

Evaluation et comparaison de logiciels de visualisation et d'exploration de génomes

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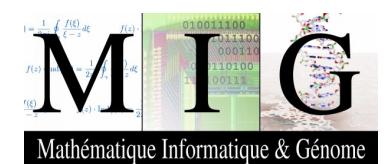
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Contexte et Objectifs

- Les besoins en visualisation de données génomiques sont très divers
 - Nombreux outils de visualisation, souvent spécifiques d'un problème donné. Quelques un génériques et adaptables.
- Comment comparer de manière objective et standardisée ces outils ?

QSOS

Qualification et Sélection de Logiciels Open-Source

Sélection

Définition



Qualification

Évaluation

Définition des critères

- 60 critères prédéfinis
- 60 nouveaux critères dans 4 catégories:
 - Technical features
 - Data content and connectivity
 - Graphical User Interface (GUI)
 - Annotation editing and creation

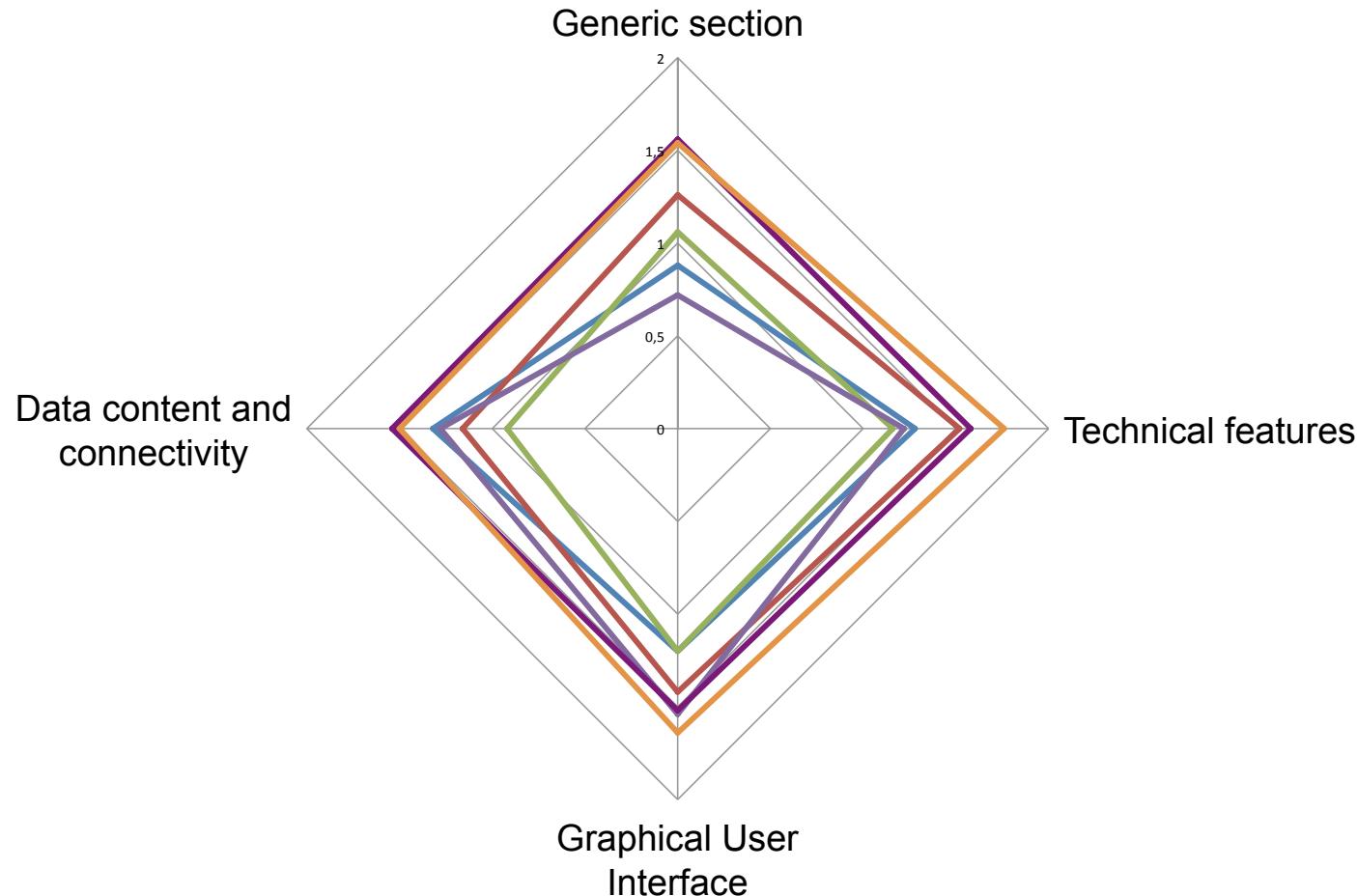
Programmes évalués

Copyright Owner	Publication Date	Application Type	Technology	Version (date eval.)
MuGeN	2003	Standalone	Perl - Gtk	20060619 (06.09)
Ensembl	EBI, EMBL, WTSI	2002	Web app	Perl CGI
Artemis / ACT	WTSI	2000	Stand alone	Java
GBrowse	CSHL (NY), UC Berkeley	2002	Web app	Perl CGI
UCSC	UC Santa Cruz	2002	Web app	C
JBrowse	UC Berkeley	2009	Web app	Ajax

Exploration des résultats

- Les critères peuvent être pondérés selon l'importance qu'on leur accorde
- 3 profils de pondération ont été prédefinis :
 - Biogiste
 - Bioinformaticien
 - Informaticien
- Visualisation sous forme de tableaux ou graphes radar.

Exemple de résultats



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Site Web

 CompaGB : Evaluation and comparison of genome browsers features [\[login / register\]](#)

[Home] [Compare GB features] [Community : making CompaGB better]

[-] 3 Graphical User Interface (GUI)

- [-] 3.1 Richness of the zooming features
- [-] 3.2 Advanced GUI visualisation techniques
- [-] 3.3 Richness of the elements of the GUI that represent the genomic annotations
- [-] 3.4 Diversity of the color code for the widgets representing the genomic annotations
- [-] 3.5 Customization of the tracks representing the genomic annotations
- [-] 3.6 Ease of navigation throughout the genome
- [-] 3.7 Richness of the ways to represent the genome
- [-] 3.8 Richness of the ways to represent the strand and frame
- [-] 3.9 Richness of the comparative genomic features
 - [-] 3.9.1 Advanced visualisation techniques for homolog display
 - [-] 3.9.2 Advanced visualisation techniques for synteny display
 - [-] 3.9.3 Advanced visualisation techniques for sequence alignment display
 - [-] 3.9.4 Abundance of genomes that can be displayed at the same time in the homolog view
 - [-] 3.9.5 Abundance of genomes that can be displayed at the same time in the synteny view
 - [-] 3.9.6 Abundance of genomes that can be displayed at the same time in the sequence alignment view
 - [-] 3.9.7 Abundance of scales available in the homologs view
 - [-] 3.9.8 Abundance of scales available in the synteny view
 - [-] 3.9.9 Abundance of scales available in the sequence alignment view

3 Graphical User Interface (GUI)

Description of the criteria and the three score : 0/Bad, 1/Average, 2/Good

Step 1 : weight the criteria

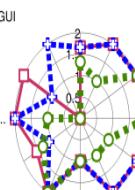
Step 2 : Select the Genome Browsers you would like to compare

Results - comparison of the selected GB

Legend :

- Ensembl genome browser
- GBrowse (March 2009)
- MuGeN (February 2009)

3.1 Richness of the zooming features ...
3.12 Internationalization 3.2 Advanced GUI visualisation t...
3.11 Customization of the GUI
3.3 Richness of the elements of ...
3.10 Richness and cleanliness of ...
3.4 Diversity of the color code ...
3.9 Richness of the comparative ...
3.5 Customization of the tracks ...



[contact] 



<http://genome.jouy.inra.fr/CompaGB>



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Conclusion et perspectives

- QSOS permet une évaluation et une comparaison complète et pondérée des outils.
- Pour que l'évaluation soit la moins biaisée possible, elle doit être multiple.
- Nous invitons les personnes intéressées à venir consulter et compléter les évaluations sur le site web.

<http://genome.jouy.inra.fr/CompaGB>

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Evaluating Genome Browsers using a Software Qualification Method

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Abstract
Genomic data are ever growing in size and diversity, thus making visualization and data mining increasingly challenging for biologists. For this purpose, numerous advanced genome visualization tools such as Genome Browsers have been recently developed. It is therefore now necessary to provide standard evaluation processes and resources to help the community to select the best software.
To assist scientists in this task, we propose the implementation of an industry promoted software qualification method (GSOS) adapted for Genome Browser evaluations, and a web resource providing numerous facilities either for visualizing current Genome Browser comparisons or performing new evaluations.

GSOS
The selection and selection of Open Source Software (GSOS) method is designed to qualify, select and compare free and open source software. An argument can be made that an argued way, GSOS provides tools for defining the list of criteria, evaluating software, and a web server to display and compare the evaluations as tables or radar graphs. It also offers the possibility of weighing the criteria fit to a user specific context.

Criteria and User Profile
A list of 40 criteria related to GSOS scope was built. These levels of scoring (full, intermediate and poor) were defined specifically for each criteria to discriminate as much as possible between the different levels of quality of the evaluated software. Some criteria are for information purposes only (no score), e.g. the type of application.

- **Technical features**, including criteria such as the type of application, ease of installation, portability, compatibility with other software, etc.
- **Data content and connectivity**, including criteria such as the possibility to display private data, supported formats, connectivity with databases or web services, export formats, etc.
- **Graphical User Interface (GUI)**, deals with criteria such as visualization techniques, interface design, etc.
- **Collaborative editing and creation**, includes criteria about the possibility of collaborative annotation, function assignment using a controlled ontology and assessment of the quality of the annotations.

It is possible to weight the criteria (ie: unimportant, average importance, essential) to reflect a particular context of utilization and therefore module the results accordingly. Three examples of profiles (biologist, computational biologist, computer scientist) are proposed as an example.

Figure 1 : Four steps of the GSOS process

Selection of Genome Browsers
An GSOS selection was done to insure a broad variety of functionalities: from simple and easily accessible software developed by a local team (Migale) to a representative selection of the most popular and well known genome browsers. We selected a large number of GBs around the world (Gbrowse, Ensemble, Webo). We also included a recent tool from the last generation of GBs that was developed with Ajax technologies (Abreo).

Table 1 : Genome Browsers evaluated

Copyright Owner	Publishing Date	Application Type	Technology	Main Audience	
Migale	INRA	2003	Standalone	Per-Org	Evaluation
Ensembl	EBI, EMBL, WTRB	2002	Web app	Per CGI	Evaluation
Artemis (ACT)	WTSI	2003	Standalone	N/A	Annotation
Gbrowse	CSE, JGI, UCSC	2002	Web app	Per CGI	Evaluation
UCSC	UCSC	2002	Web app	C	Evaluation
Abreo	UC Survey	2009	Web app	N/A	Evaluation

Conclusion
The aim of this work is two fold : (i) to improve the quality, richness and reliability of GBs evaluations and (ii) to promote software reusability and qualification procedures in the field of genomics. This does not mean that the used methodology makes GB evaluations unbiased as evaluations refer to some extent the perspective and the background of the evaluators. To overcome this problem, we believe the only way is to welcome multiple concurrent evaluations from a larger community and designed the CompaGB website with this objective in mind.

<http://genome.jouy.inra.fr/CompaGB>



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