SOFTWARE

DNAism: Exploring genomic datasets on the web with Horizon Charts.

David Rio Deiros[1*], Richard A. Gibbs[1,2] and Jeffrey Rogers[1,2]

[*]Correspondence: deiros@bcm.edu
[1]Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, USA
Full list of author information is available at the end of the article

Abstract

Background: Computational biologists daily face the need to explore massive amounts of genomic data. New visualization techniques help researchers navigate and understand these big data. Horizon Charts are a relatively new visualization method that, under the right circumstances, maximizes data density without losing graphical perception.

Results: Horizon Charts have been successfully applied to understand multi-metric time series data. We have adapted an existing Javascript library (Cubism) that implements Horizon Charts for the time series domain so that it works effectively with genomic datasets. We call this new library DNAism.

Conclusions: Users can use DNAism to leverate the power of Horizon Charts to explore their own datasets. They can create their own applications or they can expand existing ones.

Keywords: library; bioformatics; genomics; sequencing

Background

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Implementation

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Results and Discussion

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Conclusion

Computational biologists daily face the need to explore massive amounts of genomic data. New visualization techniques help researchers navigate and understand these big data. Horizon Charts are a.

Availability and requirements

- Project name: e.g. My bioinformatics project
- Project home page: e.g. http://sourceforge.net/projects/mged
- Operating system(s): e.g. Platform independent
- Programming language: e.g. Java

- Other requirements: e.g. Java 1.3.1 or higher, Tomcat 4.0 or higher
- License: e.g. GNU GPL, FreeBSD etc.
- Any restrictions to use by non-academics: e.g. licence needed

Figures

Figure 1 Horizon Charts emerge from applying a set of changes to traditional line charts **(A)**. We start by coloring the underlying area of the line chart, using different hues for positive and negative values. Next, we divide the graph in bands and apply a gradient of color that increases along with the quantitative value of the variable we are investigating **(B)**. In the next step, negative values are flipped over the baseline **(C)**, effectively reducing the vertical space by two fold. In a final step, bands are collapsed making all of them start at the baseline and providing another level of space reduction **(D)**. **We used this technique** to rapidly identify problematic samples when performing quality control on large scale sequencing. You can see the read depth across whole genome sequences from 24 rhesus macaque samples (30x coverage) for genomic region Chr17:1.1M-1.2M **(E)**. There are regions consistently underrepresented across all the samples and sample 32510 has low coverage across the whole genomic region. Note that the variable we are exploring in this example, read depth, does not contain negative values. Therefore, only green hues appear in **(E)**.

Competing interests
The authors declare that they have no competing interests.

Author's contributions
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Author details
[1]Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, USA. [2]Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, USA.

References
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Additional file descriptions text (including details of how to view the file, if it is in a non-standard format or the file extension). This might refer to a multi-page table or a figure.

Additional file 2 — Sample additional file title
Additional file descriptions text.