Abstract: The URGI genomic annotation platform, developed in the framework of the GnpAnnot project, relies on well known GMOD tools (http://gmod.org): Apollo, Chado and GBrowse. Apollo is the graphical interface for visualization and annotation edition allowing curators to edit their genes according to evidences (transcript and protein similarity, comparative genomics). Manual annotations (gene curation validated/in progress) are saved in a dedicated Chado database and shared at the same time with other community annotations members. Validated genes/pseudogenes are then committed in the second Chado database accessible by GBrowse.

References: http://www.gmod.org

Gene Prediction (Fgenesh, Eugene …)
Repeat searching (TEs, TandemRepeats)
(RepeatMasker, TRF…)
Comparison (ESTs, proteins…)
(Blastn, Blastx, Sim4…)
Comparative genomics …

Automated annotation
Result from the automated annotation have to be carefully verified by manual curation using an editing interface. This way allow to increase in quality and value annotation. We set up manual genomic annotation platform relying on the international open source Generic Model Organism Database (GMOD http://www.gmod.org) project. Here is the data flow management called “roundtrip” between Chado database, Apollo genome annotation editor and GBrowse genome browser.

Apollo development:
We are involved in the improvement of Apollo. Some bugs were fixed. New functionalities have been added. They are available in URGI version and expected in next release.
-Owner attribute filled with the username from login on chadoDB
-More information about feature are displayed

Application:
Distributed annotation system has been set up for 2 fungal genomes Botrytis cinerea, Tuber melanosporum and a plant genome Grapevine. The system for Leptosphaeria maculans genome is in progress.

Perspectives:
Whole tools of the manual curation platform will be improved, and we regularly checked last release of software used (Apollo, GBrowse). We also plan to develop a functional manual annotation system based on the same model.

Configuration files:
- apollo.cfg: Preference system
- chado-adapter.xml: Instance used, which program used, connection to DB
- files.styles // files.tiers: How preferences will be used, displayed (track color)

Chado4Apollo
Chado4GBrowse
Extract genes Curated/Validated
Update With last curated genes release
GFF3 files
Read

Apollo is a genome annotation viewer and editor. Apollo allows researchers to explore genomic annotations at many levels of detail, and to perform expert annotation curation, all in a graphical environment.

Apollo WebStart
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