Galaxy Genome Annotation

Integrating Galaxy and GMOD for genome annotation

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2018-06-28
Galaxy Genome Annotation

Tooling, training, community to assist genome annotation with Galaxy

- Automatic structural and functional annotation
- Visualisation
- Manual curation
- Release and submission to INSDC
Galaxy Tools

Galaxy tools for automatic annotation

- New tools and updates since GCC2017
- Maker, Augustus, Snap, RepeatMasker, Busco, Prokka, Antismash, ...

Visualisation

- Circos, JBrowse
GMOD integration

Interface Galaxy with the GMOD components

- Dockerized GMOD apps: JBrowse, Apollo, Tripal, Chado, ...
- Python libraries/CLI: python-chado, python-apollo, python-tripal, ...
- Tools to interact with GMOD apps: load and/or extract data

https://galaxy-genome-annotation.github.io
Use case: GGA @ useGalaxy.EU

Apollo is coming soon to useGalaxy.EU

We are currently testing the integration and seeing how we can provide a Genome Browser + Annotation Suite as a service to all of Europe. There are many GGA components and we are identifying the ones that are useful to our users and for which we can provide support when users have issues.

Email us to join the beta test
apollo@usegalaxy.eu
Use case: GGA @ BIPAA

French national platform for insect pests and related organisms

Hosting 24 genomes of non model organisms

JBrowse, Tripal, Apollo (>8000 genes curated)

https://bipaa.genouest.org
What’s next?

Training material in Galaxy Training Network

More tools

More gmod apps/modules: expression, genotyping, synteny, ...

Join us at the Collaboration Fest!
Thanks!