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# How to analyze raw sequencing data from microbiota? Using ASaiM!



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New generation of sequencing platforms coupled to numerous bioinformatics tools has led to rapid technological progress in metagenomics, metatranscriptomics and complex microbial community studies. Nevertheless, a combination of different bioinformatics tools remains necessary for efficient extraction of useful information in microbiota studies. Modular, accessible, sharable and user-friendly tools would greatly improve such studies.

We therefore developed ASaiM, an open-source **Galaxy-based framework** dedicated to microbiota data analyses.

ASaiM provides an **expertly selected collection of tools** to explore and visualize taxonomic and functional information from raw amplicon, metagenomic or metatranscriptomic sequences. To help the analyses, **several (customizable) workflows** are included. The available workflows are supported by **tutorials** and **Galaxy interactive tours** to guide the users through the analyses. Furthermore, an effort on **documentation** of ASaiM, its tools and workflows has been made (<http://asaim.readthedocs.io/>). ASaiM is implemented as **Galaxy Docker flavour** and the associated source code is available under Apache 2 license at <http://github.com/ASaiM/framework>.

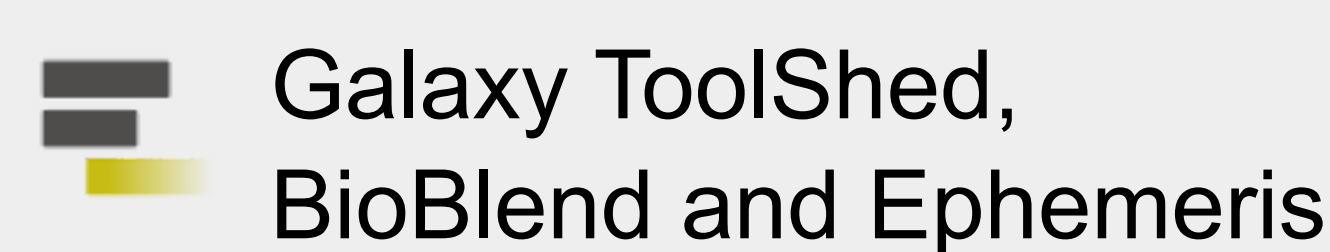
Based on the Galaxy framework, ASaiM offers sophisticated analyses to scientists without command-line knowledge. ASaiM provides a powerful framework to easily and quickly explore microbiota data in a reproducible and transparent environment.

## A framework built on the shoulders of giants

To develop a modular, accessible, redistributable, sharable and user-friendly framework for scientists working with microbiota data



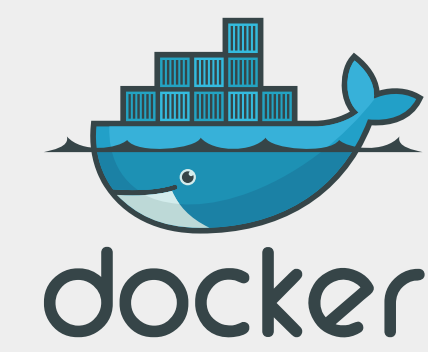
As the base



To install the Galaxy tools, the workflows and databases



To install the tools and their dependencies



To containerize and ship everything

## With a comprehensive set of microbiota related tools

**FILE AND META TOOLS**

- Data retrieval**: EBISearch, ENASearch, SRA Tools
- Text manipulation**: See documentation for the full list
- Sequence file manipulation**: See documentation for the full list
- BAM/SAM file manipulation**: SAM Tools
- BIOM file manipulation**: BIOM-Format tools

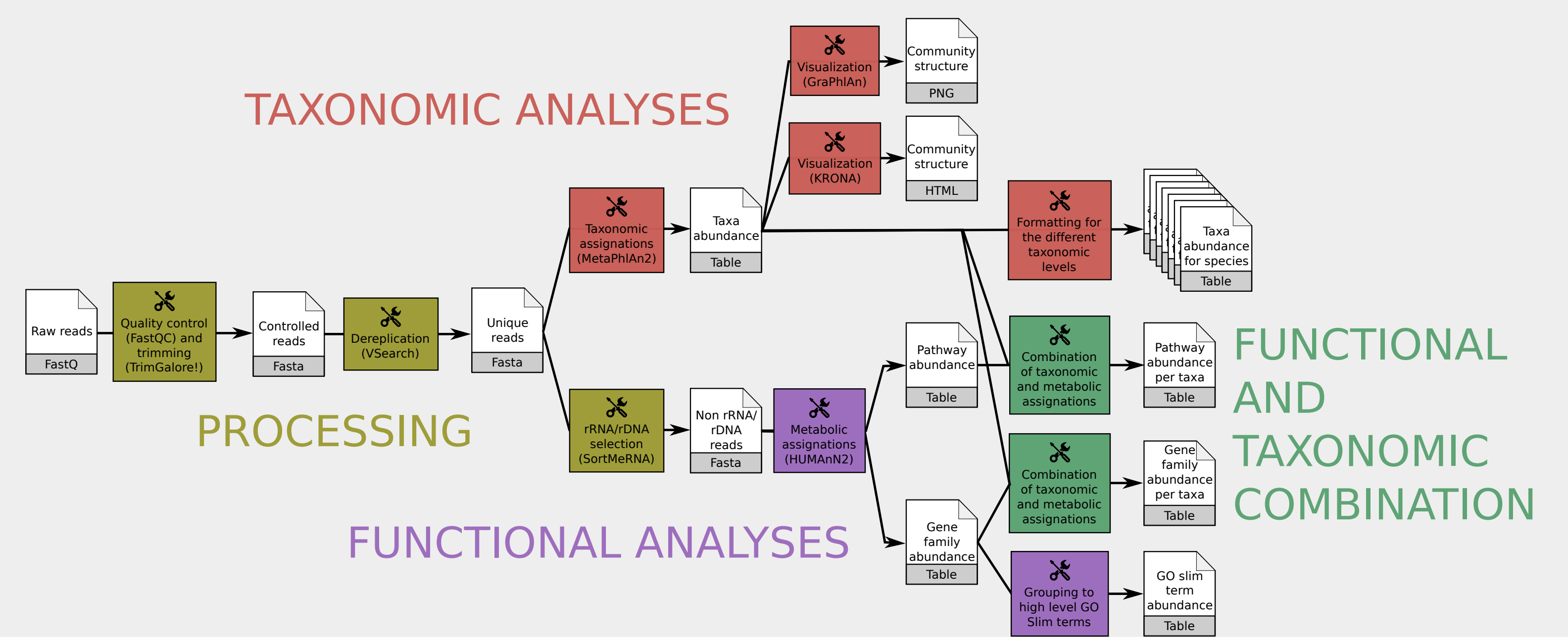
**GENOMICS TOOLS**

- Assembly**: FastQ joiner, FastQ-join
- Quality control**: FastQC, PRINSEQ, Trim Galore!, Trimmomatic
- Clustering**: CD-Hit, Format CD-HIT outputs
- Sorting**: SortMeRNA, FragGeneScan
- Similarity search**: NCBI Blast+, Diamond
- Mapping**: BWA, Bowtie
- Alignment**: HMMER3

**STRUCTURAL AND FUNCTIONAL ANALYSIS TOOLS**

- Metagenomics data manipulation**: VSEARCH
- Amplicon sequence processing**: Mothur, QIIME
- Taxonomy assignment on WGS sequences**: MetaPhlan2, Kraken
- Metabolism assignment**: HUMAnN2, PICRUST, InterProScan
- Combination of functional and taxonomic results**: Combine MetaPhlan2 and HUMAnN2
- Visualization**: Export2graphlan, GraPhlan, Krona

## With predefined and tested workflows



Main workflow to analyze raw shotgun metagenomics data

## With documentation and training

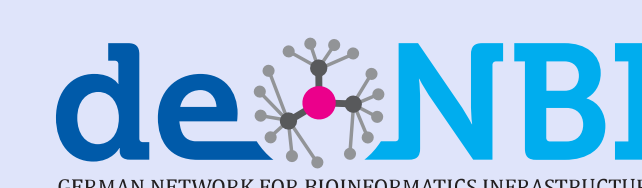
- Online documentation: <http://asaim.readthedocs.io>  
*how to use and deploy ASaiM*  
*which tools are integrated with some documentation about them*  
*which workflows are integrated and how to use them*
- Galaxy Interactive Tours inside ASaiM
- Tutorials  
Developped with the help of the Galaxy Training Network (GTN)  
Hosted in the GTN website  
<http://galaxyproject.github.io/training-material/metagenomics>

## Useful information

GitHub: <http://github.com/asaim/framework>  
Doc: <http://asaim.readthedocs.io>

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CPER 2015  
Axe T2ANSH  
(Action 3, Aliments,  
Nutrition Humaine Santé)



Check out  
our paper !

