



Jakubowska, Joanna, Hunt, Ela, Chalmers, Matthew, McBride, Martin, and Dominiczak, Anna F. (2007) VisGenome: visualization of single and comparative genome representations. *Bioinformatics*, 23 (19). pp. 2641-2642. ISSN 1367-4803

Copyright © 2007 The Authors

<http://eprints.gla.ac.uk/13843>

Deposited on: 24 February 2014

Enlighten – Research publications by members of the University of Glasgow
<http://eprints.gla.ac.uk>

Systems biology

VisGenome: visualization of single and comparative genome representations

Joanna Jakubowska^{1,*}, Ela Hunt², Matthew Chalmers¹, Martin McBride³ and Anna F. Dominiczak³

¹Department of Computing Science, University of Glasgow, G12 8QQ, Scotland, ²Department of Computer Science, ETH Zurich, 8092 Zurich, Switzerland and ³BHF Glasgow Cardiovascular Research Centre, University of Glasgow, G12 8TA, Scotland

Received on November 21, 2006; revised on July 23, 2007; accepted on July 29, 2007

Associate Editor: Alfonso Valencia

ABSTRACT

Summary: VisGenome visualizes single and comparative representations for the rat, the mouse and the human chromosomes at different levels of detail. The tool offers smooth zooming and panning which is more flexible than seen in other browsers. It presents information available in Ensembl for single chromosomes, as well as homologies (orthologue predictions including ortholog one2one, apparent ortholog one2one, ortholog many2many) for any two chromosomes from different species. The application can query supporting data from Ensembl by invoking a link in a browser.

Availability: <http://www.dcs.gla.ac.uk/~asia/VisGenome>

Contact: asia@dcs.gla.ac.uk

1 INTRODUCTION

VisGenome was designed to match the visualization needs of the BHF Blood Pressure Group at the University of Glasgow which uses a rat model of cardiovascular disease. We analyse genomic data at different levels of detail, to dissect rat and human QTLs (McBride *et al.*, 2006) in the search for candidate disease genes. QTLs are analysed in three species: the rat, the human and the mouse, and the work uses genotyping, and micro array and proteomics techniques. VisGenome supports QTL analysis by showing QTLs and the genes within each QTL in two species in one display, along with the supporting experimental data. It also shows data for a single chromosome in one display and supports zooming at an arbitrary level of detail. Current software release connects to Ensembl (Hubbard *et al.*, 2007) and can be used as an alternative viewer for a subset of that data. Extensions are being tested and an ongoing user study will guide further development.

2 FEATURES

VisGenome loads QTLs, genes, micro array probes, bands and markers, and displays pairs of homologies (orthologue

predictions) from Ensembl. It welcomes the user with a view of all rat, mouse and human chromosomes, see Figure 1. In the single chromosome representation, after choosing a chromosome of interest by clicking, a new view with detailed data about the chromosome is created. In the comparative representation, the user clicks on two chromosomes from different species and a new view representing homologies between the chosen chromosomes is created. After choosing a chromosome, the users can manipulate the view by mouse and keyboard interaction.

2.1 Navigation

VisGenome offers mouse and keyboard interaction. The users choose the representation by selecting a menu item or by typing Ctrl+S (single) or Ctrl+C (comparative). A choice is offered for marking the chromosome region of interest. The users can drag or enlarge the box enclosing the region marked on the chromosome or enter the region coordinates in the top panel.

2.2 Zooming and panning

We offer smooth zooming which supports the visual exploration of the chromosome space. Zooming and panning uses Piccolo (Bederson *et al.*, 2004). The zooming technique allows the users to keep an area of interest in focus during interaction with the data. Zooming is manipulated by the right mouse button by moving it to the right (zoom in) or to the left (zoom out). Panning uses the left mouse button. Both interactions are easy to use and the users quickly become familiar with them.

2.3 Marking a region of interest

The users can choose a chromosome region of interest. Then, the main view shows only the data for this region and the users manipulate only the data in the selected area.

2.4 Additional information

VisGenome supports the display of additional information about presented data in an info panel.

*To whom correspondence should be addressed.

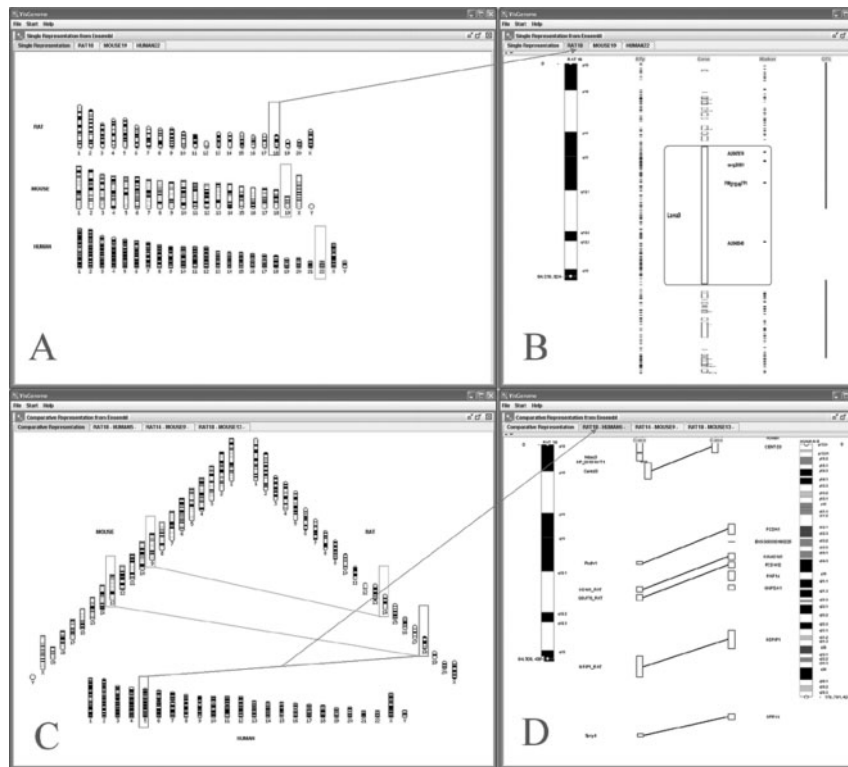


Fig. 1. (A and B) VisGenome, single chromosome view. (C and D) Comparative view. (A and C) Chromosomes from the mouse, the rat and the human. (B) An overview and detail for the rat chromosome 18. (D) An overview and detail for the rat chromosome 18 and the human chromosome 5.

2.5 Supporting data

Access to Ensembl is provided via clicking on a feature of interest which invokes Ensembl web pages in the user's browser.

3 IMPLEMENTATION

VisGenome was written and tested on Windows XP with Java 1.5, on a 2.39 GHz Pentium 4 with 512 MB RAM. VisGenome connects via JDBC to Ensembl databases for the rat, the mouse and the human. During the tests, we visualized chromosome bands, micro array probe sets, QTLs and genes. Eclipse, www.eclipse.org, was used as a development environment. The application is packaged as a jar file. The user has to install Java prior to invoking the code. 1280 × 1024 screen resolution was used for testing.

4 DISCUSSION AND CONCLUSIONS

Visualization of genome comparisons is an important research tool in biology and medicine. None of the tools we studied (Jakubowska *et al.*, 2006) fulfilled the requirement of showing in detail and overview all the data needed for our work in one display, and allowed us to study QTLs and other relevant data. VisGenome extends SyntenyVista (Hunt *et al.*, 2004) with a single genome display and presents homologies alongside QTLs and micro array probes.

Our plans are as follows. We are conducting a user study comparing VisGenome and Ensembl, to identify future improvements and assess the usability of our solution. We will broaden

the application of cartoon scaling which is not part of the current release, and requires algorithmic extensions. We will support the import of additional data from external files or web services, and local caching. We will add data import from DAS servers (Dowell *et al.*, 2001). We are preparing a follow-on release supporting user-driven choice of colours and data sources. The data will be cached, so that the tool is usable even if access to Ensembl is slow, and the user will not have to re-import the same data. An intelligent caching solution is being tested.

ACKNOWLEDGEMENTS

This work was funded by the BHF Programme (PG02012) and Chair (CH98001) Grants and the Wellcome Trust Cardiovascular Functional Genomics (WT066778/Z/01/Z) all to A.F.D., the MRC (J.J.), and by the MRC and an EU Marie-Curie Fellowship (E.H.).

REFERENCES

- Bederson, B.B. *et al.* (2004) Toolkit design for interactive structured graphics. *IEEE Trans. Softw. Eng.*, **30**, 535–546.
- Dowell, R.D. *et al.* (2001) The Distributed Annotation System. *BMC Bioinformatics*, **2**, 7.
- Hubbard, T.J.P. *et al.* (2007) Ensembl 2007. *Nucleic Acids Res.*, **35**, D610–D617.
- Hunt, E. *et al.* (2004) The Visual Language of Synteny. *OMICS*, **8**, 289–305.
- Jakubowska, J. *et al.* (2006) Granularity of genomics data in genome visualisation. Department of Computer Science, University of Glasgow. *Technical report: TR-2006-221*. <http://www.dcs.gla.ac.uk/publications/PAPERS/8212/AsiaElaMatthewCHI06.pdf>
- McBride, M.W. *et al.* (2006) Functional genomics in hypertension. *Curr. Opin. Nephrol. Hypertens.*, **15**, 145–51.