



# A Galaxy-based framework to analyze raw sequencing data from microbiota



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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



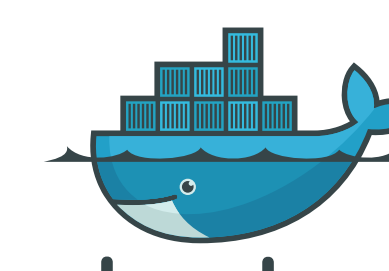
Galaxy ToolShed,  
BioBlend and Epheris

To install the Galaxy tools, the  
workflows and databases



Conda

To install the tools and  
their dependencies

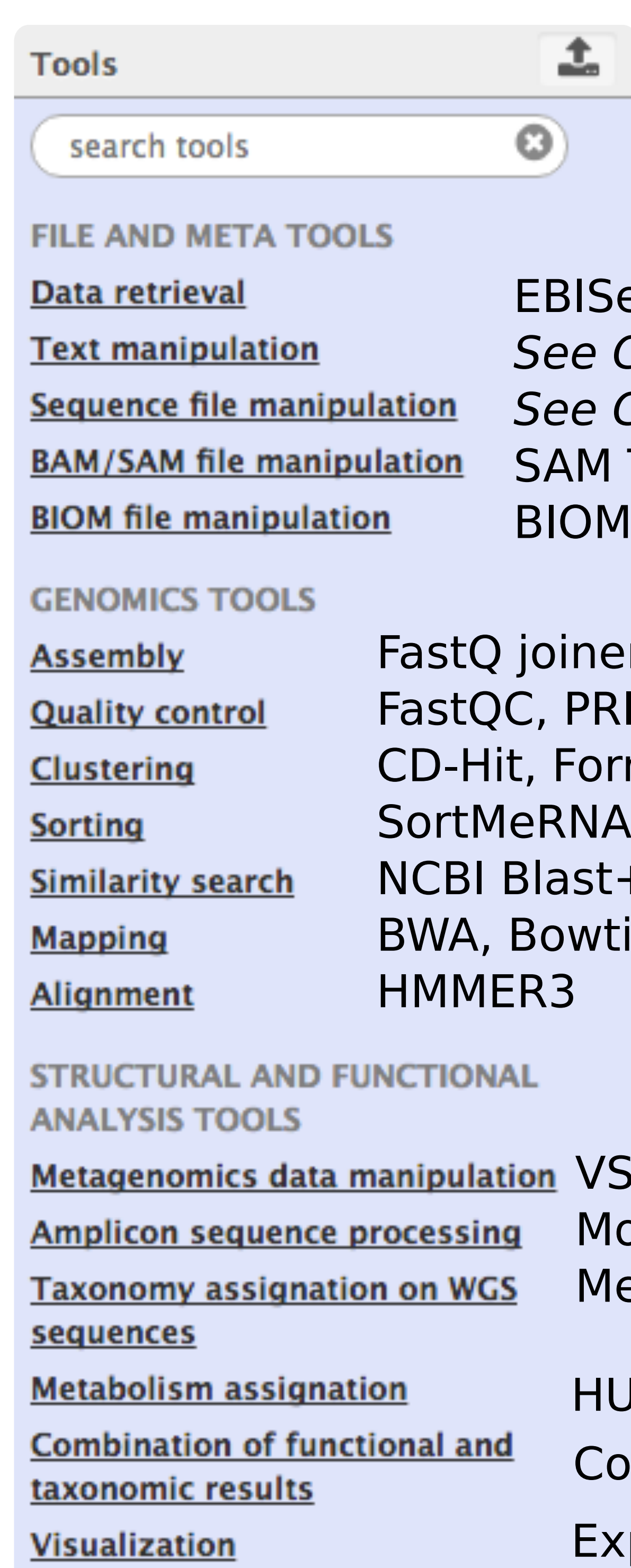


docker

To containerize and ship  
everything



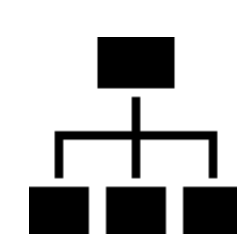
## With a comprehensive set of microbiota related tools



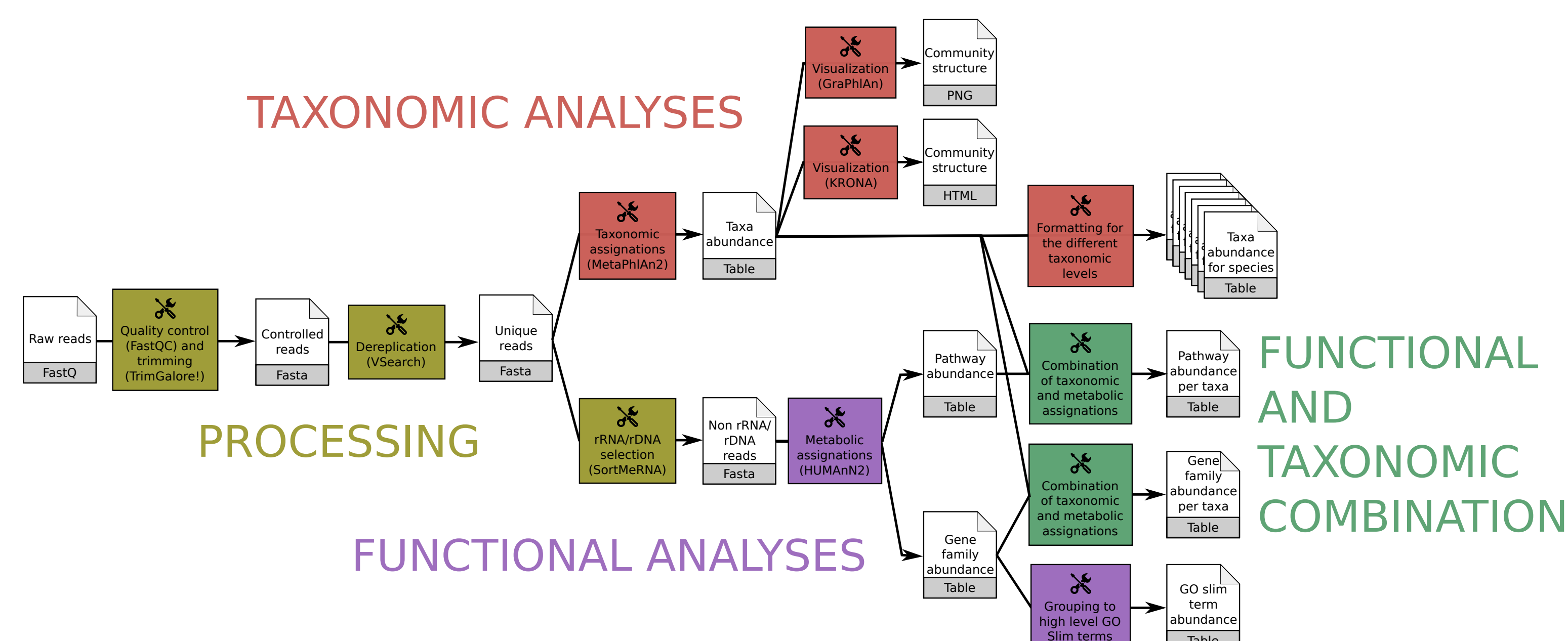
EBISearch, ENASearch, SRA Tools  
See [GitHub](#) for the full list  
See [GitHub](#) for the full list  
SAM Tools  
BIOM-Format tools

FastQ joiner, FastQ-join  
FastQC, PRINSEQ, Trim Galore!, Trimmomatic  
CD-Hit, Format CD-HIT outputs  
SortMeRNA  
NCBI Blast+, Diamond  
BWA, Bowtie  
HMMER3

VSEARCH  
Mothur, QIIME  
MetaPhlAn2, Kraken  
HUMAN2, PICRUST, InterProScan  
Combine MetaPhlAn2 and HUMAN2  
Export2graphlan, GraPhlan, Krona



## With predefined and tested workflows



Main workflow to analyze raw shotgun metagenomics data



## With documentation and training

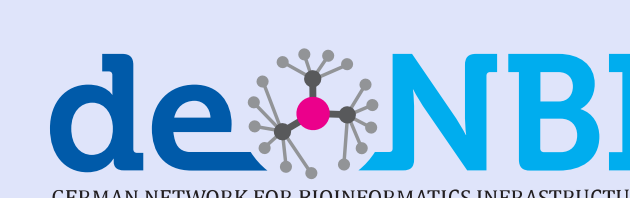
- Online documentation: <http://asaim.readthedocs.io>  
*how to use and deploy ASaiM*  
*which tools are integrated with some documentation about them*  
*which workflows are integrated and how to use them*
- Galaxy Interactive Tours inside ASaiM
- Tutorials  
Developed with the help of the Galaxy Training 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)



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