

MAPHITS: an efficient workflow for SNP detection

Computer Demo



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Summary

URGI team develops a <u>pipeline</u> (MAPHiTS) for <u>SNP detection</u> from short reads.

Features:

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

It's fully integrated in **Galaxy**.





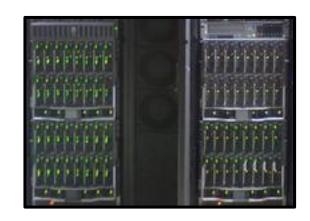
Installation of URGI Galaxy

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 managment) and a PostgreSQL Database (for Galaxy).





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Using MAPHiTS?

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Galaxy

Thanks

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