

Nathalie Choise¹, Benoit Hilselberger¹, Aminah-Olivia Keliet¹, Baptiste Brault^{1,2}, Joëlle Amselem^{1,2}, Michael Alaux¹, Sébastien Reboux¹, Isabelle Luyten¹, Delphine Steinbach¹ and Hadi Quesneville¹

¹ INRA – URGI Unité de Recherche en Génomique-Info, Centre de Versailles, FRANCE

² INRA – BIOlogie et GEstion des Risques en agriculture (BIOGER) – Champignons Pathogènes des Plantes, Centre de Versailles-Grignon, FRANCE

<http://urgi.versailles.inra.fr>

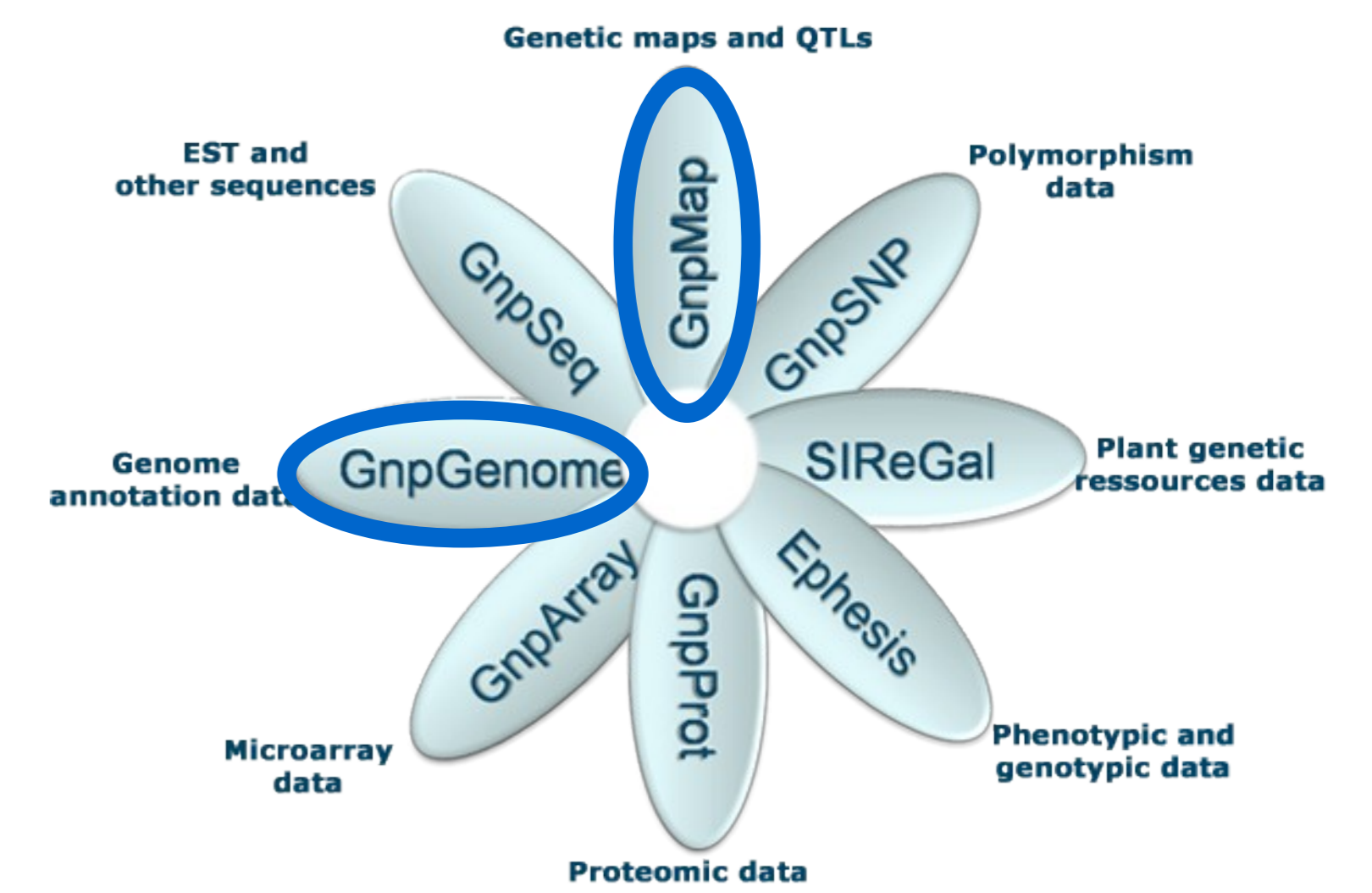


Abstract

As part of the French-Italian Public Consortium aimed to obtain a high-quality draft (12X) of the *Vitis vinifera* genome sequence of the highly homozygous genotype PN40024, the INRA-URGI bioinformatics unit is in charge to develop and maintain a genomic and genetic information system (GnplS, <http://urgi.versailles.inra.fr>) for the grape scientific community.

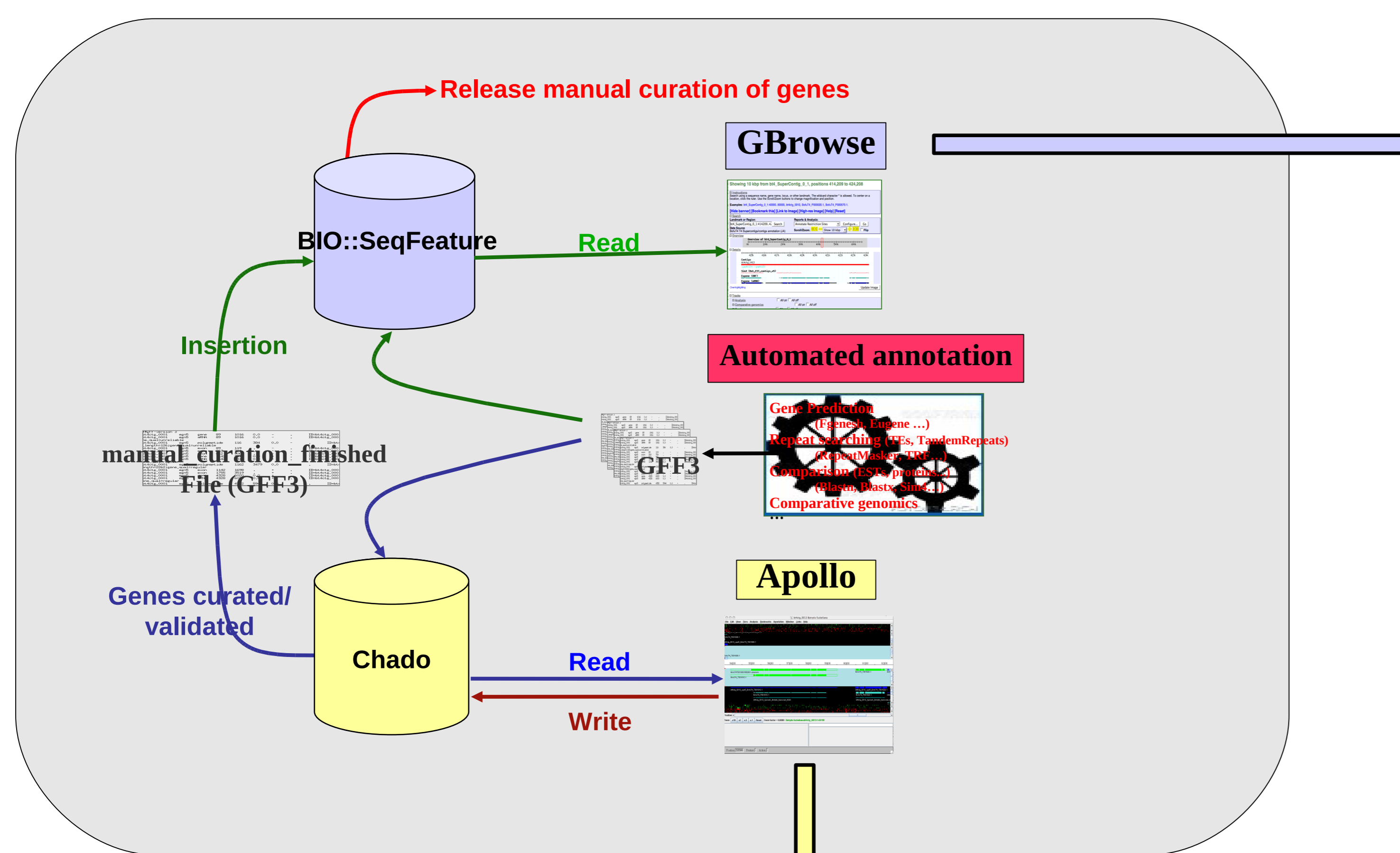
The GnpIS information system is composed of 5 genomic and 3 genetic modules.

The GnpGenome module is a multispecies database relying on the international open source Generic Model Organism Database project (GMOD, <http://www.gmod.org>). It contains the 12X *Vitis vinifera* genomic sequence assembly and its structural annotation. The GMOD project provides tools (Apollo, Chado, Gbrowse) to produce efficiently a manual curated genomic annotation. Here we present the system we have developed for the distributed annotation of the grapevine genome sequence. Apollo is the graphical annotation editor allowing curators to change the gene structures according to various evidences (ESTs, short-reads, protein similarity, comparative genomics). Manual annotations (gene curation validated or in progress) are saved in a dedicated Chado database and shared with other members of the annotation community. When validated, genes/pseudogenes curated models are committed in a second database publicly accessible by Gbrowse.



Roundtrip

Apollo ↔ Chado → BIO::SeqFeature → Gbrowse



Vitis vinifera genome browser

http://urgi.versailles.inra.fr/cgi-bin/gbrowse/grape_pub/
[*https://gpi.versailles.inra.fr/cgi-bin/gbrowse/vitis_12x/](https://gpi.versailles.inra.fr/cgi-bin/gbrowse/vitis_12x/)

- Overview
- Genetic markers
- Scaffolds
- Automatic annotation
- Transcriptomic data
- Markers
- BAC clones
- Ab initio
- automatic annotation evidences
- Repeats

Additional features: Ratio of transcriptomic experiments, GnpMAP access, Access to BAC clone distribution.

Apollo for Vitis vinifera

[*https://gpi.versailles.inra.fr/projects/Vitis/apollows.php](https://gpi.versailles.inra.fr/projects/Vitis/apollows.php)

* Restricted site for the members of the grape annotation community and before publication (for more information : urgi-contact@versailles.inra.fr)

Related publications

The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla
 Jaillon O. et al; French-Italian Public Consortium for Grapevine Genome Characterization. *Nature*.
 2007 Sep 27;449(7161):463-7.

Acknowledgements

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