Analyze your microbiota sequencing data using a Galaxy-based framework

http://frama.link/aj16

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Nowadays, complex communities of microorganisms can be studied in depth with metagenomics and metatranscriptomics, driven by evolution of sequencing techniques. Indeed, these meta'omics techniques offer insight concerning structure and functions of the studied communities. Notwithstanding, analyses of raw microbiota sequencing data are difficult because of data size and so numerous available and needed tools (1,2) for data processing.

To overcome these limitations, we have developed ASaiM, an open-source opinionated Galaxy-based framework. It is accessible via a web-based interface to help scientists in their microbiota sequence data analyses. With an expertly selected collection of tools, workflows and databases, the framework is dedicated particularly to extraction of taxonomic, metabolic and taxonomically related metabolic information from raw sequences. By its intrinsic modularity, ASaiM allows adjustement of workflows, tool parameters and used databases.

ASaiM framework is a powerful tool to analyze shotgun raw sequence data from complex communities of microorganisms. This open-source and biologist-oriented solution enhances usability, reproducibility and transparency of such studies.

Implementation

Based on a Galaxy instance with a custom configuration, ASaiM framework is integrating tools (Figure 1), specifically selected for microbiota studies. They are hierarchically organized (Figure 1) and documented (http://asaim.readthedocs.org/) to orient user choice toward best tools during analyses. These tools can be used separately or orchestrated inside workflows.

To help users with their analyses of raw microbiota sequences, a default but customizable workflow (Figure 1) is proposed in ASaiM framework. It produces accurate and precise taxonomic assignations, wide functional results (gene families, pathways, GO slim terms) and taxonomically related metabolism information, in few hours on a commodity computer. Other workflows are also pre-configured for comparative analyses.

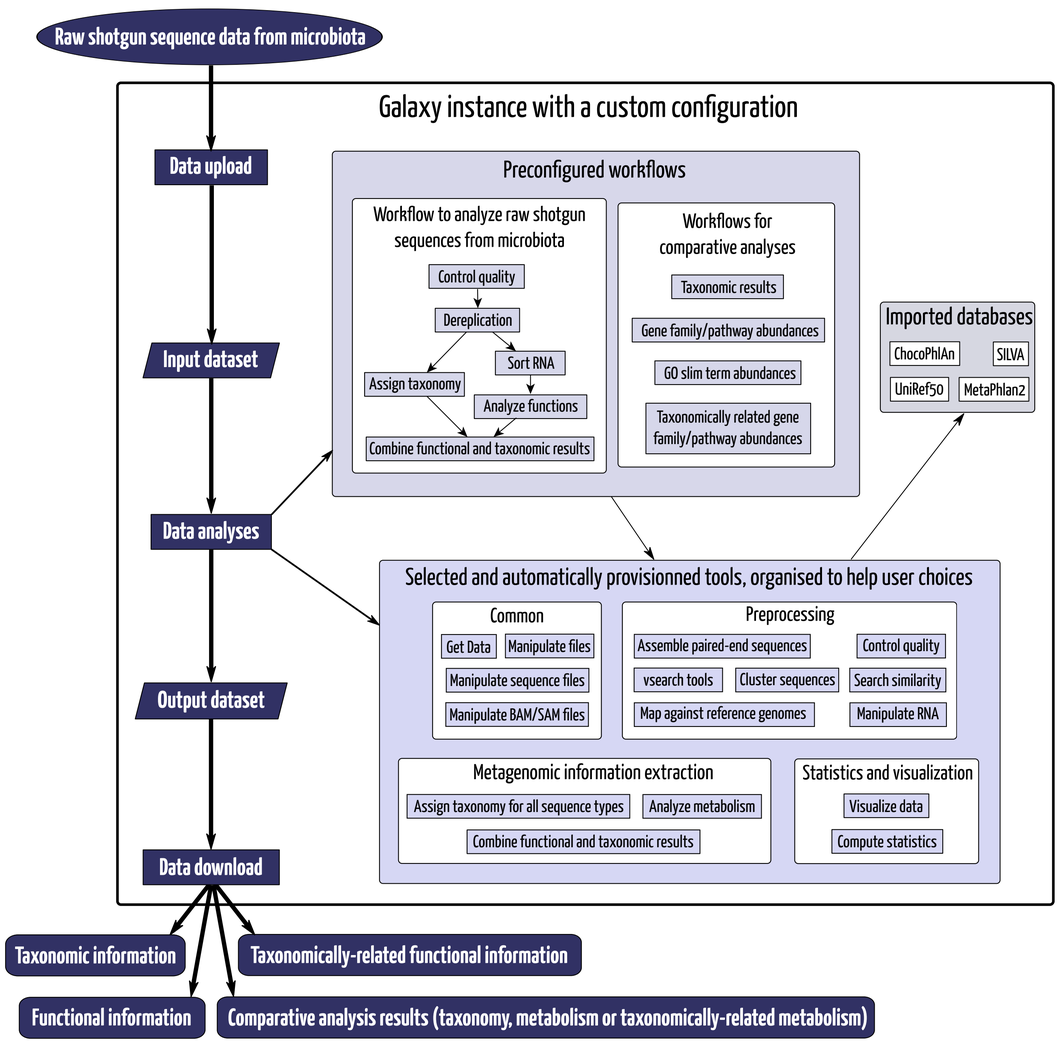
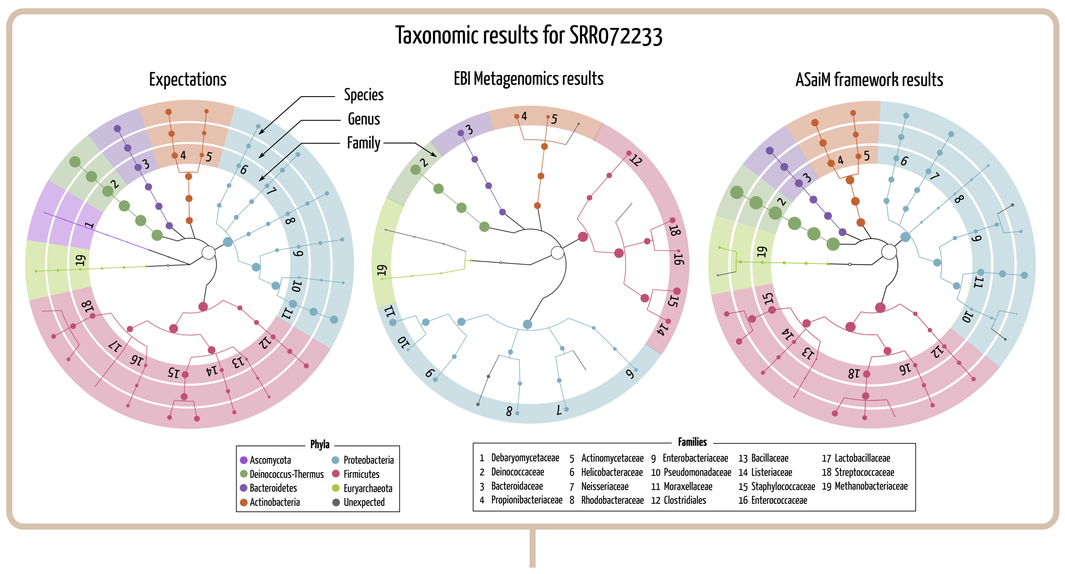
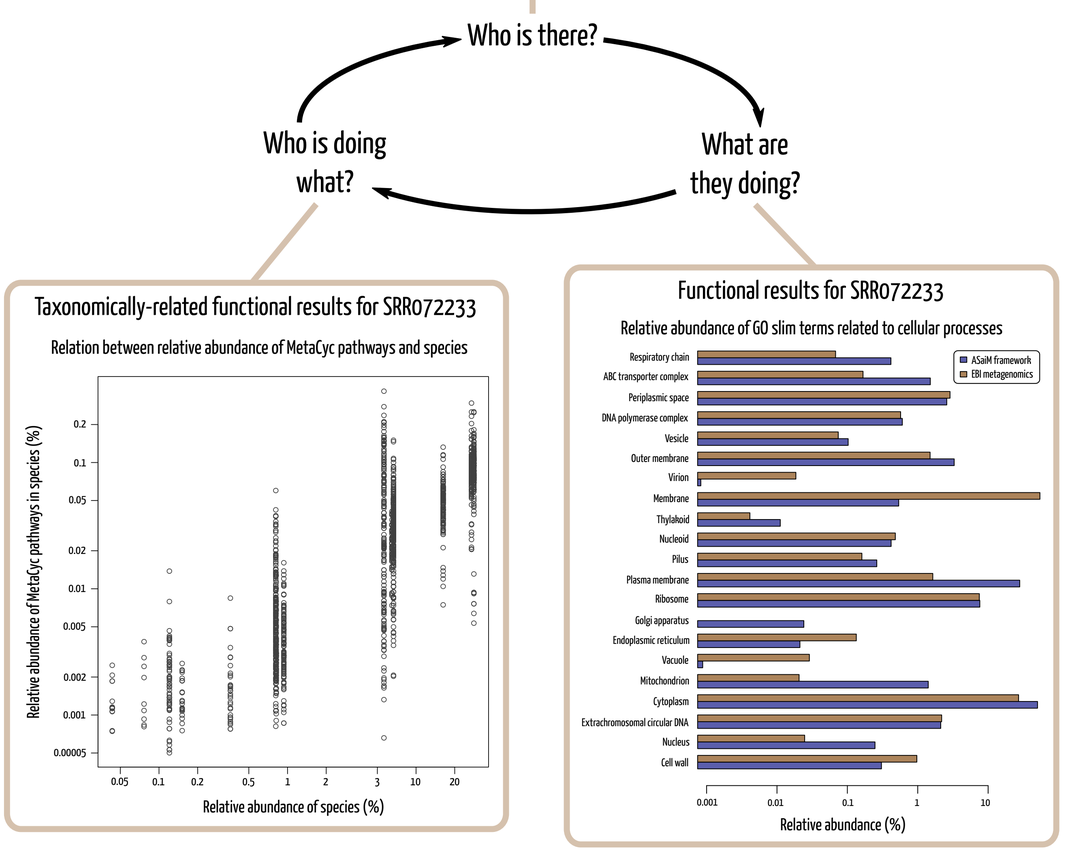


Figure 1: ASaiM framework and components of its Galaxy instance. Using scripts in framework code source, the Galaxy instance is easily configured, launched and provisioned with tools, workflows and databases.

Validation

ASaiM framework was tested on two mock metagenomic datasets from HMP metagenomes mock pilot project . These datasets are metagenomics shotgun sequences (>1,200,000 454 GS FLX Titanium single-end sequences) from a controlled community (with 22 known microbial species), available on EBI metagenomic database (SRR072232 and SRR072233). Results obtained with ASaiM framework were intensively analyzed and compared to the ones from EBI metagenomic pipeline (3, version 1.0).





Taxonomic analyses gives a great insight on community structure with complete, accurate and statistically supported information. A broad overview of metabolic profile is available with gene families, pathways and GO slim terms. The taxonomically-related functional information, specific to ASaiM framework, allows to investigate which species is involved in which metabolic function.

Details about theses analyses, more results, analyses and representations are available on https://github.com/ASaiM/hmp_mock_tests.

Further information

ASaiM framework source code is available under Apache 2 license at https://github.com/asaim/framework, as a collection of bash, Python and Ansible scripts. The source code includes framework deployment: automatic configuration of the Galaxy instance, its deployment and its provision with selected tools, workflows and needed databases.

Heavy documentation of custom configuration of Galaxy instance, tools, workflows and databases is available at https://asaim.readthedocs.org

References

(1) Mendoza *et al*, Brief Bioinfo, 16 (2015), 745-758
(2) Segata *et al*, Mol Sys Biol, 9 (2013), 66
(3) Hunter *et al*, Nucl Acids Res, 42 (2014), D600-D606

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