism, simple sequence repeat or single nucleotide relate to information such as the class of marker, for example, amplified corresponding features on remaining maps will continue to be highlighted. CMap3D also has the ability to temporarily hide maps from the alignment of correspondences or removed from the viewing window space by manipulating the object and camera positions.

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.

ACKNOWLEDGEMENTS
The authors would like to acknowledge Ben Faga, Doreen Ware and Ken Youens-Clark from the Cold Spring Harbor Laboratory and support from the Australian Genome Research Facility; Queensland Cyber Infrastructure Foundation; Australian Partnership for Advanced Computing and Queensland Faculty for Advanced Bioinformatics.

Funding: Grains Research and Development Corporation (Project DAN00117); Australian Research Council (Projects LP0882095, LP0883462 and DP0985953); National Science Foundation (NSF) DBI-0321685 and DBI-0527192.

Conflict of Interest: none declared.

REFERENCES