MAPHiTS: an efficient workflow for SNP detection

Computer Demo
Summary

URGI team develops a pipeline (MAPHiTS) for SNP detection from short reads.

Features:

- Robuste but flexible
- Easy to upgrade
- User-friendly interface (for biologists)

It’s fully integrated in Galaxy.

BRAS Marc (marc.bras@versailles.inra.fr) – Computer demo
Installation of URGI Galaxy

Galaxy is installed on URGI cluster with:

- CPU: 704 (Intel Xeon)
- RAM max: 96 Gb per job
- Storage: 60 Tb

Using Sun Grid Engine (for job management) and a PostgreSQL Database (for Galaxy).

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Using MAPHiTS?

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