

bioWeb3D: an online webGL 3D data visualisation tool

Jean-Baptiste Pettit^{*1} and John C. Marioni^{*1}

¹EMBL-EBI, European Molecular Biology Laboratory - European Bioinformatics Institute, Cambridge, CB10 1SD, UK

Email: Jean-Baptiste Pettit^{*}- jbpettit@ebi.ac.uk; John C. Marioni^{*}- marioni@ebi.ac.uk;

^{*}Corresponding author

Abstract

Background: Data visualization is an important part of biology that sometimes proves to be a bottleneck for non trained researchers. This is especially true when it comes to three dimensional (3D) data representation. Plenty of existing software provide all necessary functionalities to represent and manipulate biological 3D datasets but very few are easily accessible because (web based), cross platform and created for non expert users to quickly and efficiently view 3D data before an eventual finer analysis. **Results:** An online HTML5/webGL based 3D visualisation tool has been developed to allow biologists to quickly and easily view interactive and customizable three dimensional representations of their data along with multiple layers of information. Using the WebGL library Three.js written in Javascript, bioWeb3D allows the simultaneous visualisation of multiple large datasets inputted via a simple JSON file, which can be read and analysed locally thanks to HTML5 capabilities. **Conclusions:** Using basic 3D representation technique in an technologically innovative context (webGL) we are able to provide a program tool that is not intended to compete with professional 3D representation software but can be very useful for a quick and intuitive representation of reasonably large 3D datasets.

Content

Text and results for this section, as per the individual journal's instructions for authors.

Section title

Sub-heading for section

Sub-sub heading for section

Sub-sub-sub heading for section

Author's contributions

Text for this section ...

Acknowledgements

Text for this section ...

References

1. Freeman T C BMvDSMPGRFSTJEA Goldovsky L: **Construction, visualisation, and clustering of transcription networks from microarray expression data.** *PLoS Comput Biol.* 2007, **3(10)**:2032–42.

Figures

Figure 1 - Sample figure title

A short [1] description of the figure content should go here.

Figure 2 - Sample figure title

Figure legend text.

Tables

Table 1 - Sample table title

Here is an example of a *small* table in L^AT_EX using `\tabular{...}`. This is where the description of the table should go.

My Table		
A1	B2	C3
A2
A3	..	.

Additional Files

Additional file 1 — Sample additional file title

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.