Integration of experiments results coming from the meta-analysis of QTLs (meta-QTLs) in the URGI information system GnpIS

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Abstract URGI is an INRA bioinformatics unit dedicated to plants and pest genomics. We develop and maintain an information system called GnpIs, for plants of agronomical interest. This information system includes data corresponding to different themes such as transcriptomic, polymorphism, genetic resources, genotypic/environment interaction, physical map, genetic annotation and genetic mapping. We present here the work done in the frame of the bioinformatics project ANR MetaQTL whose aim was 1) to improve GnpIS genetic mapping module to include QTL meta-analysis and their results (meta-QTL), 2) to integrate on URGI Web site, the new version of the analysis and visualization map software, BioMercator, developed at INRA Moulon and 3) to promote the use of the two tools simultaneously.
Keywords meta-QTL, meta-analysis, BioMercator, data.

Goal

The first aim of the bioinformatics project, ANR MetaQTL, was to develop a new enhanced version of BioMercator software offering 1) improved with state-of-the-art map compilation and QTL meta-analysis algorithms 2) a wizard tool to assist a user in genetic/physical/sequence-based map integration and 3) a new module for projection of QTL/metaQTL onto physical/sequence map. This new version provides end-user with a unique user-friendly workbench for genetic/physical data integration. The second aim of the project was to promote the sharing of results produced with BioMercator, by extending the URGI Information System GnpIS and its genetic database module GnpMap to 1) store this new data and 2) make them available for query or display at the genetic map and genome levels.

Queries
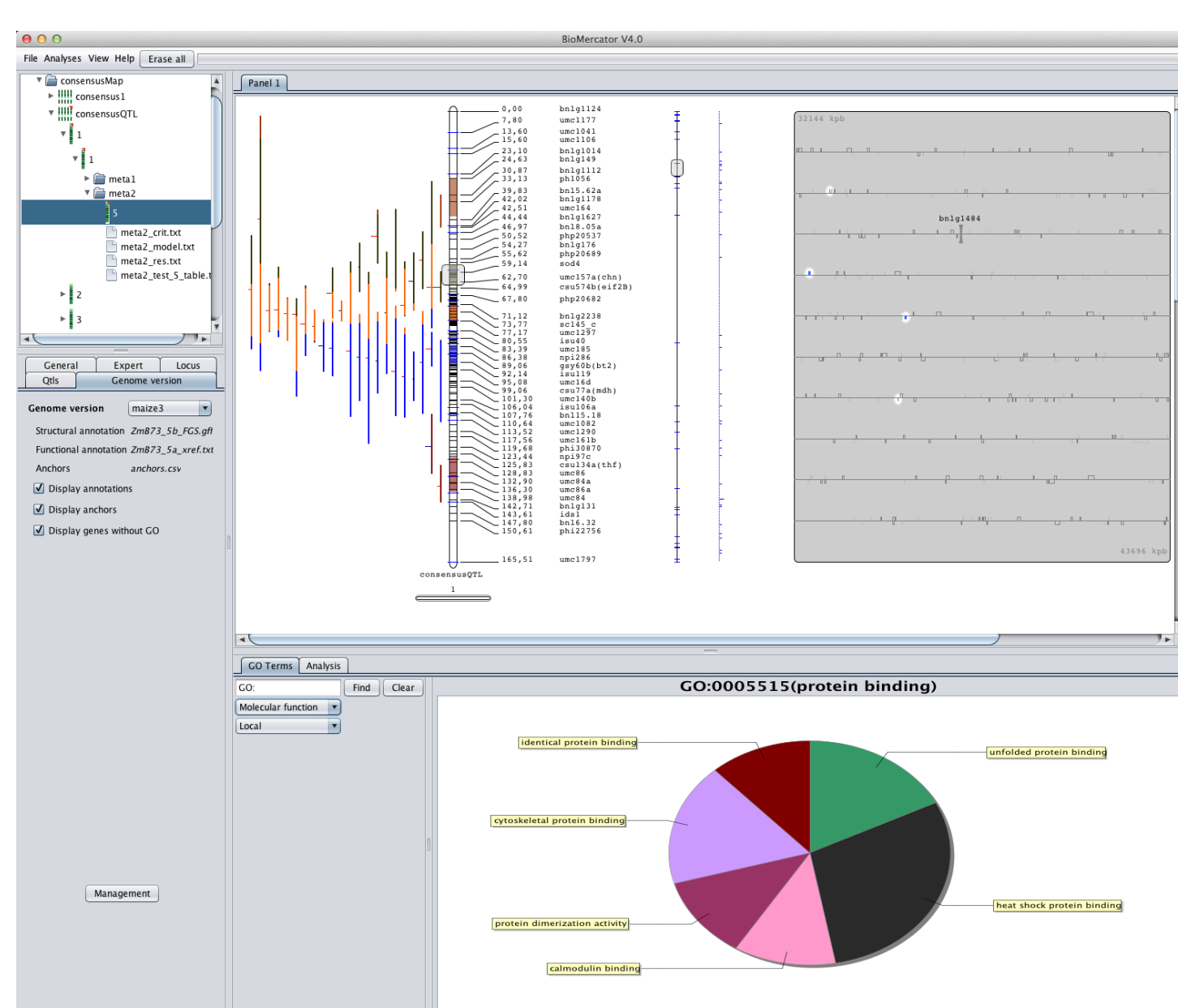

GnpMap can therefore be easily populated with these data allowing end-user to construct powerful queries such as listing meta-QTLs linked to traits of interest.
Some examples of the new version of the GnpMap interface with wheat meta-QTLs (*J. Legouis & al.*) are presented below.
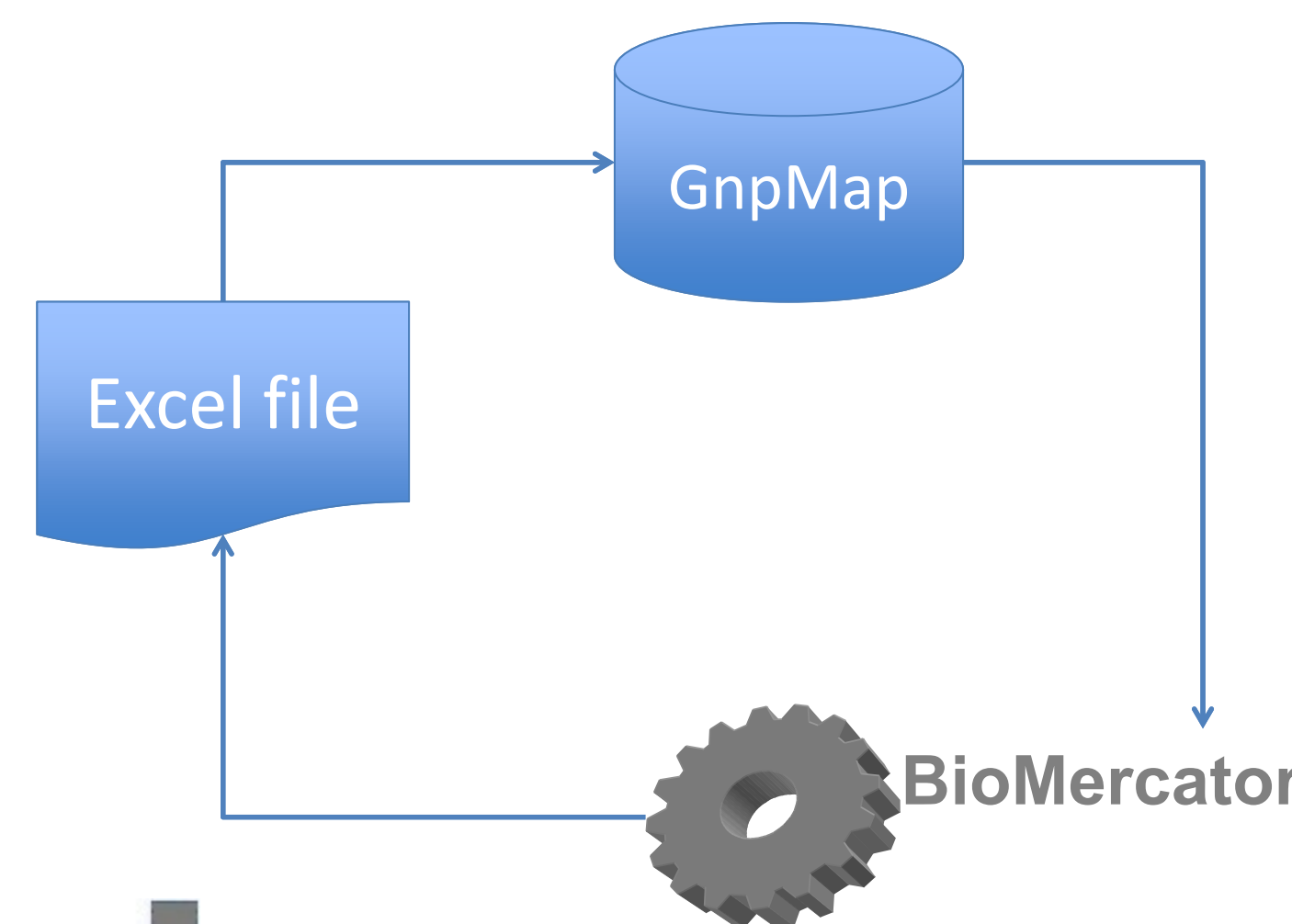
BioMercator

New compact graphical representations have been developed 1) a chromosome cascading zoom allows the user to enlarge a region of chromosome as deep as he needs, while keeping an overview of the whole chromosome map. 2) A new compact QTL track summarizing QTL data along the chromosomes has been developed. 3) For whole map representation, each chromosome can be enlarged independently at the user convenience in order to focus on regions of interest. 4) Genome sequencing consortium usually deliver gene annotation and genetic/physical anchor loci.
These data can be loaded in BioMercator v4. QTL and metaQTL can be projected onto the genome and it is then easy to search for genes included in confidence intervals. In addition BioMercator v4 can display and export the functional annotation of the corresponding genes.

Data submission

Data from GnpMap can be export in standardized exchange XML file used by BioMercator. BioMercator output and meta-analysis results can be automatically exported in the URGI GnpMap exchange format (Excel file). http://urgi.versailles.inra.fr/Data/Mapping/Data-submission
A processing tool (checking and conversion) and a tool for loading data in GnpIS were developed.

Results

Standardized XML file was chosen to be the communication format used between GnpIS web interface and BioMercator. It is therefore possible to launch BioMercator directly from the genetic mapping interface (details cards and results table) to display map. This feature is available now for project partners and will be available to public after publication.

Conclusions

We developed BioMercator v4 and we extended GnpIS, a unique software and database to mine, integrate, display and query QTLs and meta-QTLs altogether with genome structural and functional annotation. Within the frame of this project, these tools have been used to process many datasets including maize, poplar, peach tree, wheat and sunflower. The tight collaboration between bioinformatics and genetics groups has been very powerful at ensuring the success of the project. The tool is available for query on the URGI web site at http://urgi.versailles.inra.fr/GnpMap. A final version will be available before the end of 2012, taking into account last developments.