INSTITUT DE BIOLOGIE PARIS · SEINE

BIOINFORMATICS IBPS - ARTbio

ARTbio works with the Galaxy system, a collaborative open source platform dedicated to scientific and biomedical research. The Galaxy servers enable computational data analyses with a user-friendly interface. They provide both traceability and reproducibility of the analyses which can be shared for collaboration and publication.

OUR SERVICES

- We assist you in the experimental and computational design of high-throughput sequencing analyses using Galaxy servers.
- We help you choose the tools and workflow best adapted to your analyses.
- We provide advanced training in Galaxy usage.

Our services are fully accessible to both public and private structures. Please contact us for pricing.

OUR EXPERTISE

- We have an extensive knowledge of the Galaxy software and its use, from raw data acquisition to publication.
- We constantly integrate newly launched software and methods into the Galaxy toolpack.
- We ensure project quality and optimal interaction with users by using continuous integration technologies and the AGILE guidelines.
- We continuously improve our Galaxy expertise through our own research in RNA biology, epigenetics, metagenomics and bioinformatics, which we publish in peer reviewed scientific journals.

OUR TECHNOLOGY

- We use the R, Python, Perl and Bash programming languages, the Git and Mercurial revision control software, and continuous integration tools such as Planemo and Jenkins.
- We implement virtualization and container technologies (e.g. Docker) in order to make analyses reproducible in any hardware infrastructure.
- We can increase our computing resources on demand thanks to cloud infrastructures such as that provided by the *Institut Français de Bioinformatique*.

CONTACT

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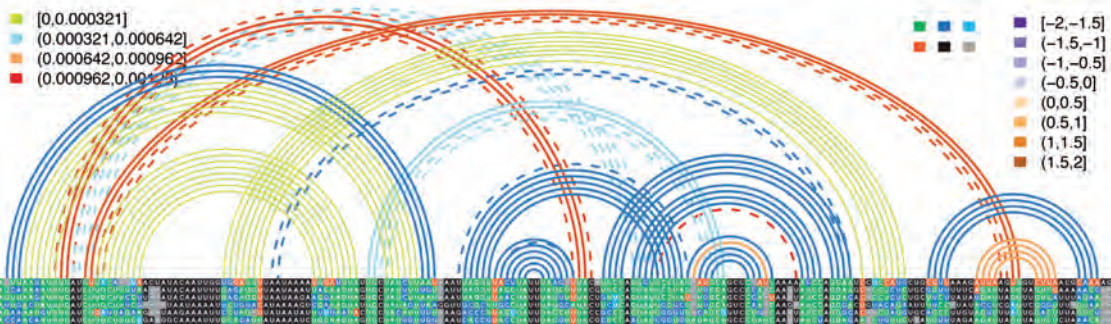
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DEVELOPMENTS

■ Project support

We have recently provided advanced support to many Next Generation Sequencing (NGS) projects, including studies of epigenetic functions of piRNAs[1], antiviral RNA interference[2] or roles of miRNAs in stem cell differentiation[3].

■ Tools

We developed and made publicly available the « mississippi » suite of tools (for mi, si and pi RNA) for mining small RNA sequencing datasets[4]. We are currently releasing a set of Galaxy workflows aimed at detecting viruses or identifying new viral species from small RNA sequencing datasets[5]. We are also developing the DockerToolFactory, which allows execution of customized R, python, perl or bash scripts without leaving the Galaxy environment[6].

■ Methodology developments

We are working to improve continuous integration (based on virtualization methods (e.g. Planemo, Jenkins CI, Virtual machines, Docker and Deployment in Cloud).

EQUIPMENT

Servers
- Server Dell 24 core, 128 GB RAM, 12 TB RAID storage.
- Server Dell 16 core, 96 GB RAM, 25 TB RAID storage.
- Access to IFB cloud infrastructure (www.france-bioinformatique.fr)

Galaxy servers online
- http://mississippi.fr (public)
- http://lbcd41.snv.jussieu.fr (restricted access)

1. A. de Vanssay et al., Paramutation in Drosophila linked to emergence of a piRNA-producing locus. *Nature*. 490, 112-15 (2012).
2. P. Miesen et al., Distinct sets of PIWI proteins produce arbovirus and transposon-derived piRNAs in Aedes aegypti mosquito cells. *Nucleic Acids Res*. (2015), doi:10.1093/nar/gkv590.
3. A. Jouneau et al., Naive and primed murine pluripotent stem cells have distinct miRNA expression profiles. *RNA*. 18, 253-64 (2012).
4. https://testtoolshed.g2.bx.psu.edu/view/mvdbeek/mississippi_toolsuite/
5. https://toolshed.g2.bx.psu.edu/view/drosofff/suite_visitor2/
6. https://bitbucket.org/mvdbeek/dockertoolfactory