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Poster presentation

System level visualization of eQTLs and pQTLs

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Effective visualisation of syntenic genome areas and QTLs derived from physiological and expression data is an unresolved issue. We are investigating genomic visualizations including SyntenyVista2 and Der Browser3 in order to establish the best way to integrate and display these data, and support the use of synteny in the identification of genes responsible for cardiovascular phenotypes. We are showing information regarding eQTLs and pQTLs for the rat1 integrated with data from Ensembl. Initial data representation uses Der Browser. We are also integrating the addition of further data from the MGI, OMIM and RGD. In the next step we will serve these data using SyntenyVista and possibly some other package.

Genomics visualization programs such as SyntenyVista, Apollohttp://www.fruitfly.org/annot/apollo/, Artemishttp://www.sanger.ac.uk/Software/Artemis/, BugViewhttp://www.gla.ac.uk/~dpl1n/BugView/, Der Browserhttp://doolittle.ibls.gla.ac.uk/leader/derBrowser/, Ensemblhttp://www.ensembl.org/index.html, ACThttp://www.sanger.ac.uk/Software/ACT/, and RatView are possible candidates in this investigation. We are comparing the systems in terms of functionality, ease of use, data coverage, and support for data analysis. Our aim is to characterize the space of possible solutions in order to choose the most effective ones. At the moment the information is more clearly presented in SyntenyVista, but we still do not have all the relevant information that the biologists wish to see, and do not have a solution for database connectivity, although it might be possible to adapt this from Apollo. Current work is addressing these concerns. User tests are now being planned to assess the effectiveness of our methodology.

References
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