

### BioMercator: A complete framework to integrate QTL, meta-QTL, genome annotation and genome-wide association studies

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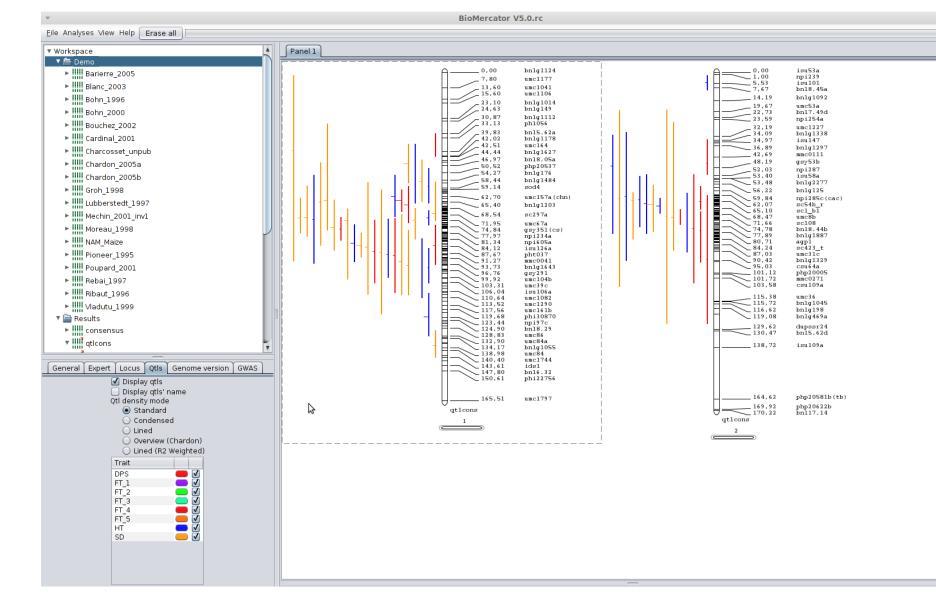
# BioMercator : A complete framework to integrate QTL, meta-QTL, genome annotation and genome-wide association studies

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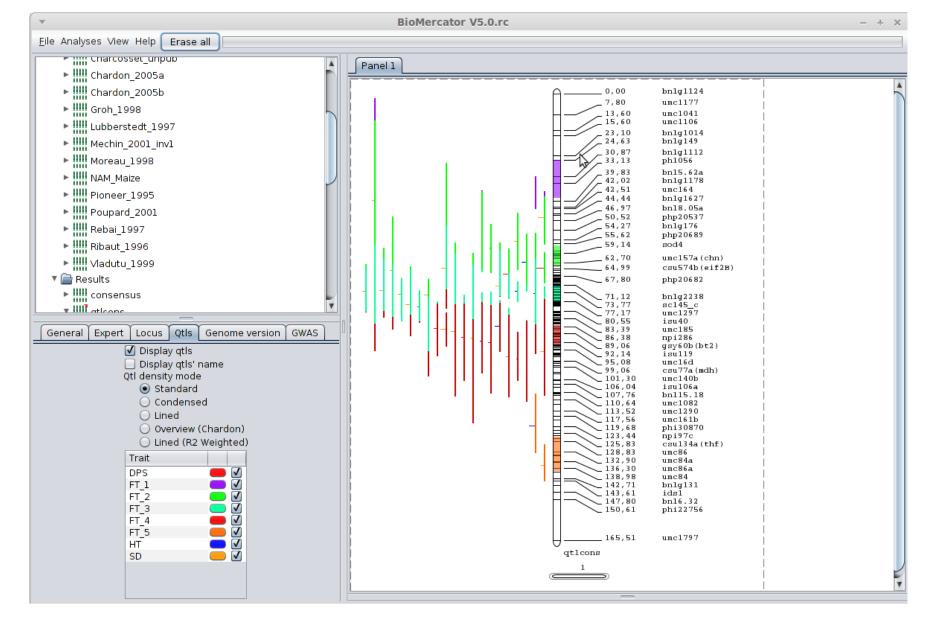
INRA, UMR Génétique Quantitative et Evolution - Le Moulon, F-91190 Gif-sur-Yvette, France

## Genetic maps compilation & QTL meta-analysis



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Compilation of genetic maps combined to QTL metaanalysis has proven to be a powerful approach contributing to the identification of candidate genes underlying quantitative traits. One of the most interesting properties of meta-QTL (or consensus QTL) is its confidence interval (IC) often shorter than IC of corresponding QTLs, decreasing the number of candidate gene to consider. BioMercator enables compilation and visualization of a large number of genetic maps, from different sources (literature, database, own experiment etc.). BioMercator enables also QTL meta-analysis using



Genetic map compiled. This map is the result of the compilation of the « Demo » folder. QTLs have been projected on the result map. Veyrieras methods<sup>[1]</sup>. Meta-analysis are run at the chromsome level and QTLs from related traits can be jointly subjected to a single meta-analysis by grouping corresponding traits into meta-traits.

[1] Jean-Baptiste Veyrieras, Bruno Goffinet and Alain Charcosset. MetaQTL: a package of new computational methods for the meta-analysis of QTL mapping experiments. BMC Bioinformatics (2007), 8:49

QTLs meta-analysis. Meta-QTLs are represented by colored section on the chromosome. The former QTLs are colored according to the clustering result of the meta-analysis.



## Structural and functionnal annotation view

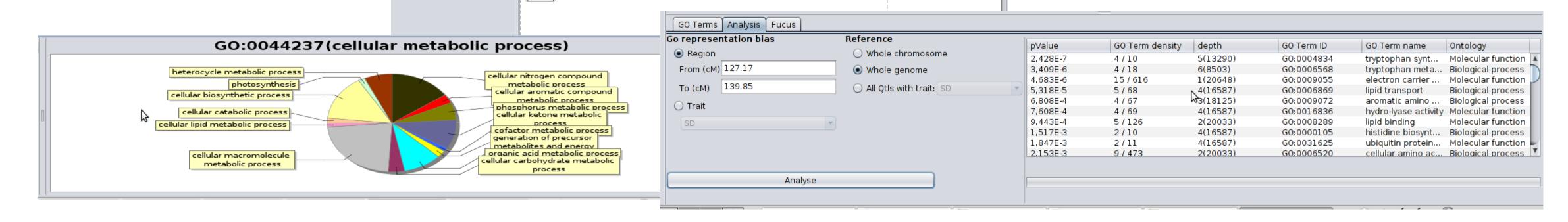
The next step after QTL localization is to identify the genes at this locus and their functions.

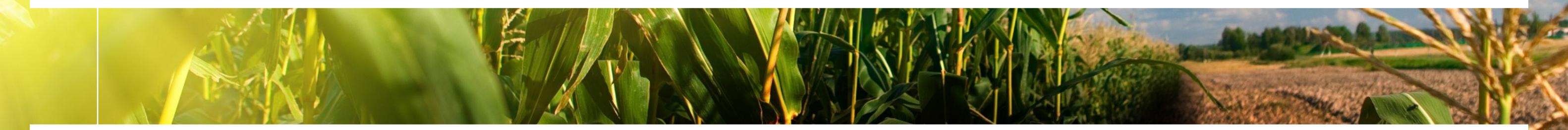
Thus, BioMercator enables to load structural (GFF3 format) and functionnal annotation (Based on the Gene Ontology) and to link these information to the genetic map. BioMercator provides tools to visualize and analyse these information.

<b>v</b>	BioMercator V5.0.rc	
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► IIIII Vladutu 1999	Panel 1	
► IIIII Vladutu_1999 ▼ 🔓 Results		
	0,00 bnlg1124	
► consensus	7,80 umc1177 283775 kpb	
▼ IIIII qtlcons	13,60 unc1041 unc1500	
<b>v</b> 1	23,10 bnlg1014	
· · ·	_ 30,87 bnlg1112	
v 1	- 33,13 ph1056	
🔻 🚞 Chrl	39,83 bn15.62a /_42,02 bn1g1178	
5	44,44 hpig1627	
	46,97 bn18.05a 50,52 php20537	
Chrl_res.txt	54,27 bnlg176	
Chr1_FT_5_table.txt	55,62 php20689 59,14 sod4	
Chr1_model.txt	62,70 umc157a (chn)	
► Canal _ model back	64,99 cmu574b(eif2B)	
▶ 2	67,80 php20682	
	71,12 bnlg2238 73,777 gs145_c 777,17 umc1297	
General Expert Locus Qtls	77,17 umc1297 80,55 izu40	
Genome version GWAS	85,38 npi286	
	89,06 gay60b(bt2) 92,14 iau119	
Genome version 🛛 🛛 🗖	95,08 unc16d 99,06 cmv77a (mdh)	
	101,30 umc140b 106,04 isu106a	
GWAS GWAS.txt	107,76 bn115.18	
	110,64 unc1082 bnlg1055	
Structural annotation ZmB73_5b_FGS.gff	117,56 umc161b 119,68 phi30870	
Functional annotation ZmB73_5a_xref.txt	125,83 cm134a(thf)	
Anchors anchors.csv	128,83 unc86 132,90 unc84a	
Database links dblinks.txt	136,30 unc86a 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
Association Result GWAS.txt	142,71 bnlg131 143,61 idel	
✓ Display annotations	147,80 bn16.32 150,61 phi22756	
	Ψ	
Display anchors	291309 kpb	
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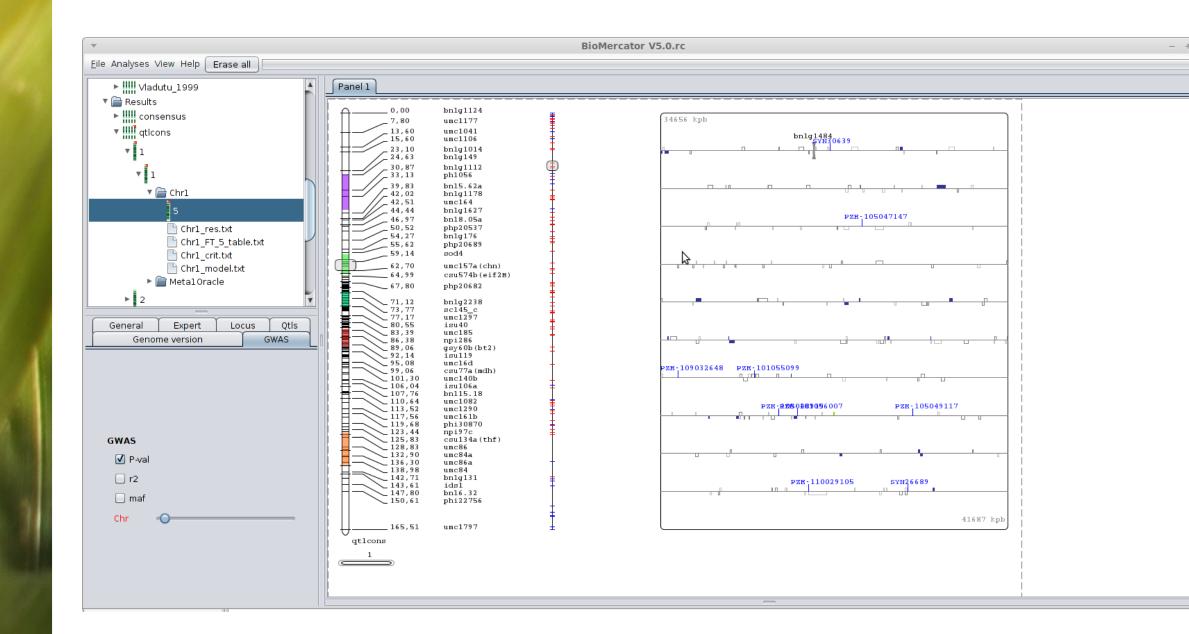
In the main panel, the genes are drawn in the browser (figure at the top) with little boxes, colored according to their GO annotation. The pie chart (bottom left) depicts the GO of the genes located at the focused region. A clic on a subsection of the pie chart highlight the genes in the genome browser.

BioMercator provides also some tools to evaluate the overrepresentation of a GO id in a focused region (bottom right)

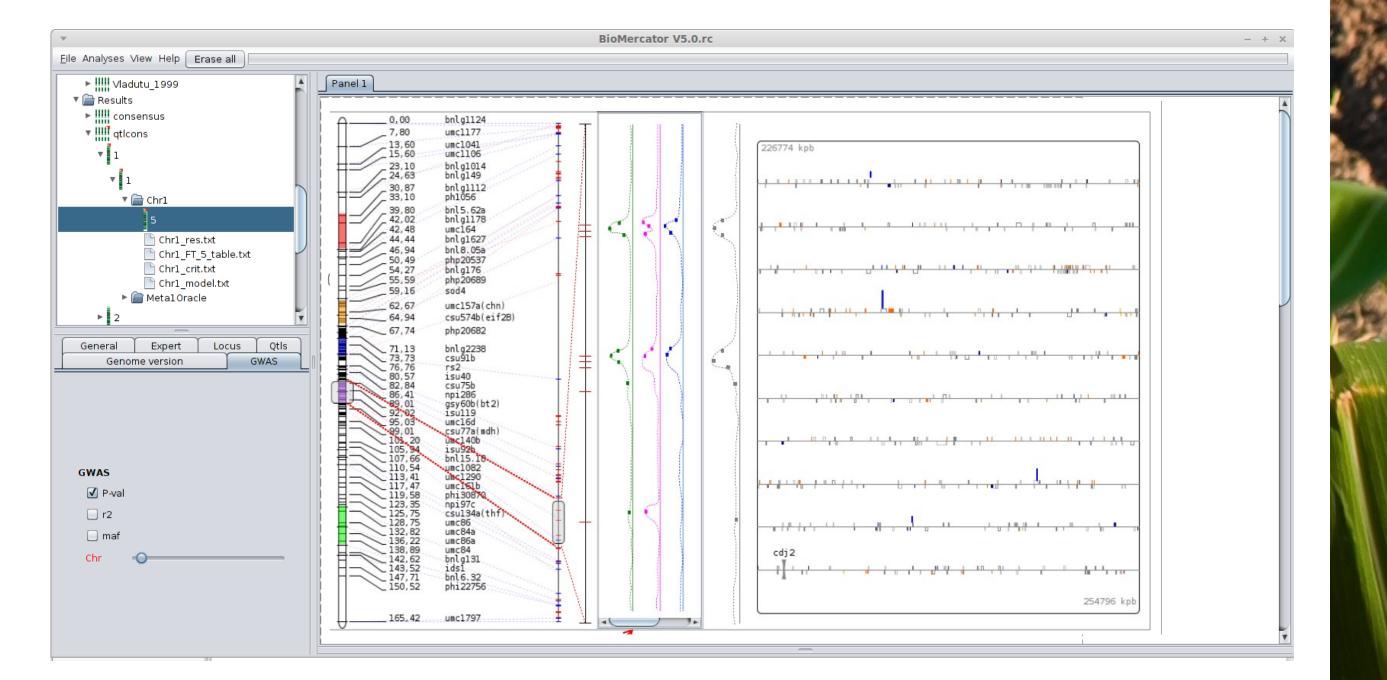




## **GWAS view & GWAS meta-analysis**



In order to improve candidate genes detection we aim to provide new methods like genome wide (GWAS). association studies **BioMercator enables GWAS results** loading in BioMercator (GnpAsso format<sup>[2]</sup>). Currently, one GWAS can be loaded in BioMerator and results can be filtered according to the pvalue or the R2. In the left figure, the relevant markers are depicted with a little blue stick.



The left picture shows a template of what we aim to develop next year for Biomercator.

[2] https://urgi.versailles.inra.fr/Projects/GnpAsso

