



FROGS : Find Rapidly OTUs with Galaxy Solution

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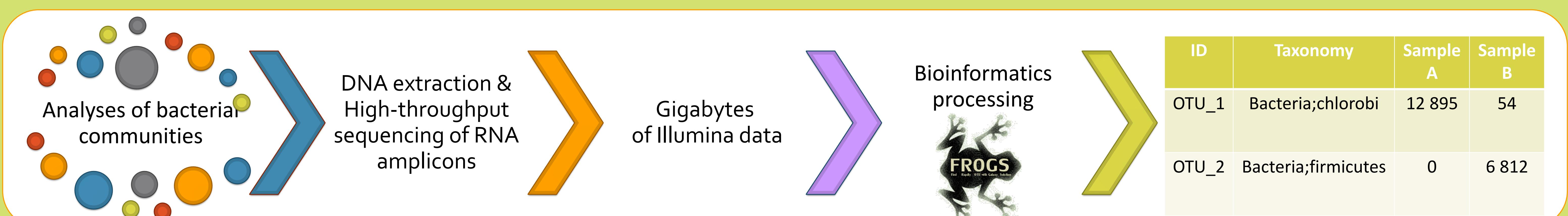
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FROGS: Find Rapidly OTUs with Galaxy^[5] Solution

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*These authors have contributed equally to the present work.

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User-friendly

+

Accuracy

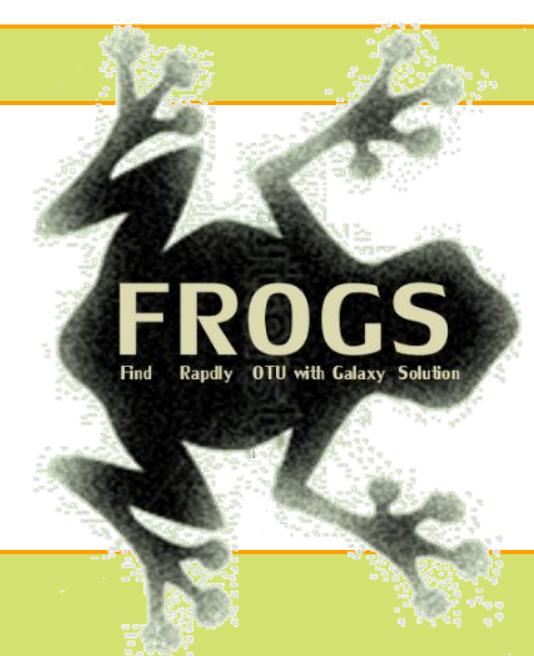
+

Speed

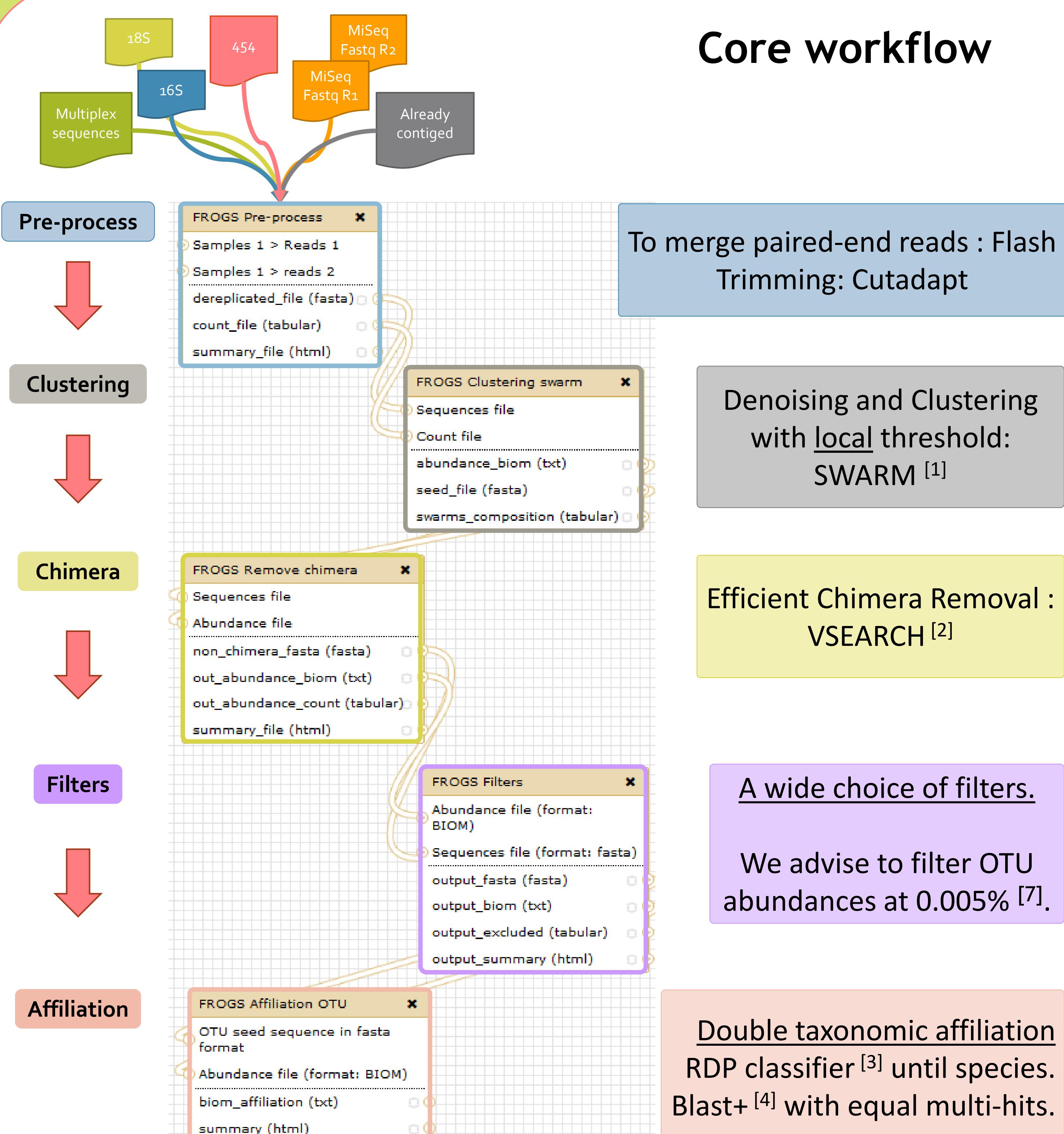
+

Scalability

=



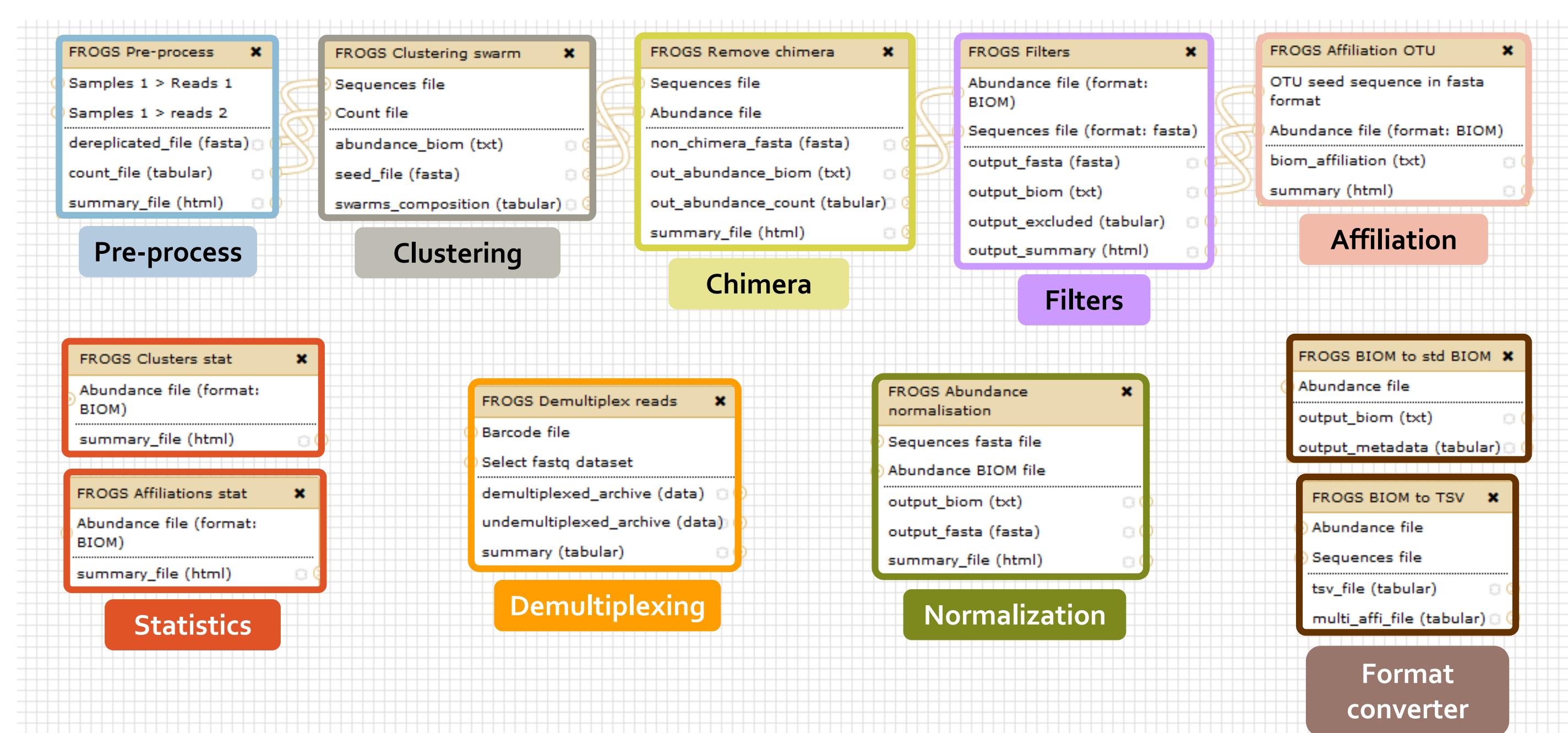
Core workflow



FROGS = complete analyze

Access : <http://galaxy-workbench.toulouse.inra.fr>

Interconnectable with BIOM format



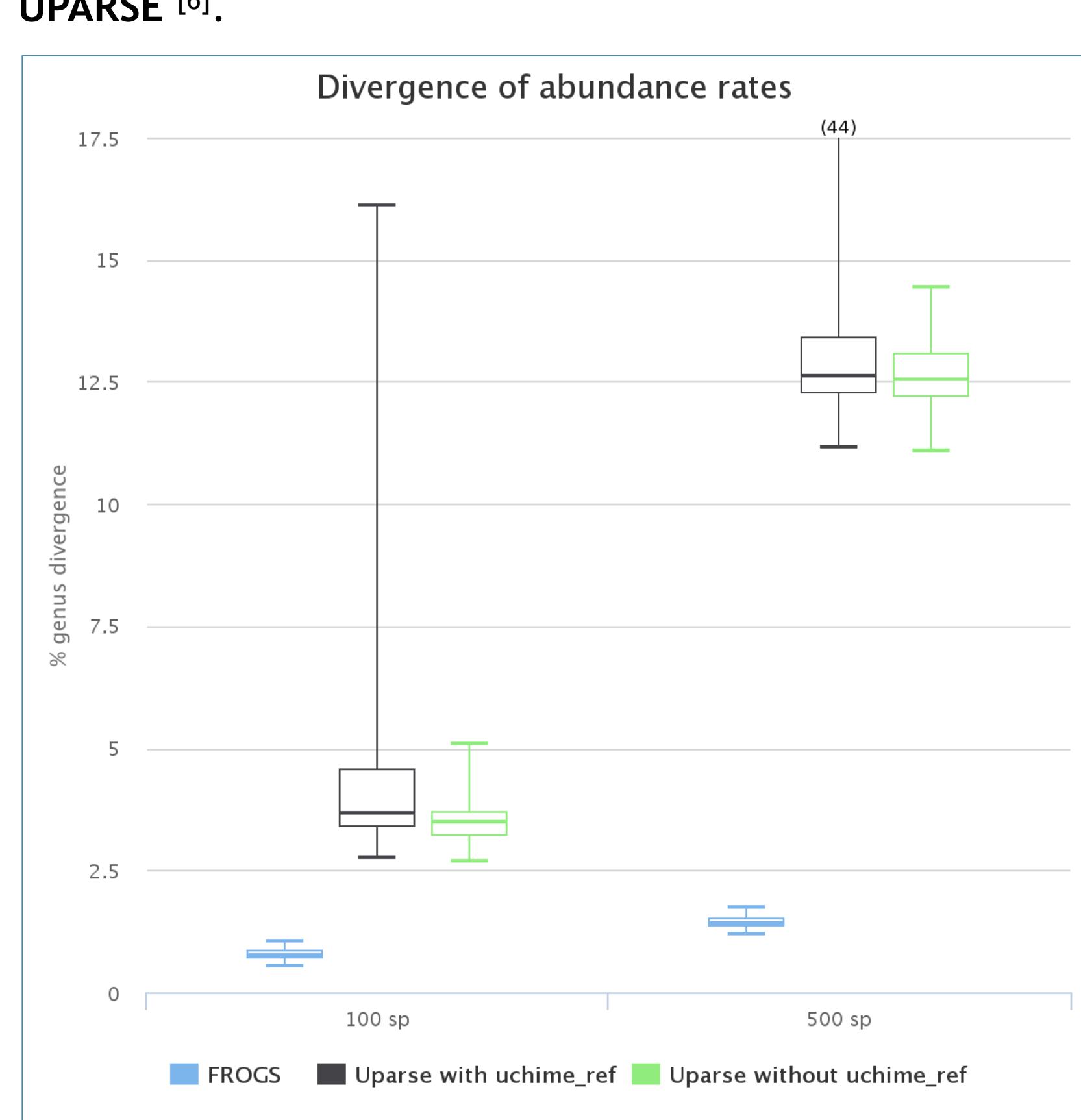
Great graphics outputs



Accuracy on simulated data set

For the tests we use two sets of species manually extracted from LTP 115. These species were chosen to obtain near and distant species in the same dataset.

For each set of species we generate 5 artificial runs of 10 samples. In each sample the abundance of species following a power law. The ranking of species abundance is randomly determined in each sample. Then, an Illumina error profile is applied on reads and 20 % of chimera are added. All the runs are processed after FROGS preprocess by FROGS and UPARSE [6].



Speed on real datasets

9 600 000 sequences of a complete MiSeq run

Preprocess : 9 300 000 sequences

15 min

Swarm clustering : 680 000 clusters

10 hours

Chimera removal : 556 700 non-chimeric cl.

15 min

Filtering : 556 200 OTUs

*filter OTU abundances at 0.005%

PhiX removal

~8 min

RDP affiliation

~25 min

Blast affiliation

~5 min

500 OTUs

~11 hours

Announcements

- Evaluate FROGS on others metrics and datasets (mock community, real already known community).
- Add other databases for affiliation (greengenes, ITS).
- Add FROGS in the toolshed.
- Github** repository available <https://github.com/geraldinepascal/FROGS.git>
- Training sessions:** Toulouse (December and April) & Jouy-en-Josas (January and in spring)

References

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- [6] Edgar. (2013) UPARSE: Highly accurate OTU sequences from microbial amplicon reads.
- [7] Bokulich (2013) Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing