Training on Galaxy: Metagenomics

November 2017

Find, Rapidly, OTUs with Galaxy Solution

FRÉDÉRIC ESCUDIÉ* and LUCAS AUER*, MARIA BERNARD, LAURENT CAUQUIL, SARAH MAMAN, MAHENDRA MARIADASSOU, SYLVIE COMBES, GUILLERMINA HERNANDEZ-RAQUET, GÉRALDINE PASCAL

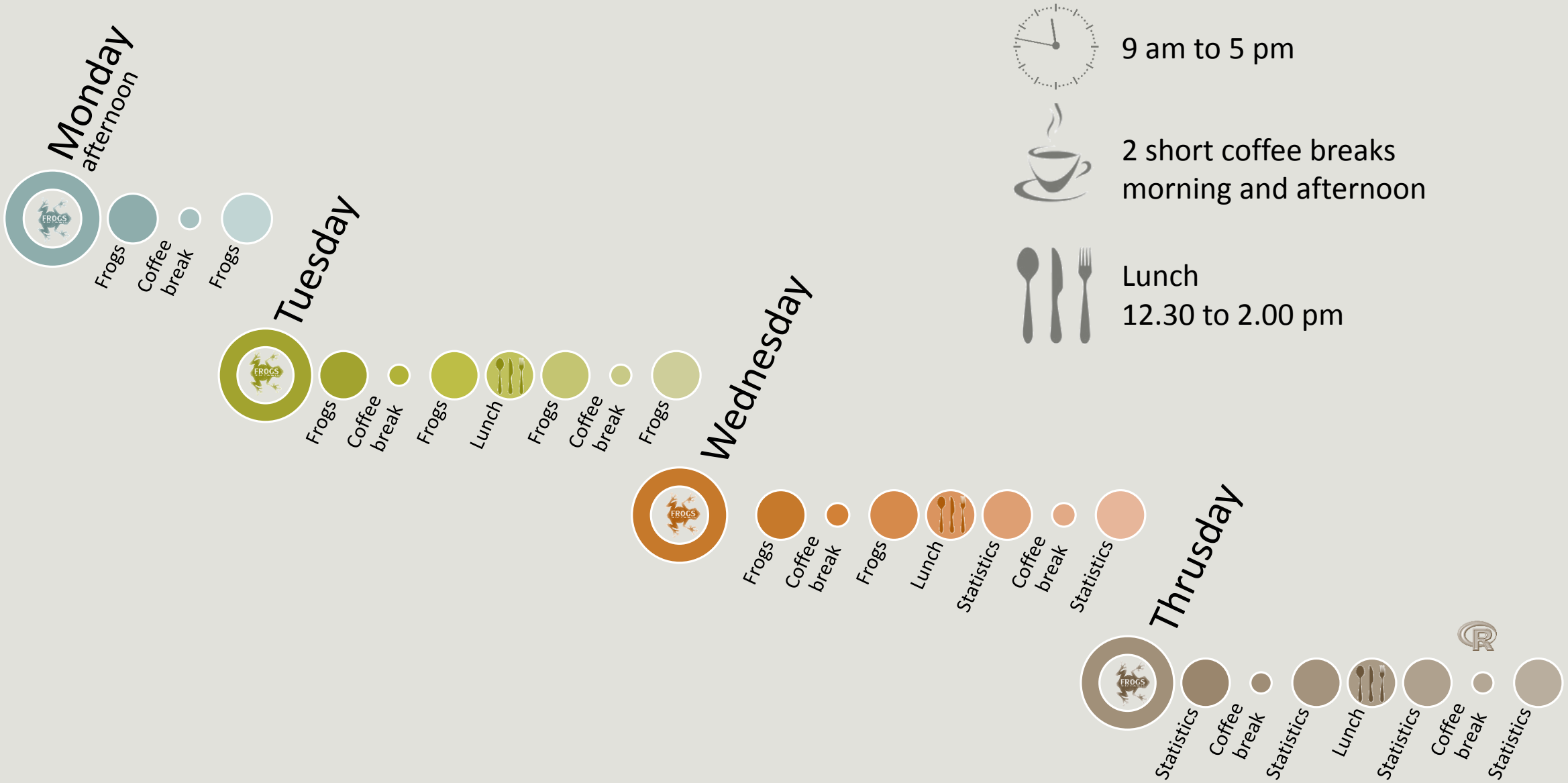
*THESE AUTHORS HAVE CONTRIBUTED EQUALLY TO THE PRESENT WORK.

Feedback:

What are your needs in “metagenomics"?

454 / MiSeq ?

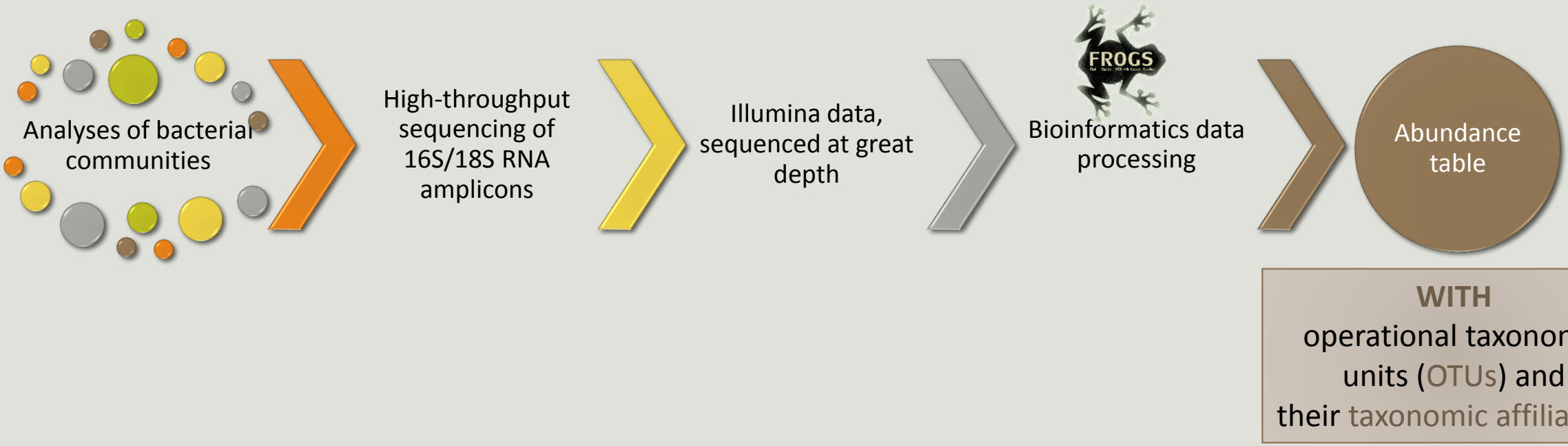
Your background ?


Monday
afternoon
Frogs
Coffee break
Frogs
Tuesday
Frogs
Coffee break
Frogs
Lunch
Frogs
Coffee break
Frogs
Wednesday
Frogs
Coffee break
Frogs
Lunch
Statistics
Coffee break
Statistics
Thrusday
Statistics
Coffee break
Statistics
Lunch
Statistics
Coffee break
Statistics
9 am to 5 pm
2 short coffee breaks
morning and afternoon
Lunch
12.30 to 2.00 pm

Overview

- Objectives
- Material: data + FROGS
- Data upload into galaxy environment
- Demultiplex tool
- Preprocessing
- Clustering + Cluster Statistics
- Chimera removal
- Filtering
- Affiliation + Affiliation Statistics
- Normalization
- Tool descriptions
- Format transformation
- Workflow creation
- Download data
- Some figures

Objectives



WITH
operational taxonomic units (OTUs) and their taxonomic affiliation.

OTUs for ecology

Operational Taxonomy Unit:
a grouping of similar sequences that can be treated as a single « species »

Strengths:

- Conceptually simple
- Mask effect of poor quality data
  - Sequencing error
  - In vitro recombination (chimera)

Weaknesses:

- Limited resolution
- Logically inconsistent definition

Objectives

	Affiliation	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6
OTU1	Species A	0	100	0	45	75	18645
OTU2	Species B	741	0	456	4421	1255	23
OTU3	Species C	12786	45	3	0	0	0
OTU4	Species D	127	4534	80	456	756	108
OTU5	Species E	8766	7578	56	0	0	200

Why FROGS was developed ?

The current processing pipelines struggle to run in a reasonable time.

The most effective solutions are often designed for specialists making access difficult for the whole community.

In this context we developed the pipeline FROGS*: « Find Rapidly OTU with Galaxy Solution ».*

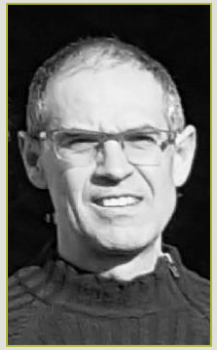
Who is in the FROGS group?

Frédéric ESCUDIÉ

Maria BERNARD

Developers

Lucas AUER



Laurent CAUQUIL

Sylvie COMBES

Guillermina HERNANDEZ-RAQUET

Biology experts

Sarah MAMAN

Galaxy support

Mahendra MARIADASSOU

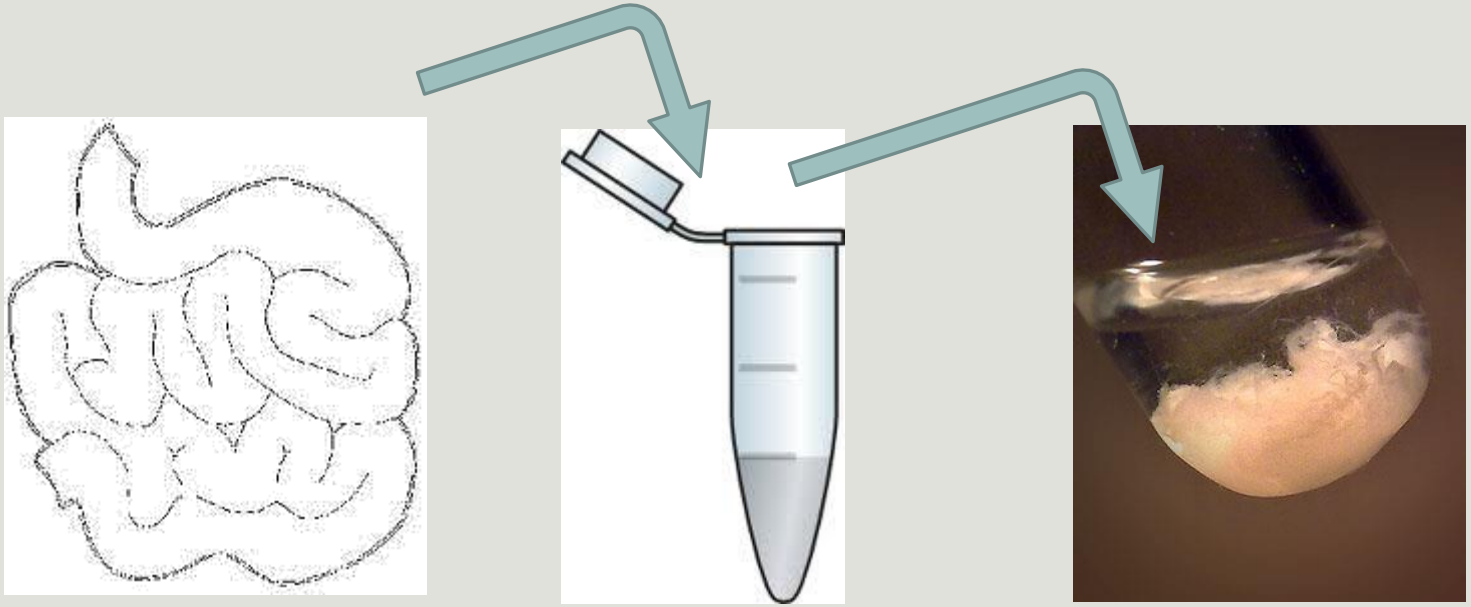
Statistical expert

Géraldine PASCAL

Coordinator

Material

Sample collection and DNA extraction



« Meta-omics » using next-generation sequencing (NGS)

DNA

RNA

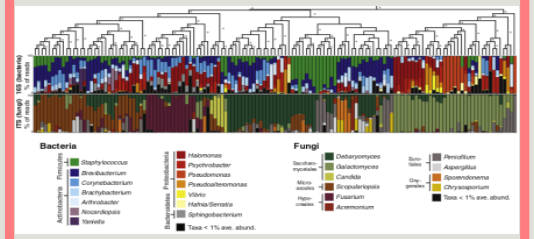
Metagenomics

Metatranscriptomics

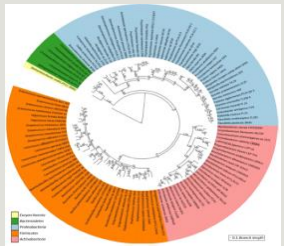
Amplicon sequencing

Shotgun sequencing

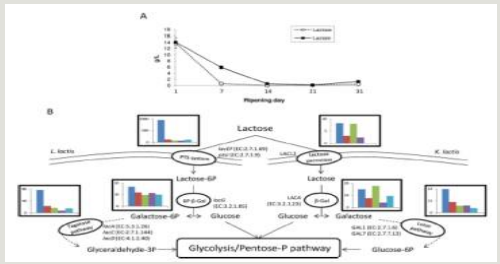
RNA sequencing

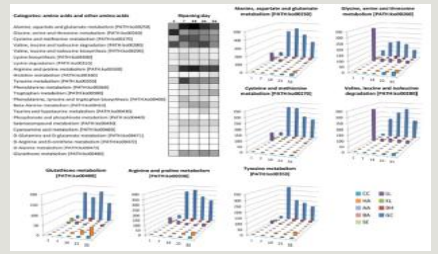


Wolfe *et al.*, 2014



Almeida *et al.*, 2014





Dugat-Bony *et al.*, 2015

Who is here?

What can they do?

What are they doing?

The gene encoding the small subunit of the ribosomal RNA

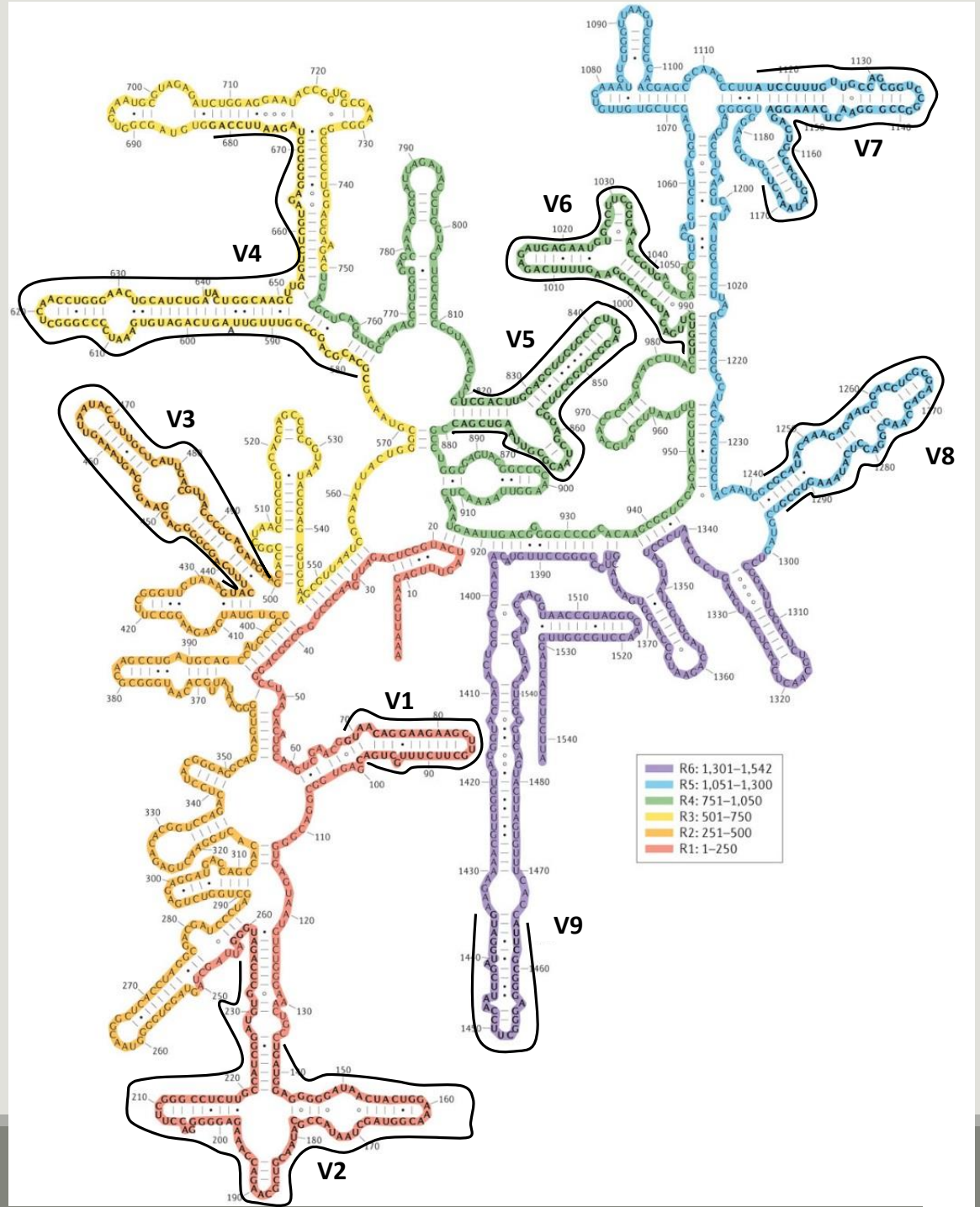
The most widely used gene in **molecular phylogenetic** studies

Ubiquist gene : **16S rDNA** in prokayotes ; **18S rDNA** in eukaryotes

Gene encoding a ribosomal RNA : non-coding RNA (not translated), part of the small subunit of the ribosome which is responsible for the translation of mRNA in proteins

Not submitted to lateral gene transfer

Availability of databases facilitating comparison
(Silva 2015: >22000 type strains)

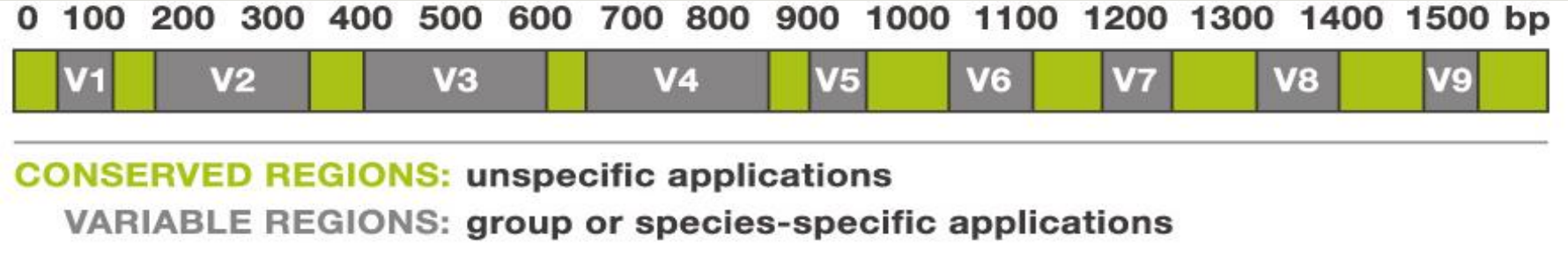


Secondary structure of the 16S rRNA of *Escherichia coli*

In red, fragment R1 including regions V1 and V2;
in orange, fragment R2 including region V3;
in yellow, fragment R3 including region V4;
in green, fragment R4 including regions V5 and V6;
in blue, fragment R5 including regions V7 and V8;
and in purple, fragment R6 including region V9.

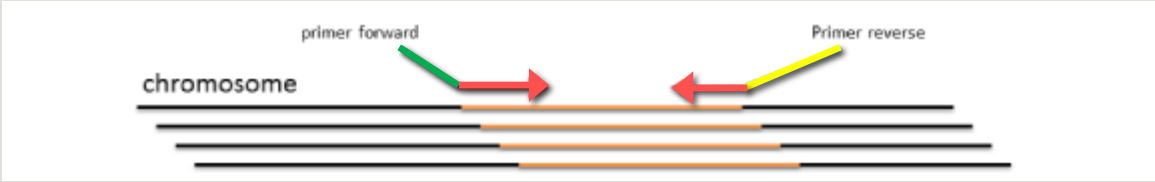
Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences
Pablo Yarza, et al.
Nature Reviews Microbiology 12, 635–645 (2014) doi:10.1038/nrmicro3330

The gene encoding the small subunit of the ribosomal RNA

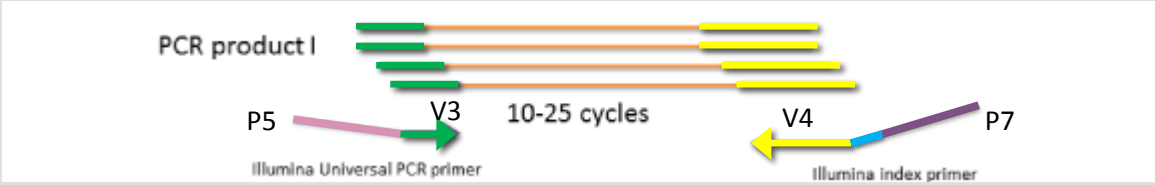


Steps for Illumina sequencing

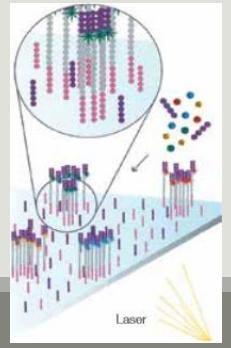
- 1st step : one PCR

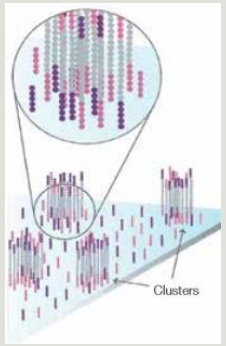


- 2nd step: one PCR



- 3rd step: on flow cell, the cluster generations
- 4th step: sequencing





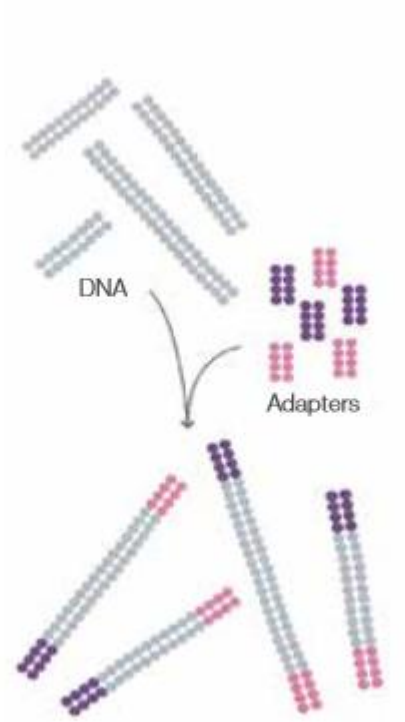
Amplification and sequencing

« Universal » primer sets are used for **PCR amplification** of the phylogenetic biomarker

The primers contain adapters used for the sequencing step and barcodes (= tags = MIDs) to distinguish the samples (multiplexing = sequencing several samples on the same run)

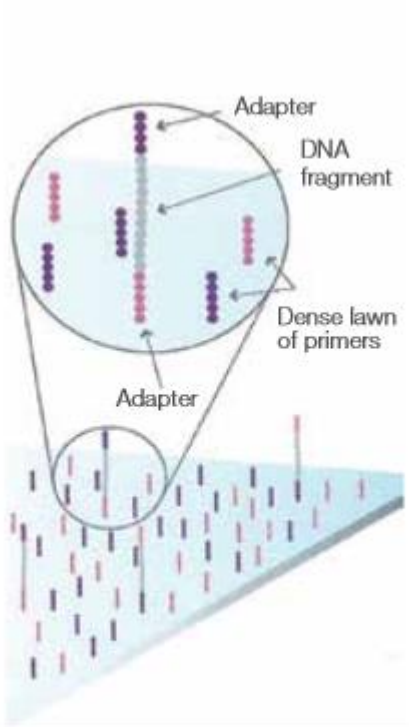
Cluster generation

Prepare Genomic DNA Sample



Randomly fragment genomic DNA and ligate adapters to both ends of the fragments.

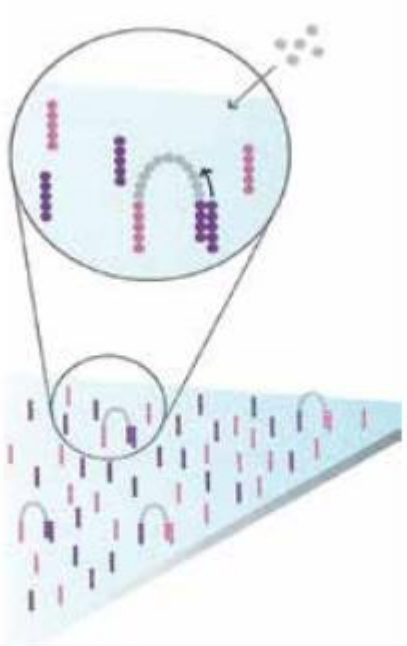
Attach DNA to Surface



Bind single-stranded fragments randomly to the inside surface of the flow cell channels.

Attach DNA to surface

Bridge Amplification

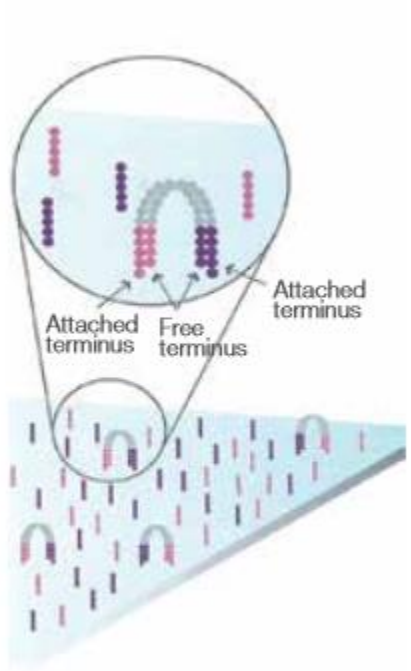


Add unlabeled nucleotides and enzyme to initiate solid-phase bridge amplification.

Bridge amplification

Cluster generation

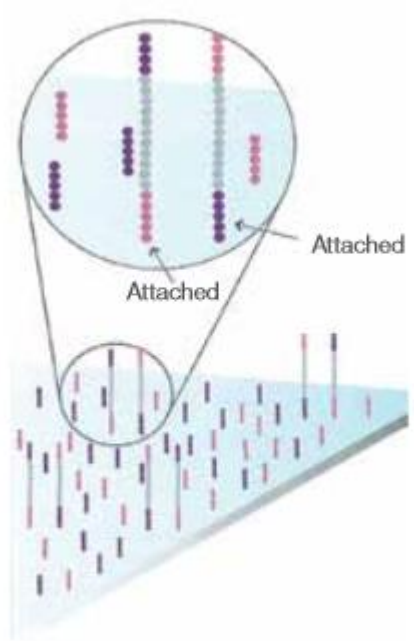
Fragments Become Double Stranded



The enzyme incorporates nucleotides to build double-stranded bridges on the solid-phase substrate.

Fragments become double stranded

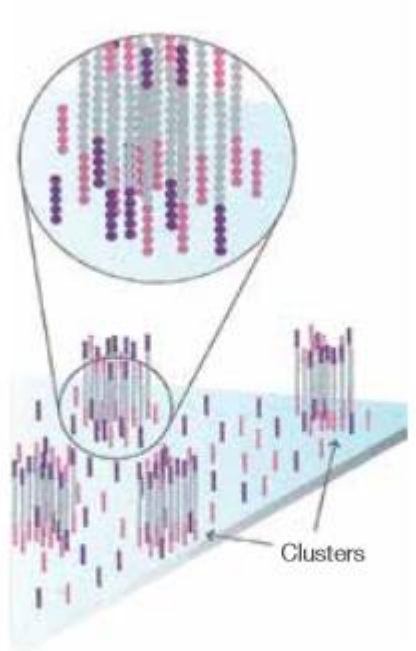
Denature the Double-Stranded Molecules



Denaturation leaves single-stranded templates anchored to the substrate.

Denature the double-stranded molecule

Complete Amplification

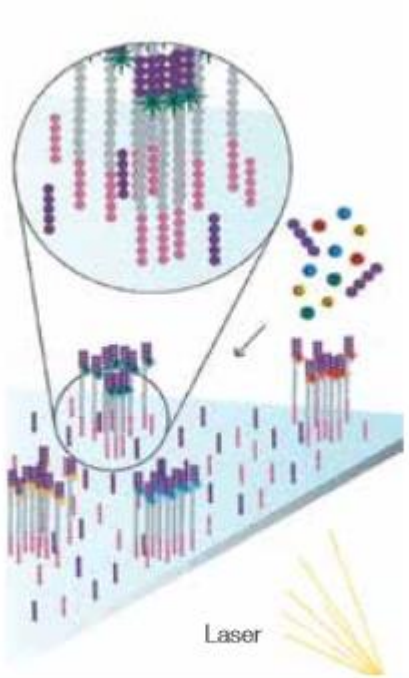


Several million dense clusters of double-stranded DNA are generated in each channel of the flow cell.

Cycle of new strand synthesis and denaturation to make multiple copies of the same sequence (amplification)
Reverse strands are washed

Sequencing by synthesis

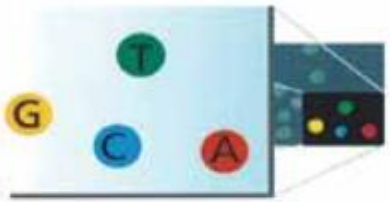
Determine First Base



The first sequencing cycle begins by adding four labeled reversible terminators, primers, and DNA polymerase.

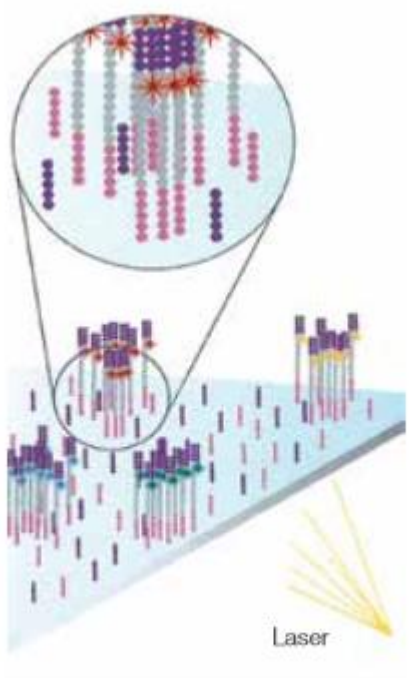
Light signal is more strong in cluster

Image First Base



After laser excitation, the emitted fluorescence from each cluster is captured and the first base is identified.

Determine Second Base



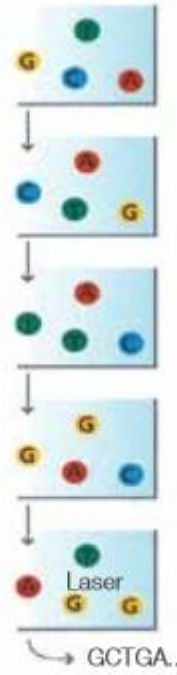
The next cycle repeats the incorporation of four labeled reversible terminators, primers, and DNA polymerase.

Sequencing by synthesis

Image Second Chemistry Cycle

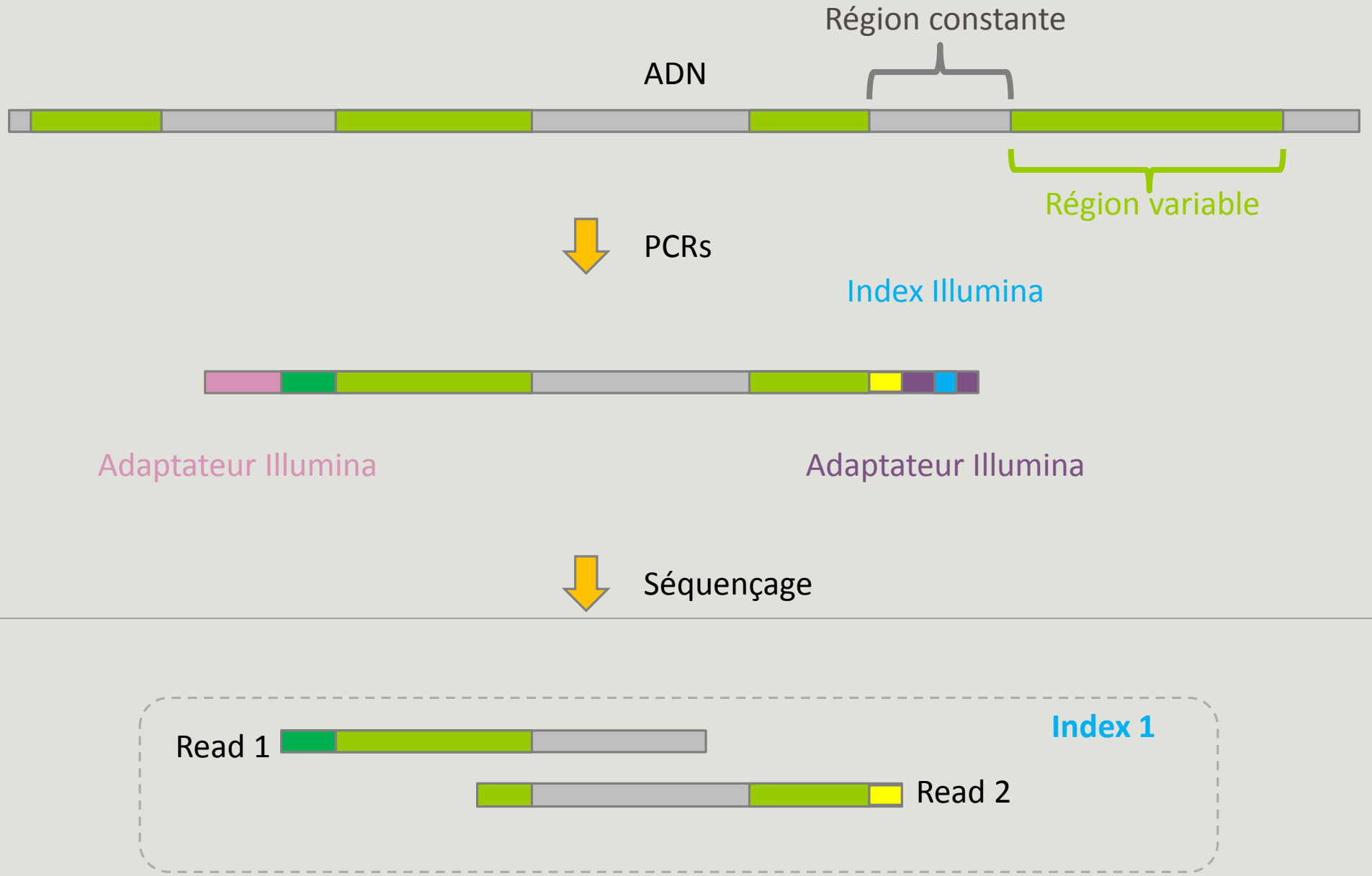
After laser excitation, the image is captured as before, and the identity of the second base is recorded.

Sequencing Over Multiple Chemistry Cycles

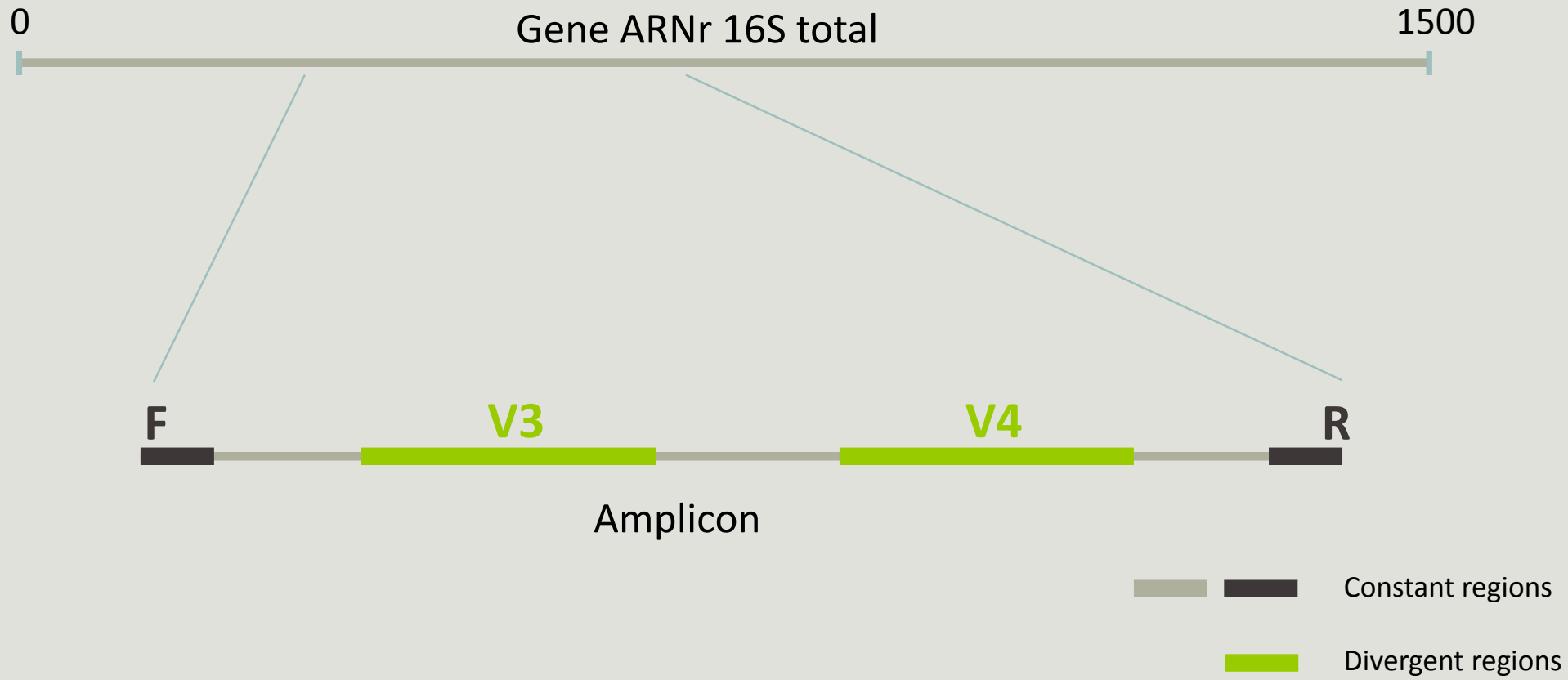


The sequencing cycles are repeated to determine the sequence of bases in a fragment, one base at a time.

Barcode is read, so cluster is identified.
After first sequencing (250 or 300 nt of Reverse strand), fragment form bridges again and Forward strand can be sequenced also.


Région constante
ADN
Région variable
PCRs
Index Illumina
Adaptateur Illumina
Adaptateur Illumina
Séquençage
Index 1
Read 1
Read 2

Identification of bacterial populations may be not discriminating



Amplification and sequencing

Sequencing is generally perform on **Roche-454** or **Illumina MiSeq** platforms.

Roche-454 generally produce ~ 10 000 reads per sample

MiSeq ~ 30 000 reads per sample

Sequence length is **>650 bp** for pyrosequencing technology (Roche-454) and **2 x 300 bp** for the MiSeq technology in paired-end mode.

Methods

Which bioinformatics solutions ?

	Disadvantages
QIIME	Installation problem Command lines
UPARSE	Global clustering command lines
MOTHUR	Not MiSeq data without normalization Global hierarchical clustering Command lines
MG-RAST	No modularity No transparence

FROGS
Find Rapdly OTU with Galaxy Solution

QIIME allows analysis of high-throughput community sequencing data
J Gregory Caporaso et al, Nature Methods, 2010; doi:10.1038/nmeth.f.303
Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities.
Schloss, P.D., et al., Appl Environ Microbiol, 2009, doi: 10.1128/AEM.01541-09

UPARSE: Highly accurate OTU sequences from microbial amplicon reads
Edgar, R.C. et al, *Nature Methods*, 2013, dx.doi.org/10.1038/nmeth.2604
The metagenomics RAST server – a public resource for the automatic phylogenetic and functional analysis of metagenomes
F Meyer et al, BMC Bioinformatics, 2008, doi:10.1186/1471-2105-9-386

FROGS ?

Use platform Galaxy

Set of modules = Tools to analyze your “big” data

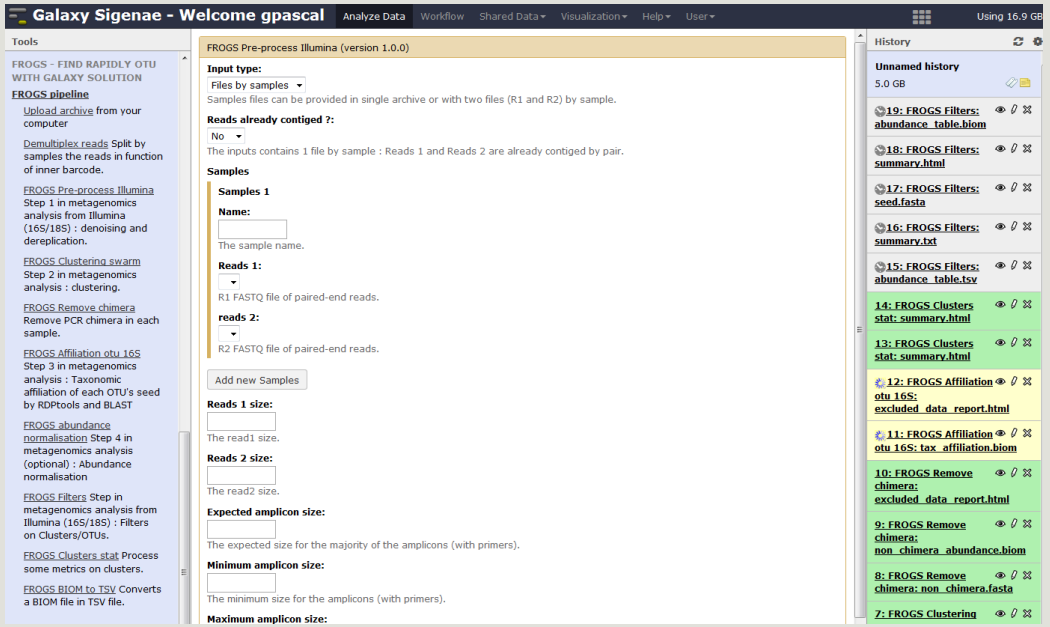
Independent modules

Run on Illumina/454 data 16S, 18S, and 23S

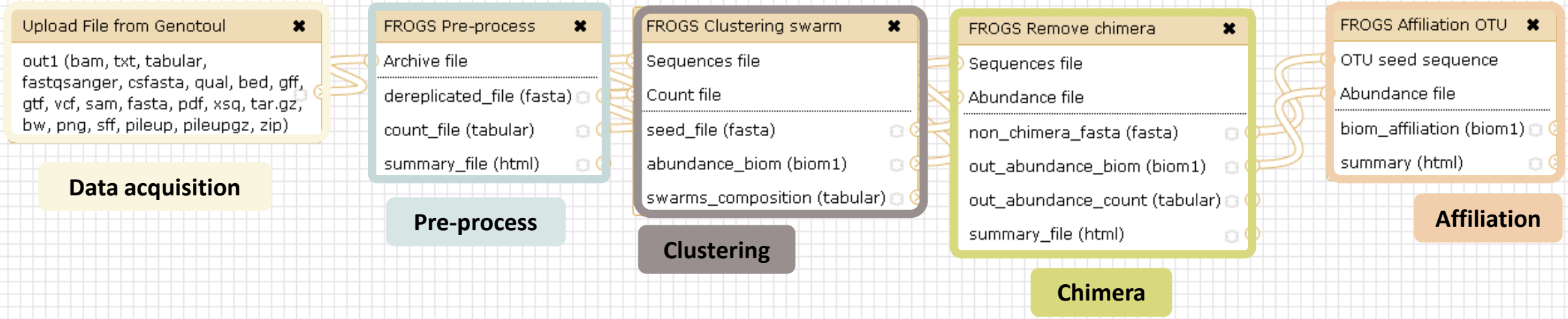
New clustering method

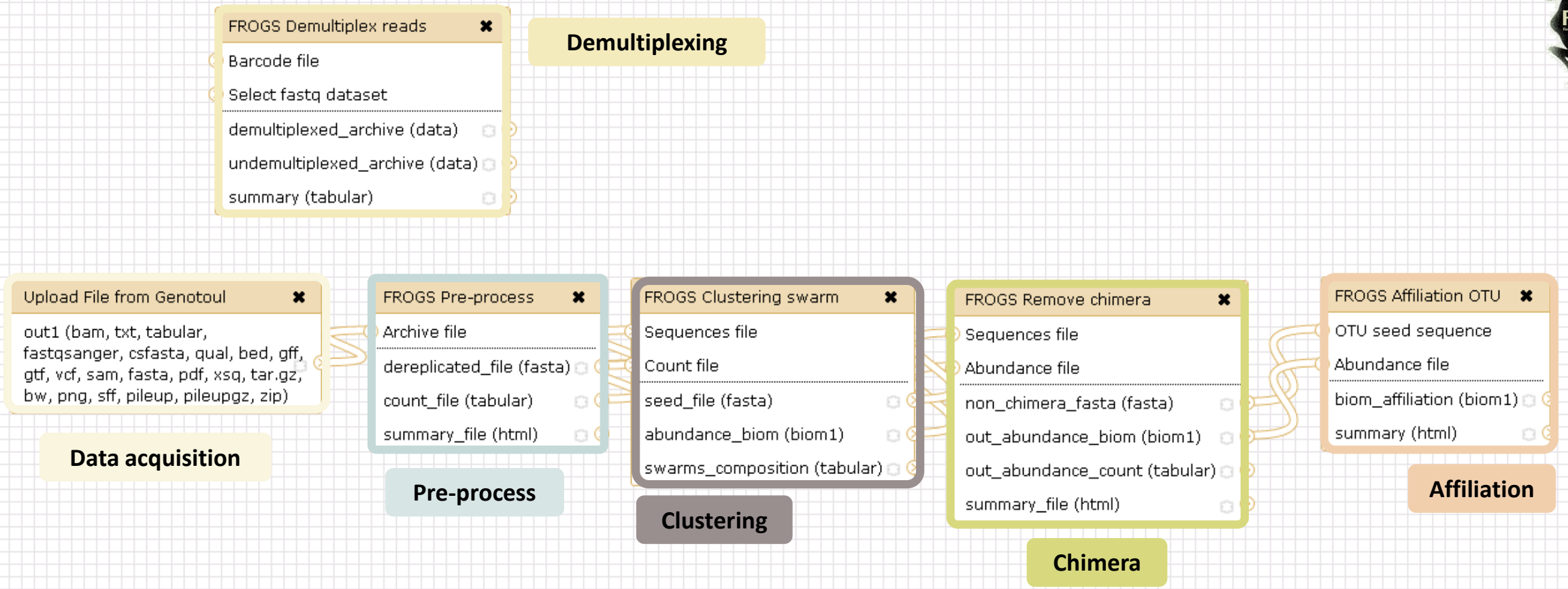
Many graphics for interpretation

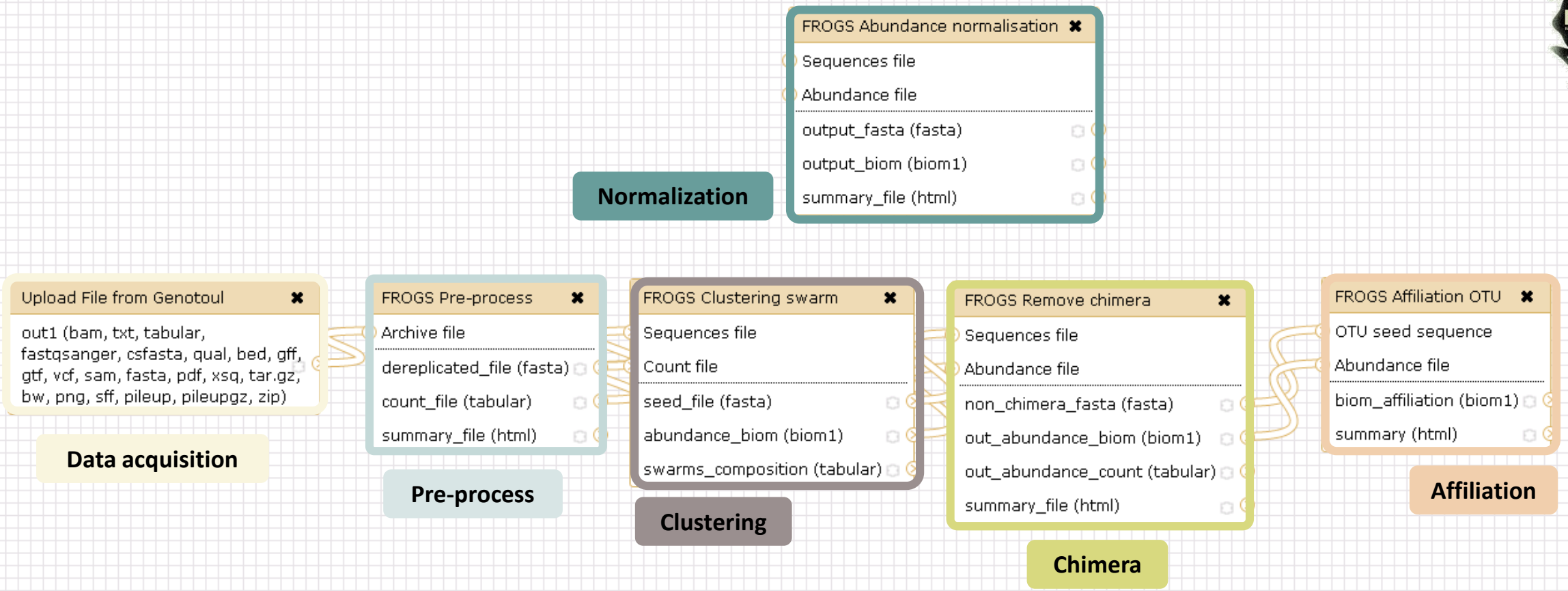
User friendly, hiding bioinformatics infrastructure/complexity



FROGS Pipeline




FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation


FROGS Abundance normalisation
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
summary_file (html)
Normalization
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
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FROGS Pre-process
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swarms_composition (tabular)
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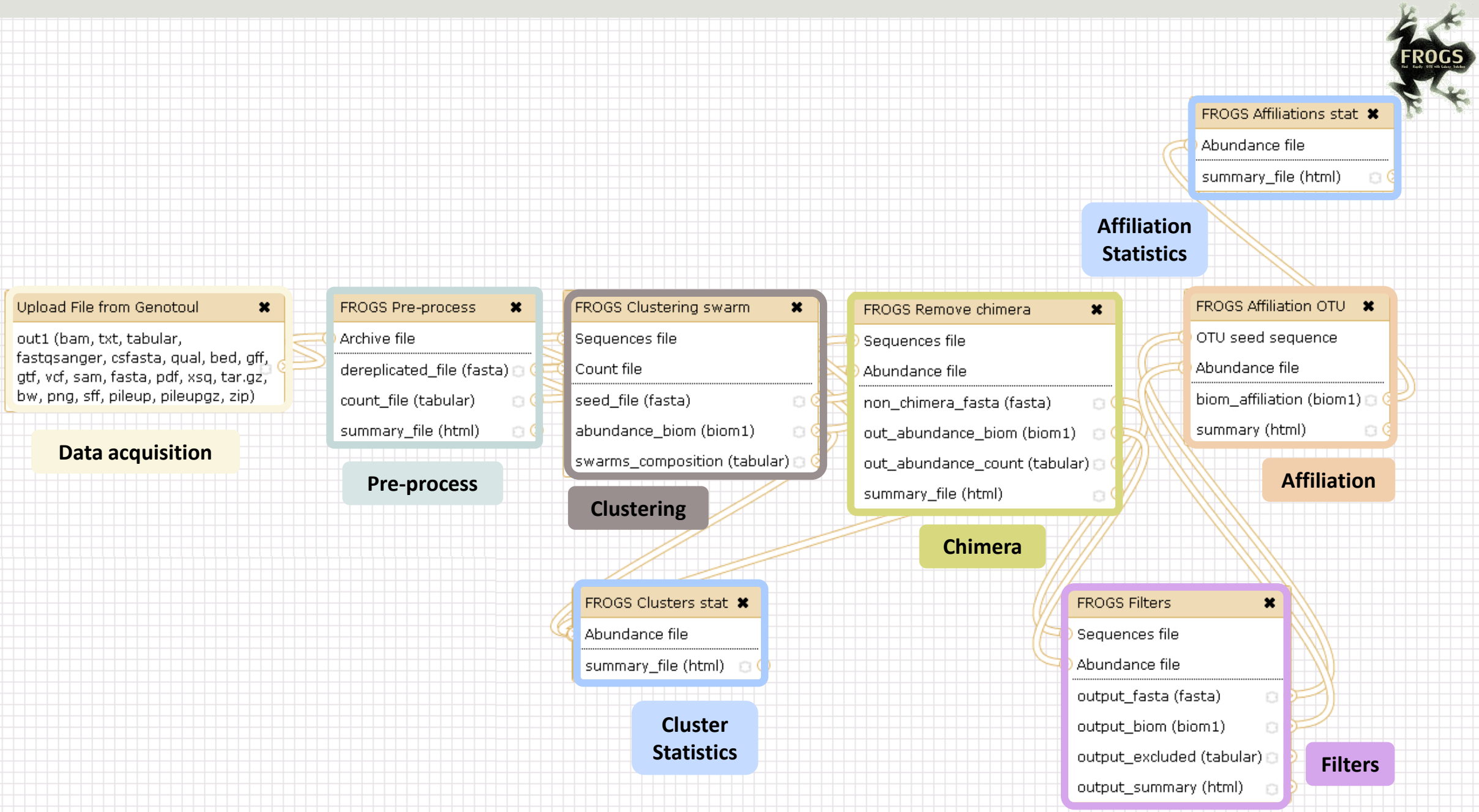
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation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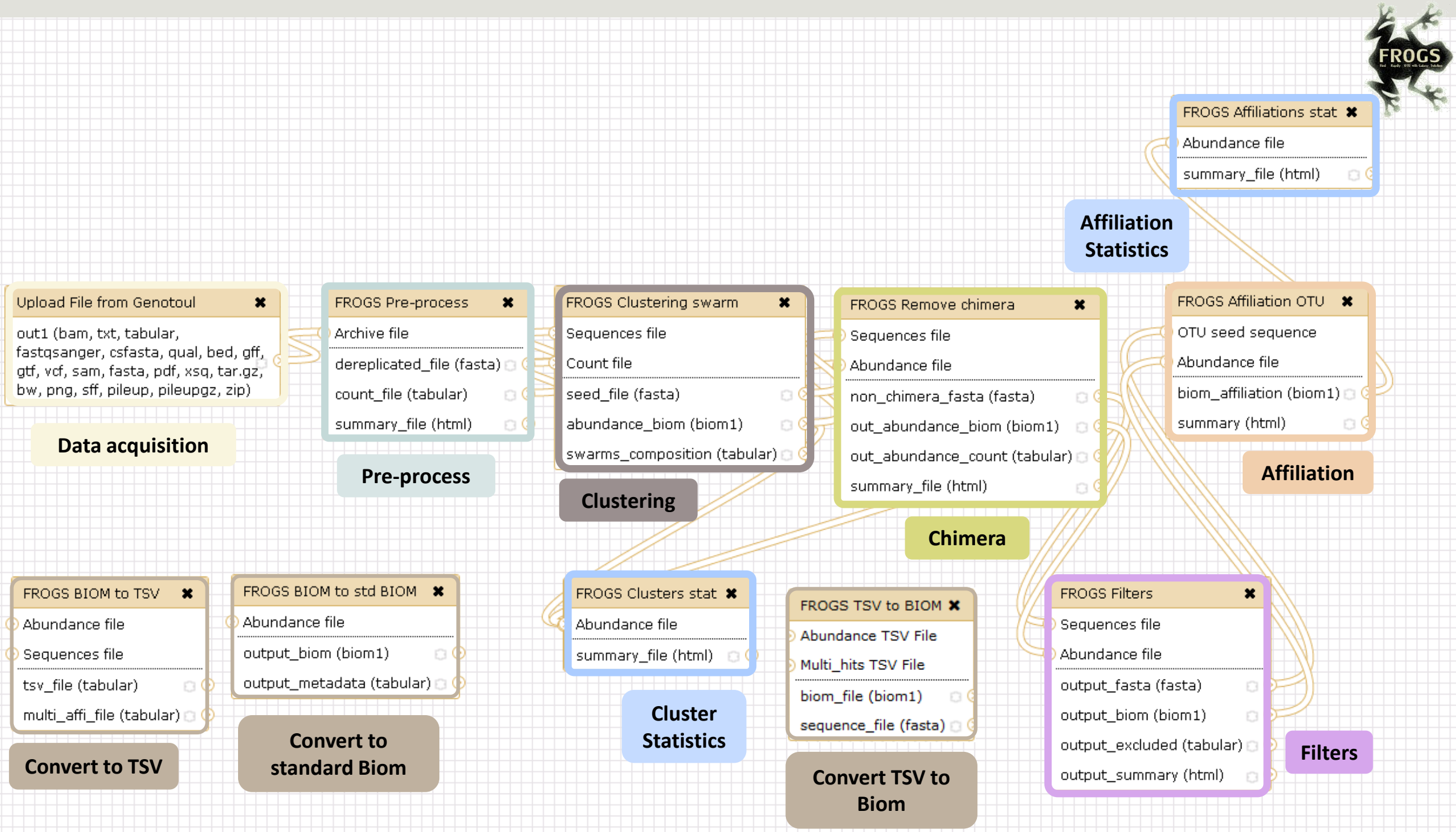
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliations stat
Abundance file
summary_file (html)
Affiliation Statistics
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters


Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
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Sequences file
Count file
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FROGS Remove chimera
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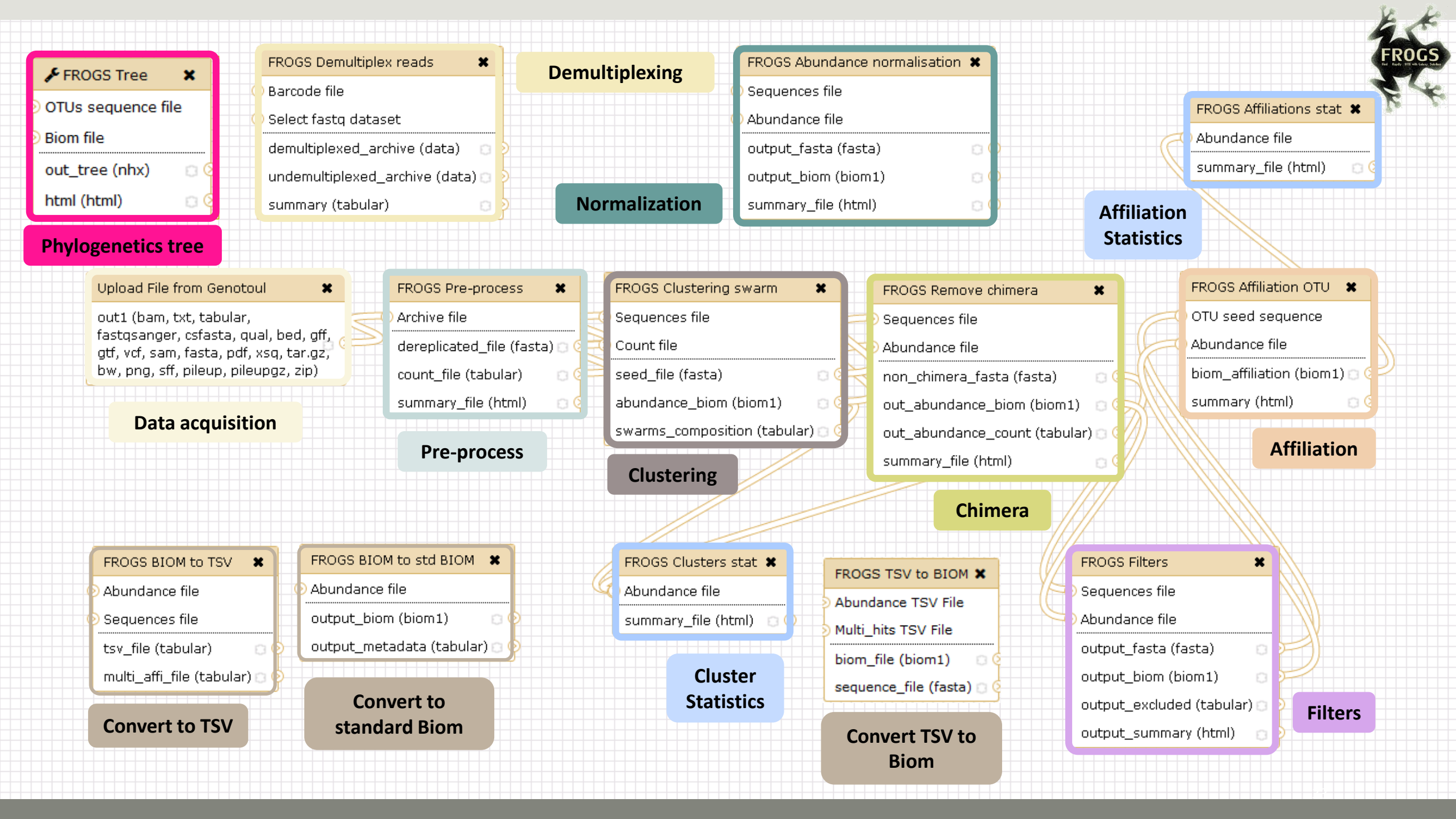
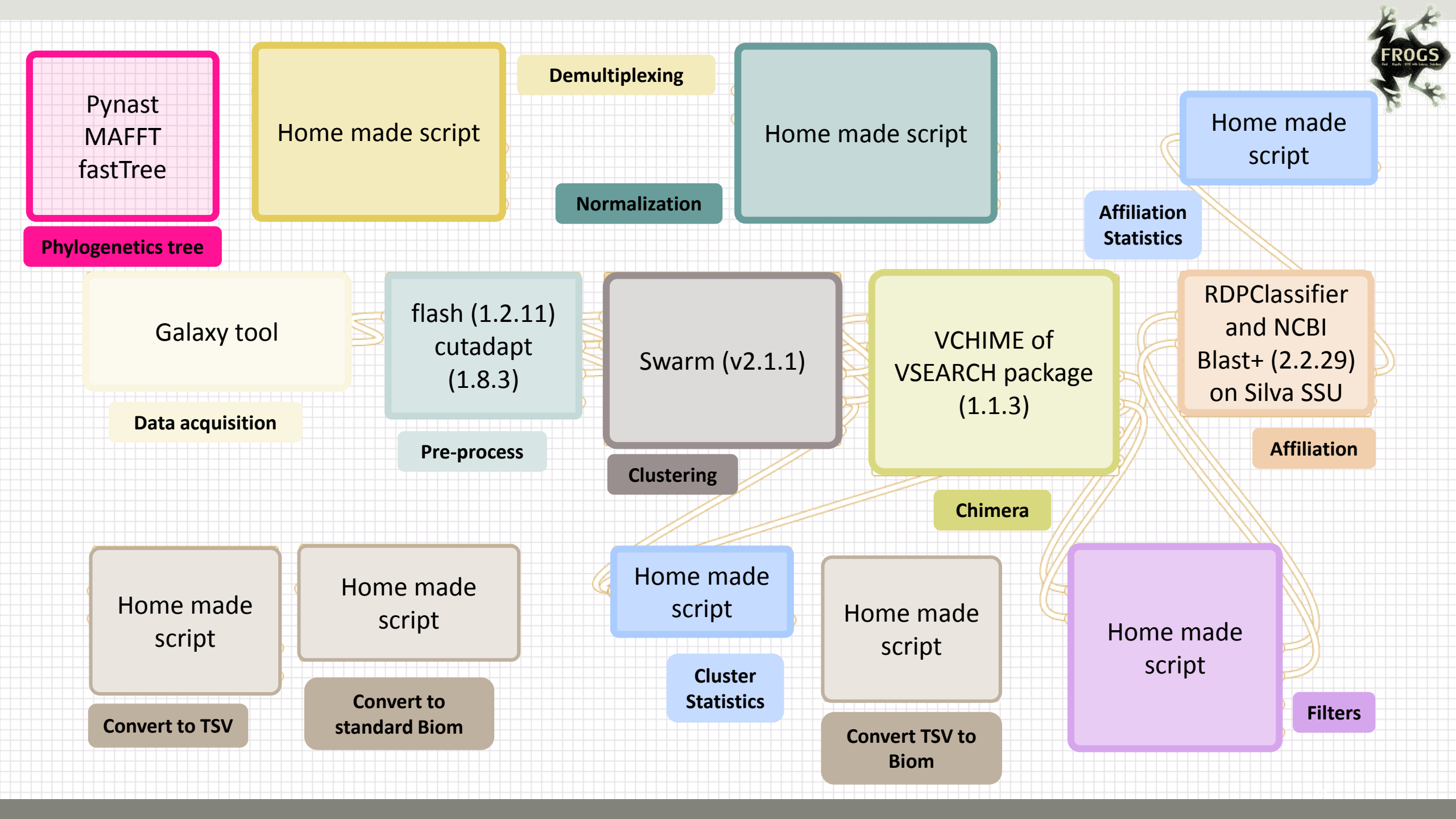
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliations stat
Abundance file
summary_file (html)
Affiliation Statistics
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
Convert to TSV
FROGS BIOM to std BIOM
Abundance file
output_biom (biom1)
output_metadata (tabular)
Convert to standard Biom
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS TSV to BIOM
Abundance TSV File
Multi_hits TSV File
biom_file (biom1)
sequence_file (fasta)
Convert TSV to Biom
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters

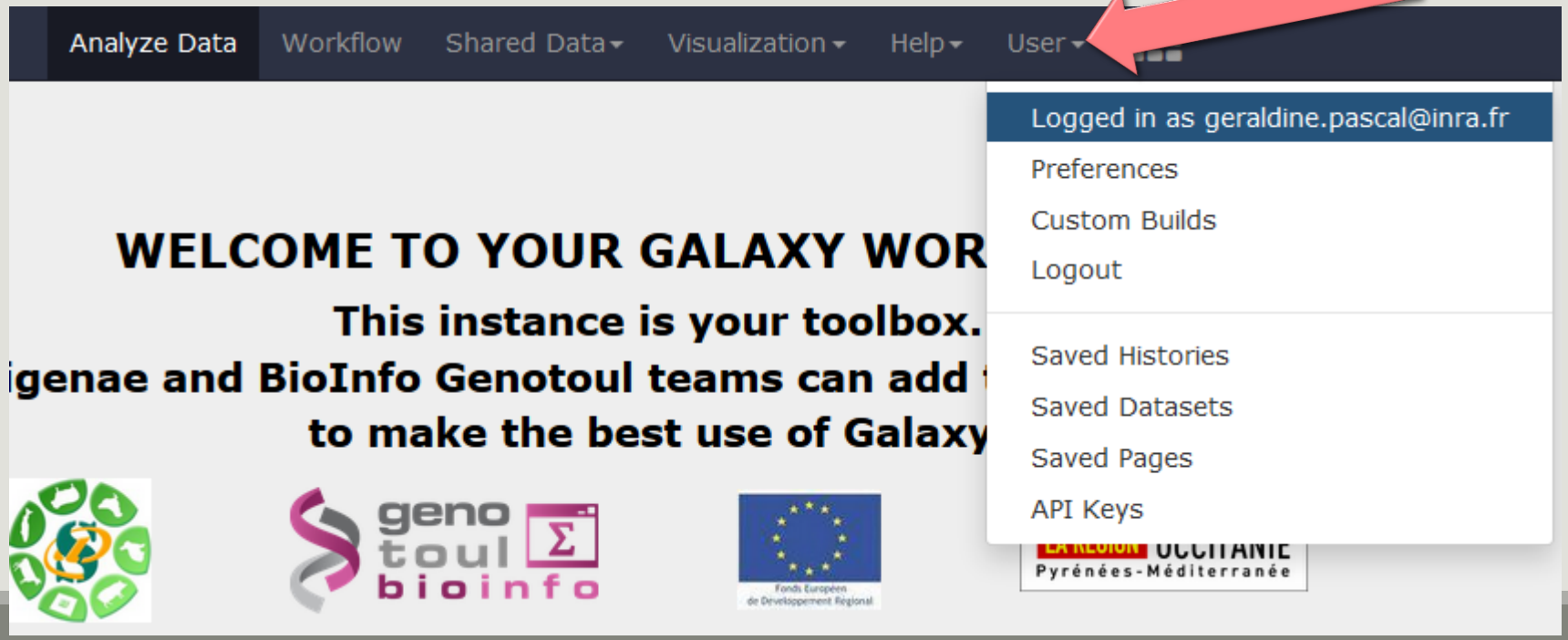

FROGS Tree
OTUs sequence file
Biom file
out_tree (nhx)
html (html)
Phylogenetics tree
FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
FROGS Abundance normalisation
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
summary_file (html)
Normalization
FROGS Affiliations stat
Abundance file
summary_file (html)
Affiliation Statistics
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
Convert to TSV
FROGS BIOM to std BIOM
Abundance file
output_biom (biom1)
output_metadata (tabular)
Convert to standard Biom
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS TSV to BIOM
Abundance TSV File
Multi_hits TSV File
biom_file (biom1)
sequence_file (fasta)
Convert TSV to Biom
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters


Pynast
MAFFT
fastTree
Phylogenetics tree
Home made script
Demultiplexing
Normalization
Home made script
Home made script
Affiliation Statistics
Galaxy tool
Data acquisition
flash (1.2.11)
cutadapt
(1.8.3)
Pre-process
Swarm (v2.1.1)
Clustering
VCHIME of
VSEARCH package
(1.1.3)
Chimera
RDPClassifier
and NCBI
Blast+ (2.2.29)
on Silva SSU
Affiliation
Home made script
Convert to TSV
Home made script
Convert to standard Biom
Home made script
Cluster Statistics
Home made script
Convert TSV to Biom
Home made script
Filters

Together go to visit FROGS

In your internet browser (Firefox, chrome, Internet explorer) :

http://sigenae-workbench.toulouse.inra.fr/




Galaxy
Analyze Data
Workflow
MAIN MENU
Help
User
Using 78.6 G
Tools
METAGENOMICS
FROGS - Find Rapidly Otu with Galaxy Solution
FROGS Demultiplex reads Split by samples the reads in function of inner barcode.
FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication.
FROGS Clustering swarm Step 2 in metagenomics analysis : clustering.
FROGS Remove chimera Step 3 in metagenomics analysis :
FROGS Affiliation OTU Step 4 in metagenomics analysis : Taxonomic affiliation of each OTU's seed by RDPtools and BLAST
FROGS Clusters stat Process some metrics on clusters.
FROGS Affiliations stat Process some metrics on taxonomies.
FROGS BIOM to std BIOM Converts a FROGS BIOM in fully compatible BIOM.
FROGS BIOM to TSV Converts a BIOM file in TSV file.
FROGS TSV to BIOM Converts a TSV file in BIOM file.
FROGS Abundance normalisation
AVAILABLE TOOLS
FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication. (Galaxy Version 1.5.0)
Options
Sequencer
Illumina
Select the sequencer family used to produce the sequences.
Input type
Files by samples
Samples files can be provided in single archive or with two files (R1 and R2) by sample.
Reads already contiged ?
No
The inputs contain 1 file by sample : Reads 1 and Reads 2 are already contiged by pair.
Samples
1: Samples
Name
The sample name.
Reads 1
No fastq dataset available.
R1 FASTQ file of paired-end reads.
reads 2
No fastq dataset available.
R2 FASTQ file of paired-end reads.
Insert Samples
Reads 1 size
The read1 size.
Reads 2 size
The read2 size.
Expected amplicon size
TOOL CONFIGURATION AND EXECUTION
History
search datasets
Hantagulumic
29 shown, 14 deleted
20.42 MB
43: FROGS BIOM to std BIOM: blast_metadata.tsv
42: FROGS BIOM to std BIOM: abundance.biom
41: FROGS Abundance normalisation: normalized.biom
40: FROGS Abundance normalisation: normalized.biom
39: FROGS Abundance normalisation: normalized.fasta
38: FROGS Abundance normalisation: report.html
37: FROGS Abundance normalisation: normalized.biom
36: FROGS Abundance normalisation: normalized.fasta
30: FROGS BIOM to TSV: multi_hits.tsv
29: FROGS BIOM to TSV: abundance.tsv
23: FROGS Affiliation OTU:
DATASETS HISTORY

Demultiplexing

Pre-process

Clustering

Chimera

Filters

Affiliation

Cluster Stat

Affiliation Stat

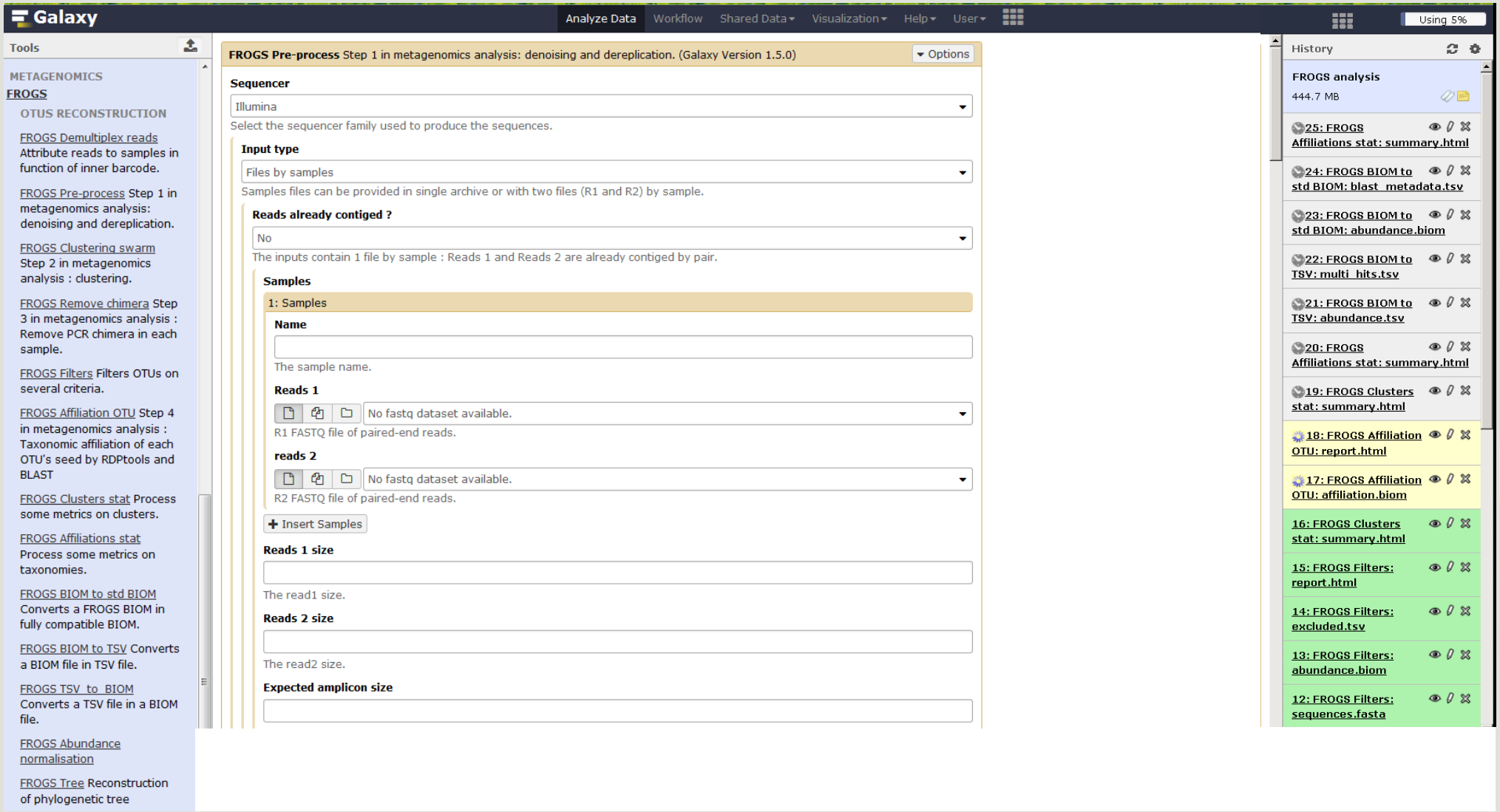
Biom to std Biom

Biom to TSV

TSV to Biom

Normalization

Phylogenetics Tree

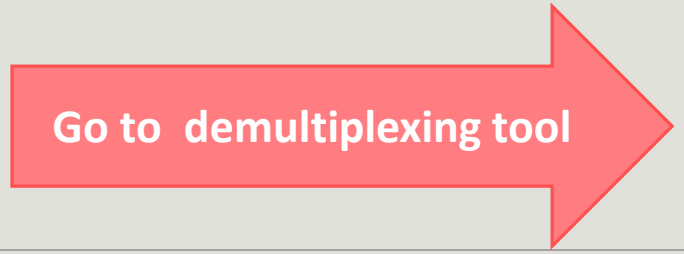


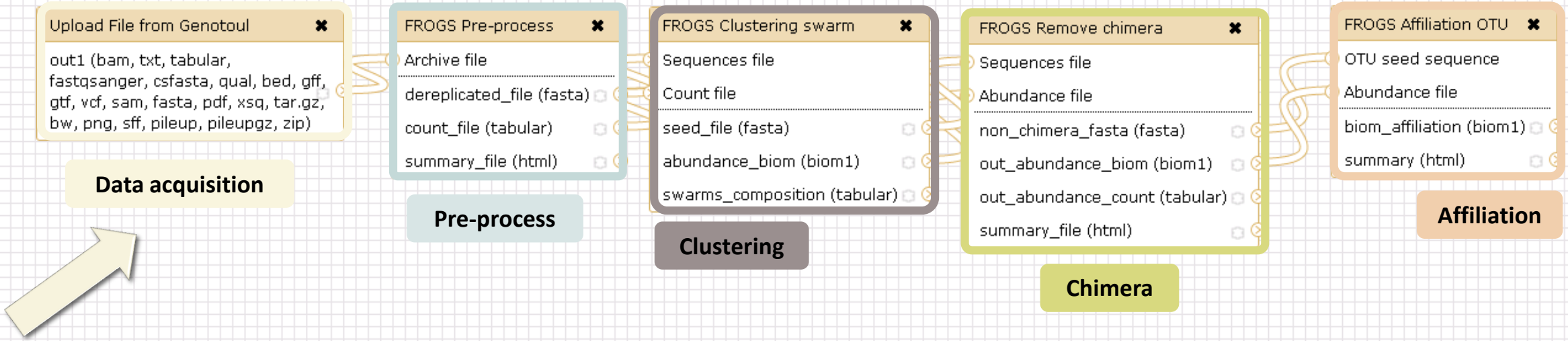
Waiting to run

Currently running

Result files

Upload data




Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
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seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation

What kind of data ?

4 Upload → 4 Histories

Multiplexed data

Pathobiomes rodents and ticks

multiplex.fastq

barcode_forward.tabular

454 data

Freshwater sediment metagenome

454.fastq.gz

SRA number

- SRR443364

MiSeq
R1 fastq + R2 fastq

Farm animal feces metagenome

sampleA_R1.fastq

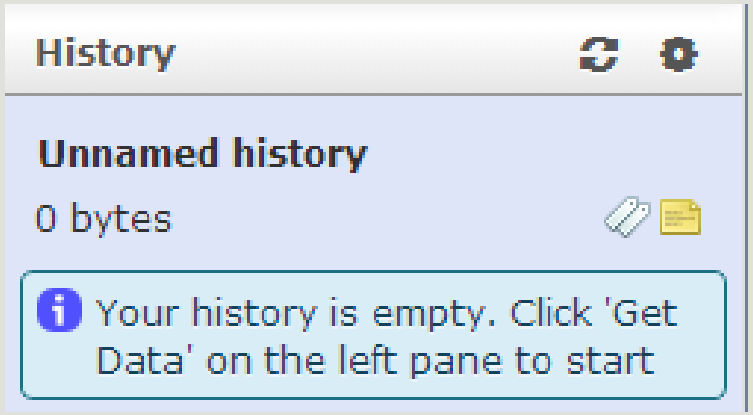
sampleA_R2.fastq

MiSeq merged fastq in archive tar.gz

Farm animal feces metagenome

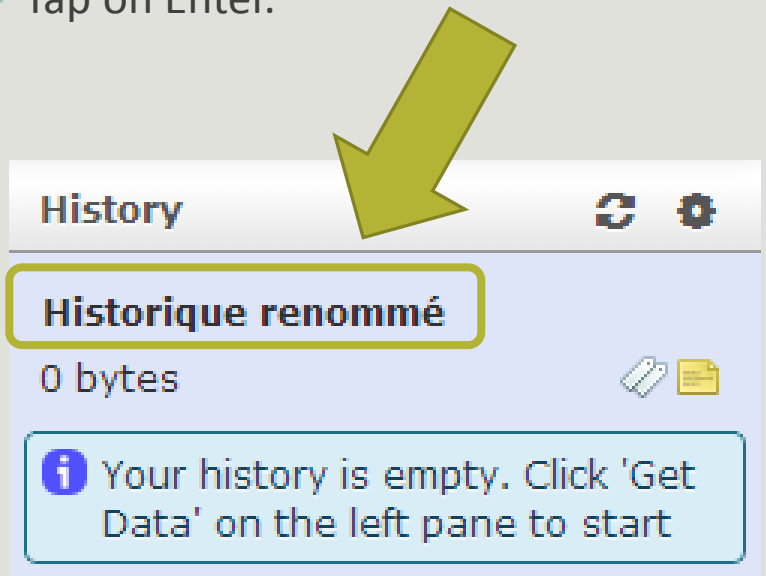
100spec_90000seq_9samples.tar.gz

1ST CONNEXION



RENAME HISTORY

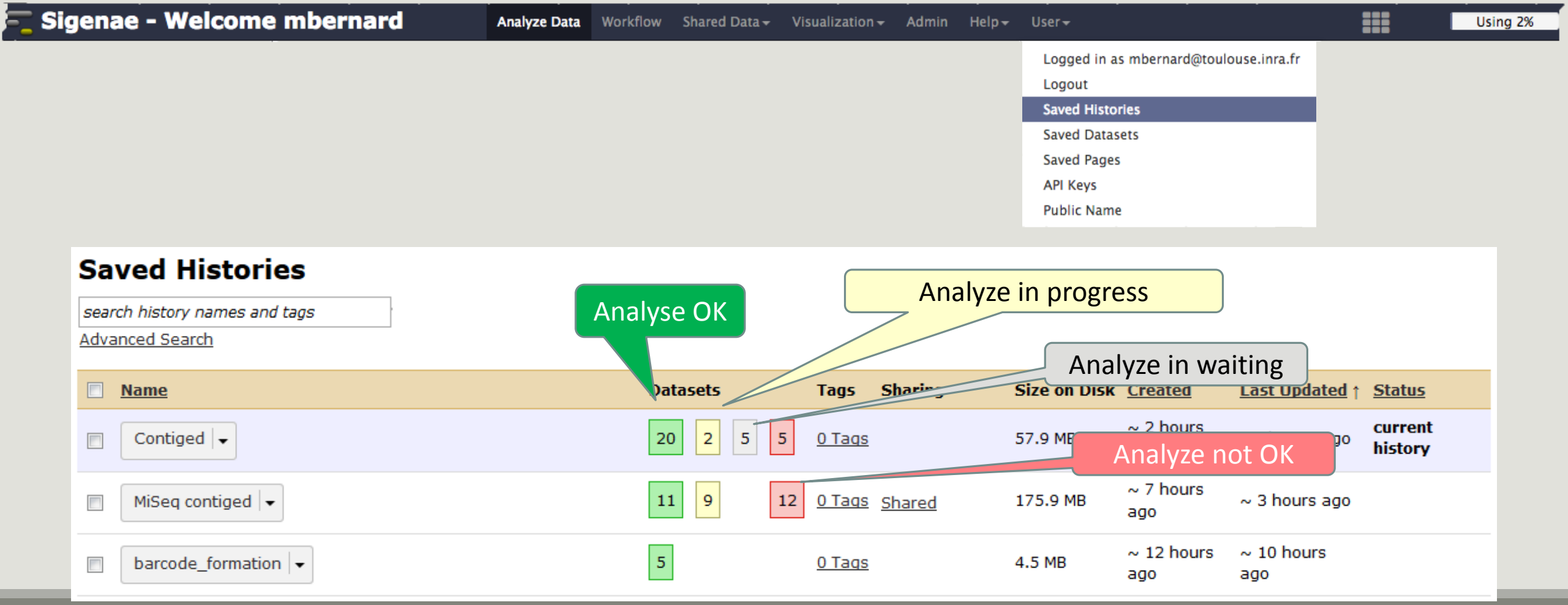
- click on Unnamed history,
- Write your new name,
- Tap on Enter.



History gestion

- Keep all steps of your analysis.
- Share your analyzes.
- At each run of a tool, a new dataset is created. The data are not overwritten.
- Repeat, as many times as necessary, an analysis.
- All your logs are automatically saved.
- Your published histories are accessible to all users connected to Galaxy (Shared Data / Published Histories).
- Shared histories are accessible only to a specific user (History / Option / Histories Shared With Me).
- To share or publish a history: User / Saved histories / Click the history name / Share or Publish

Saved Histories



Your turn! - 1

LAUNCH UPLOAD TOOLS

Accounts:








- anemone
- arome
- aster
- bleuet
- camelia
- capucine
- chardon
- clematite
- cobee
- coquelicot
- cosmos
- Password: f1o2r3!

Your turn: exo 1

Create the 1st history **multiplexed**

Import files « **multiplex.fastq** » and « **barcode_forward.tabular** » present in the **Genotoul** folder /work/formation/FROGS/

Create the 2nd history **454**

Import file « **454.fastq.gz** » present in the **Genotoul** folder /work/formation/FROGS/
(datatype fastq or fastq.gz is the same !)

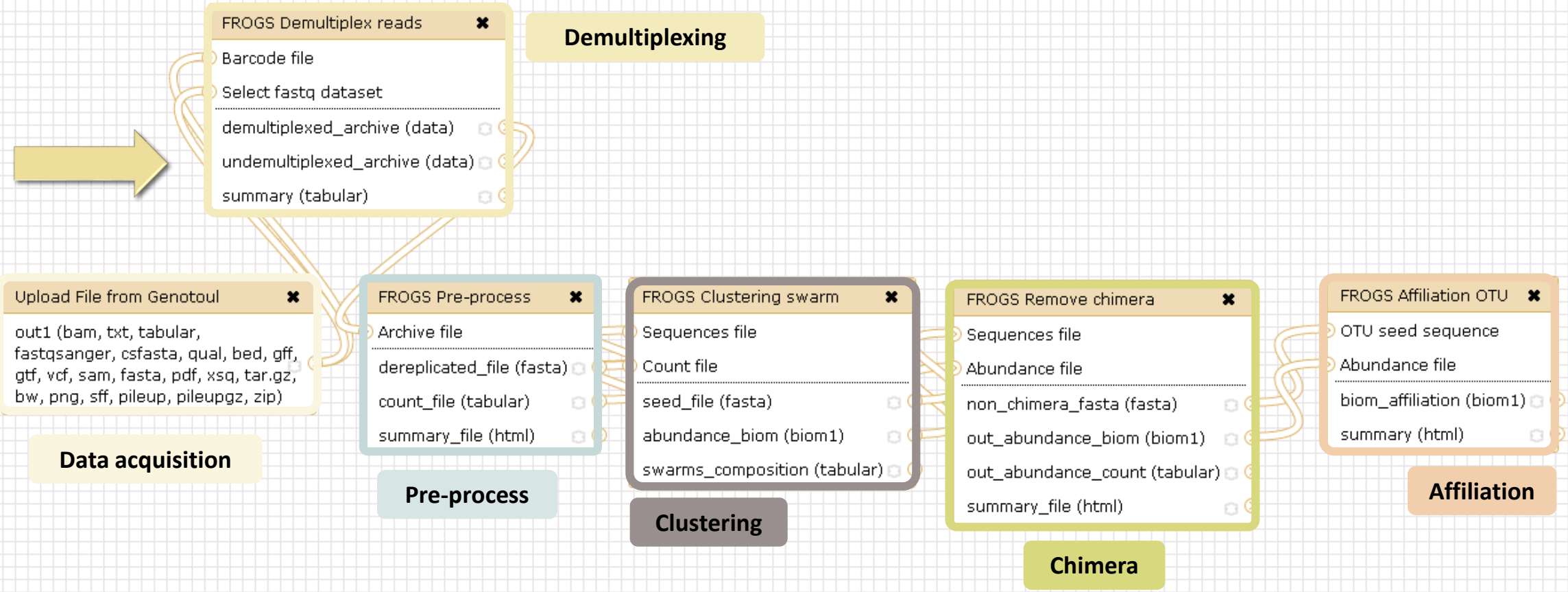
Create the 3rd history **MiSeq R1 R2**

Import files « **sampleA_R1.fastq** » and « **sampleA_R2.fastq** » present in the **Genotoul** folder /work/formation/FROGS/

Create the 4th history **MiSeq merged**

Import archive file « **100spec_90000seq_9samples.tar.gz** » present in the **Genotoul** folder /work/formation/FROGS/

Demultiplexing tool


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
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FROGS Pre-process
Archive file
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count_file (tabular)
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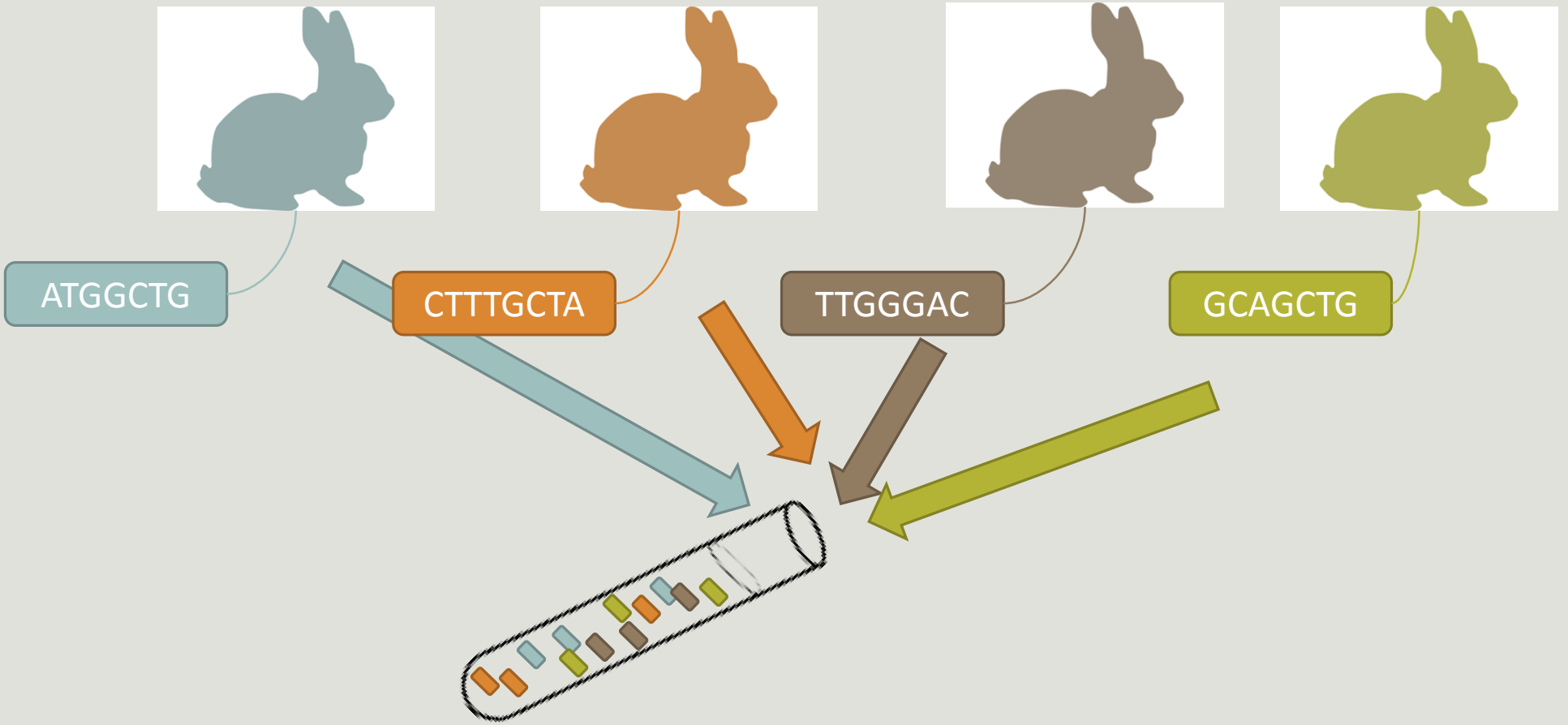
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation

Barcoding ?



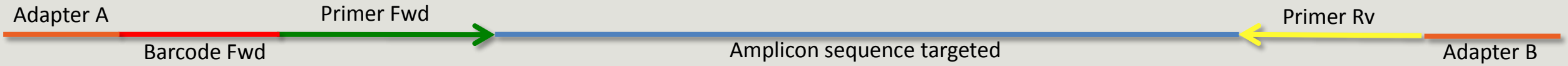
Demultiplexing

Sequence demultiplexing in function of barcode sequences :

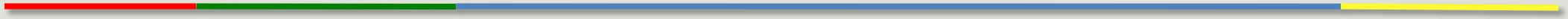
- In forward
- In reverse
- In forward and reverse

Remove unbarcoded or ambiguous sequences

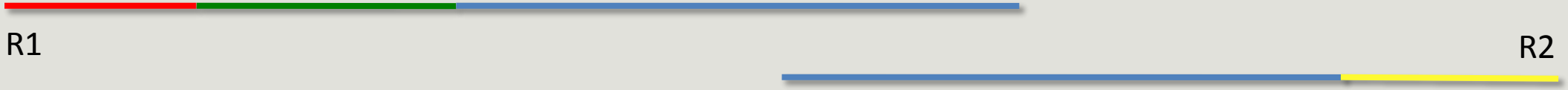
Demultiplexing forward



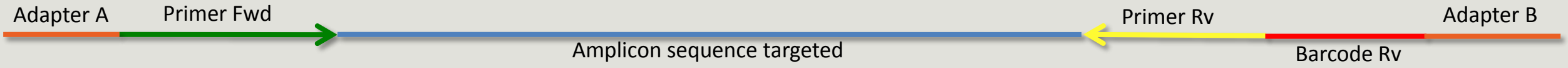
Single-end sequencing



Paired-end sequencing

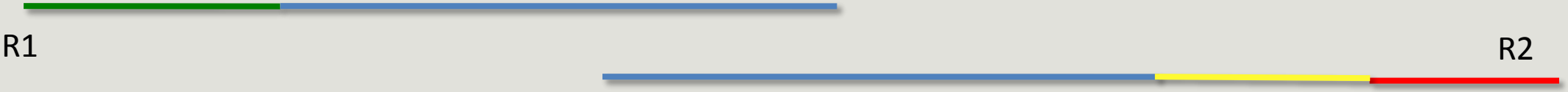


Demultiplexing reverse

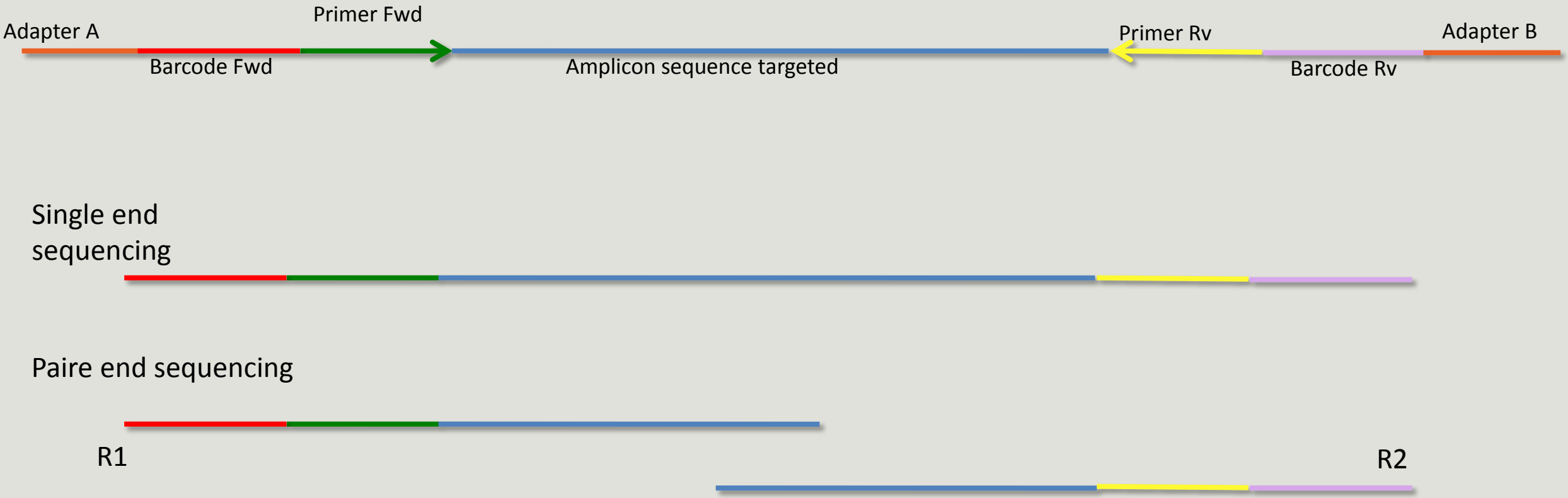


Single end sequencing

Paire end sequencing



Demultiplexing forward and reverse

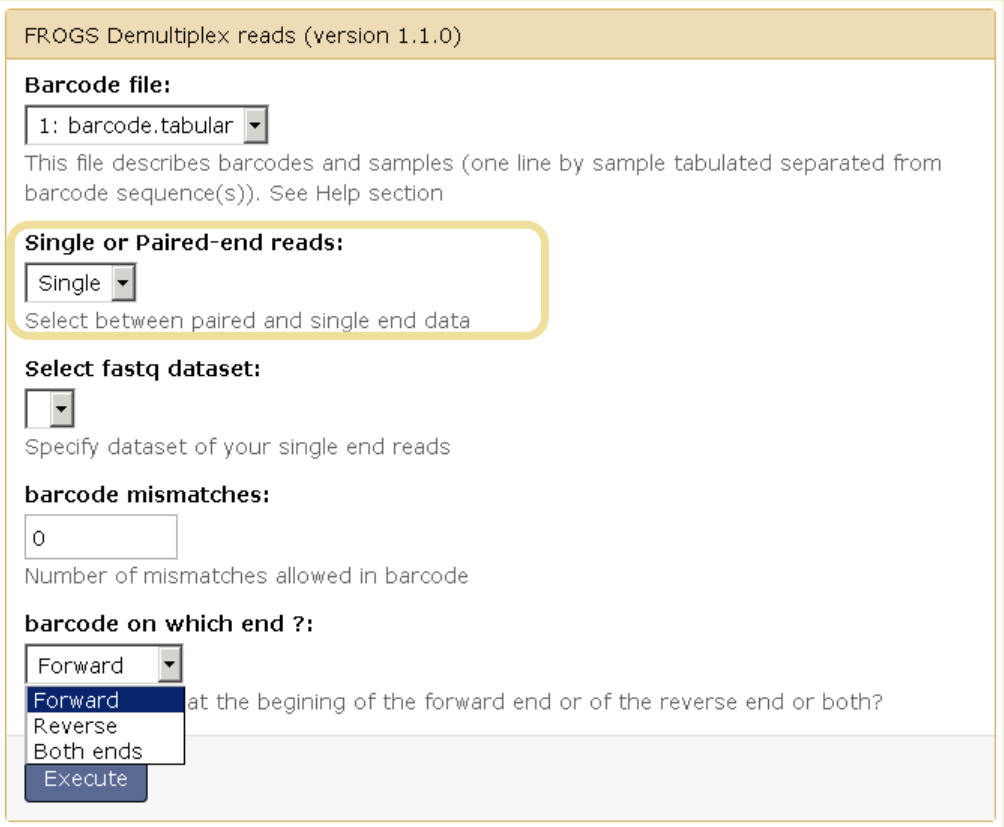


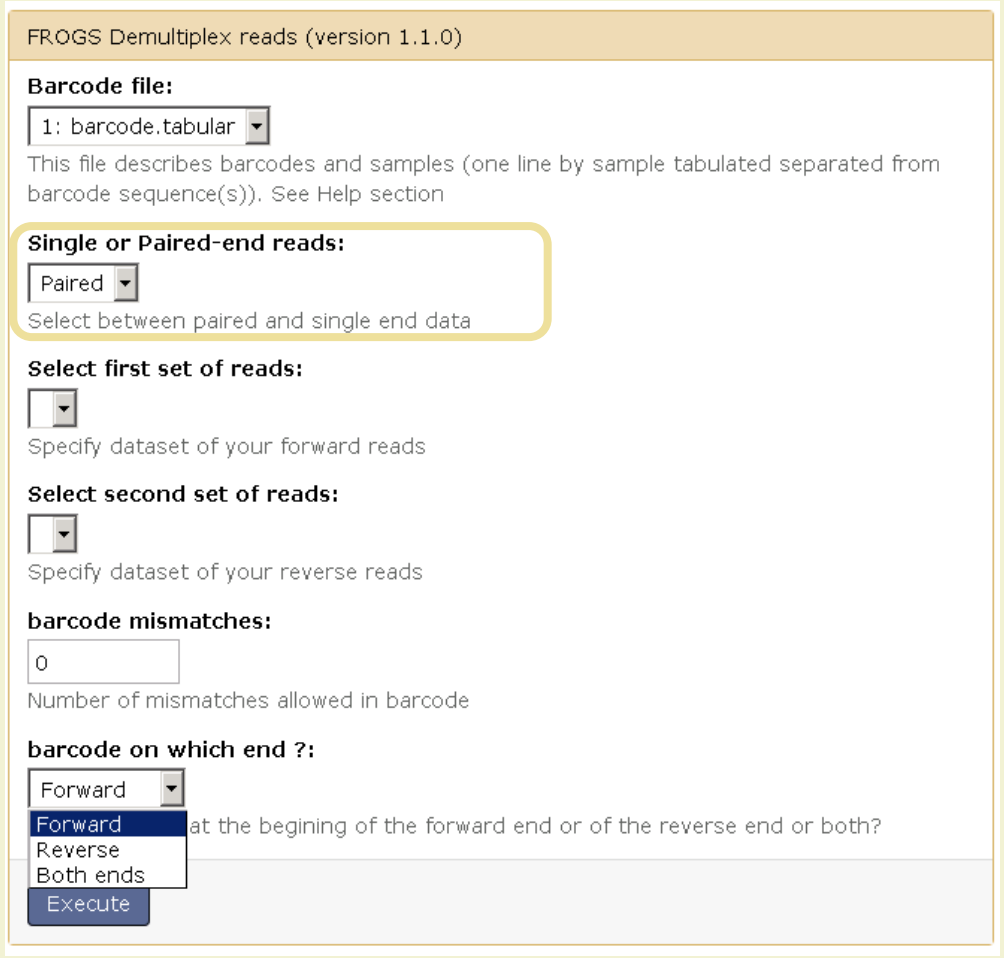
Your turn! - 2

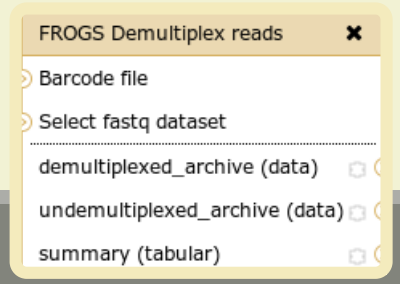
LAUNCH DEMULTIPLEX READS TOOL

multiplexed

The tool parameters depend on the input data type







Demultiplexing

multiplexed

Exercise 2

In **multiplexed** history launch the demultiplex tool:

« The Patho-ID project, rodent and tick‘s pathobioms study, financed by the metaprogram INRA-MEM, studies zoonoses on rats and ticks from multiple places in the world, the co-infection systems and the interactions between pathogens. In this aim, thay have extracted hundreads of or rats and ticks samples from which they have extracted 16S DNA and sequenced them first time on Roche 454 plateform and in a second time on Illumina Miseq plateform. For this courses, they authorized us to publicly shared some parts of these samples. »

Parasites & Vectors (2015) 8:172 DOI 10.1186/s13071-015-0784-7. **Detection of Orientia sp. DNA in rodents from Asia, West Africa and Europe.** Jean François Cosson, Maxime Galan, Emilie Bard, Maria Razzauti, Maria Bernard, Serge Morand, Carine Brouat, Ambroise Dalecky, Khalilou Bâ, Nathalie Charbonnel and Muriel Vayssier-Taussat

multiplexed

Exercise 2

In **multiplexed** history launch the demultiplex tool:

Data are single end reads
→ only 1 fastq file

Samples are characterized by one barcode in forward strands
→ multiplexing « forward »

Inputs :

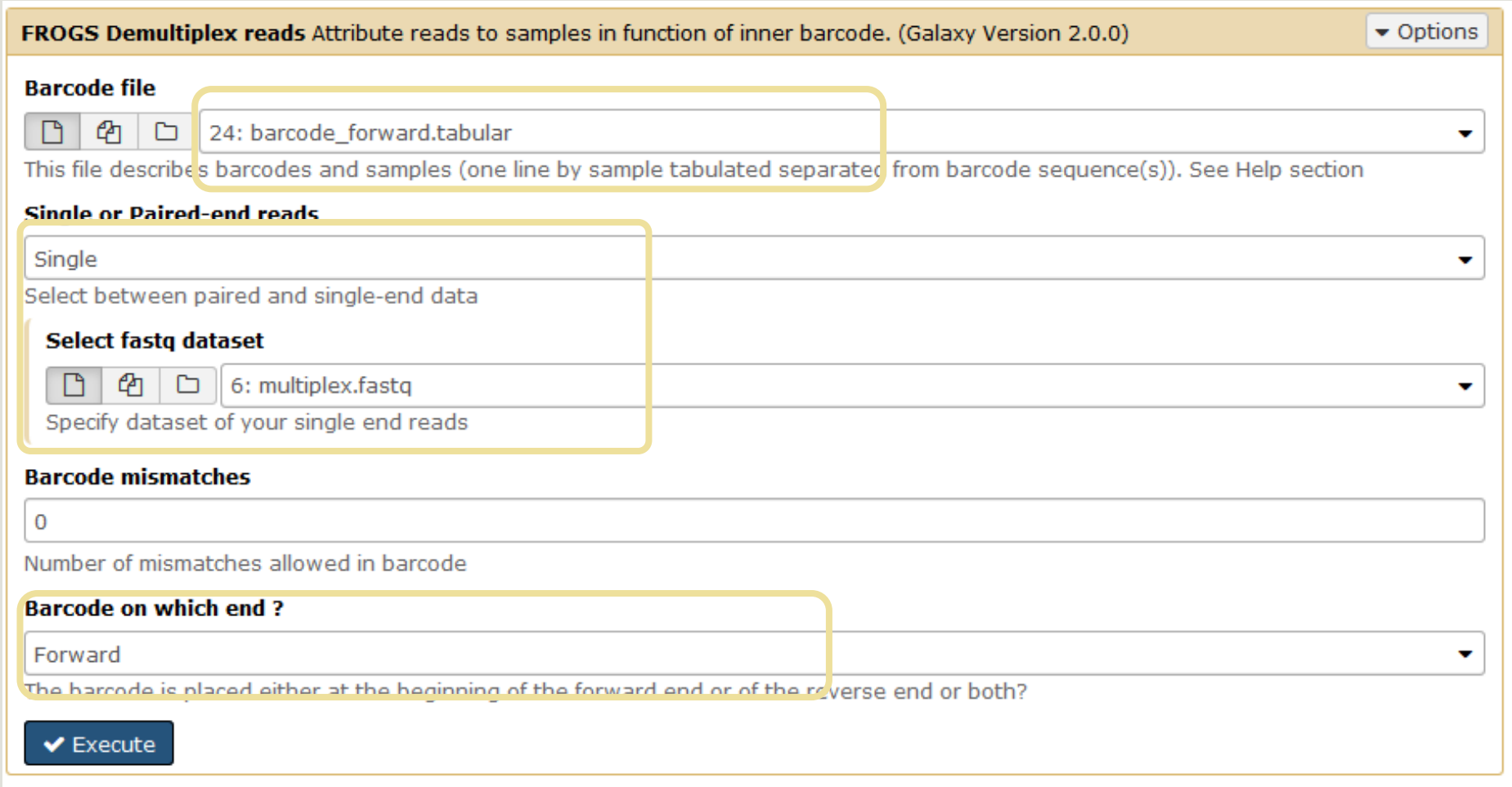
multiplexed

Exercise 2

Demultiplex tool asks for 2 files: one « fastq » and one « tabular »

1. Play with pictograms 
2. Observe how is built a fastq file. 
3. Look at the stdout, stderr when available (in the  pictogram)

multiplexed



multiplexed

Advices

For your own data

- Do not forget to indicate barcode sequence as they are in the fastq sequence file, especially if you have data multiplexed via the reverse strand.
- For the mismatch threshold, we advised you to let the threshold to 0, and if you are not satisfied by the result, try with 1. The number of mismatch depends on the length of the barcode, but often those sequences are very short so 1 mismatch is already more than the sequencing error rate.
- If you have different barcode lengths, you must demultiplex your data in different times beginning by the longest barcode set and used the "unmatched" or "ambiguous" sequence with smaller barcode and so on.
- If you have Roche 454 sequences in sff format, you must convert them with some program like sff2fastq

multiplexed

Results

9: FROGS Demultiplex reads: report

8: FROGS Demultiplex reads: undemultiplexed.tar.gz

7: FROGS Demultiplex reads: demultiplexed.tar.gz

1	2
#sample	count
ambiguous	0
MgArd0009	91
MgArd0017	166
MgArd0038	1208
MgArd0029	193
unmatched	245
MgArd0001	119
MgArd0081	246
MgArd0046	401
MgArd0054	243
MgArd0073	474
MgArd0062	1127

With barcode mismatches >1 sequence can corresponding to several samples.
So these sequences are non-affected to a sample.

Sequences without known barcode.
So these sequences are non-affected to a sample.

A tar archive is created by grouping one (or a pair of) fastq file per sample with the names indicated in the first column of the barcode tabular file

multiplexed

Format: Barcode

BARCODE FILE is expected to be tabulated:

- first column corresponds to the sample name (unique, without space)
- second to the forward sequence barcode used (None if only reverse barcode)
- optional third is the reverse sequence barcode (optional)

Take care to indicate sequence barcode in the strand of the read, so you may need to reverse complement the reverse barcode sequence. Barcode sequence must have the same length.

Example of barcode file.
The last column is optional, like this, it describes sample multiplexed by both fragment ends.

```
MgArd00001          ACAGCGT          ACGTACA
```

multiplexed

Format : FastQ

FASTQ : Text file describing biological sequence in 4 lines format:

- first line start by "@" correspond to the sequence identifier and optionally the sequence description. "@Sequence_1 description1"
- second line is the sequence itself. "ACAGC"
- third line is a "+" following by the sequence identifier or not depending on the version
- fourth line is the quality sequence, one code per base. The code depends on the version and the sequencer

```
@HNHOSKD01ALD0H
ACAGCGTCAGAGGGGTACCAGTCAGCCATGACGTAGCACGTACA
+
CCCFFFFFFHHHHHJJIJJJHHFF@DEDDDDDDD@CDDDDACDD
```

multiplexed

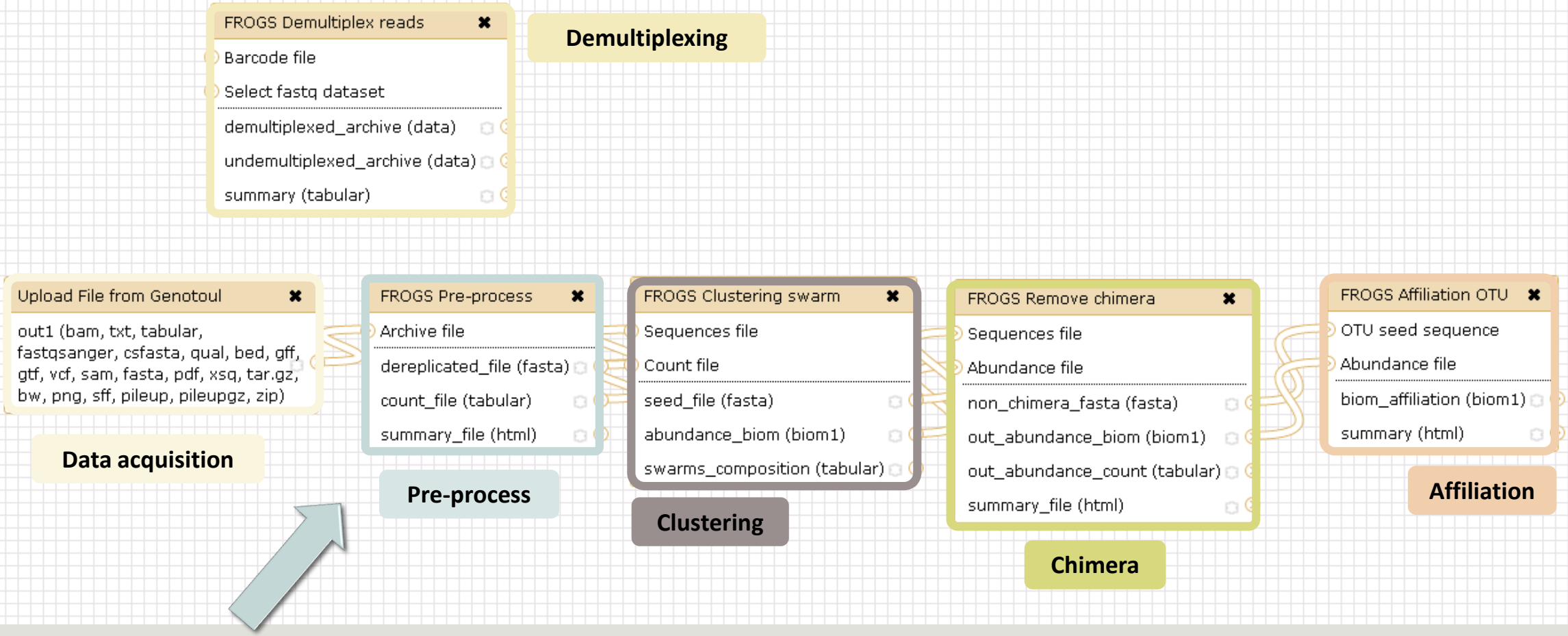
How it works ?

For each sequence or sequence pair the sequence fragment at the beginning (forward multiplexing) of the (first) read or at the end (reverse multiplexing) of the (second) read will be compare to all barcode sequence.

If this fragment is equal (with less or equal mismatch than the threshold) to one (and only one) barcode, the fragment is trimmed and the sequence will be attributed to the corresponding sample.

Finally fastq files (or pair of fastq files) for each sample are included in an archive, and a summary describes how many sequence are attributed for each sample.

Pre-process tool


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
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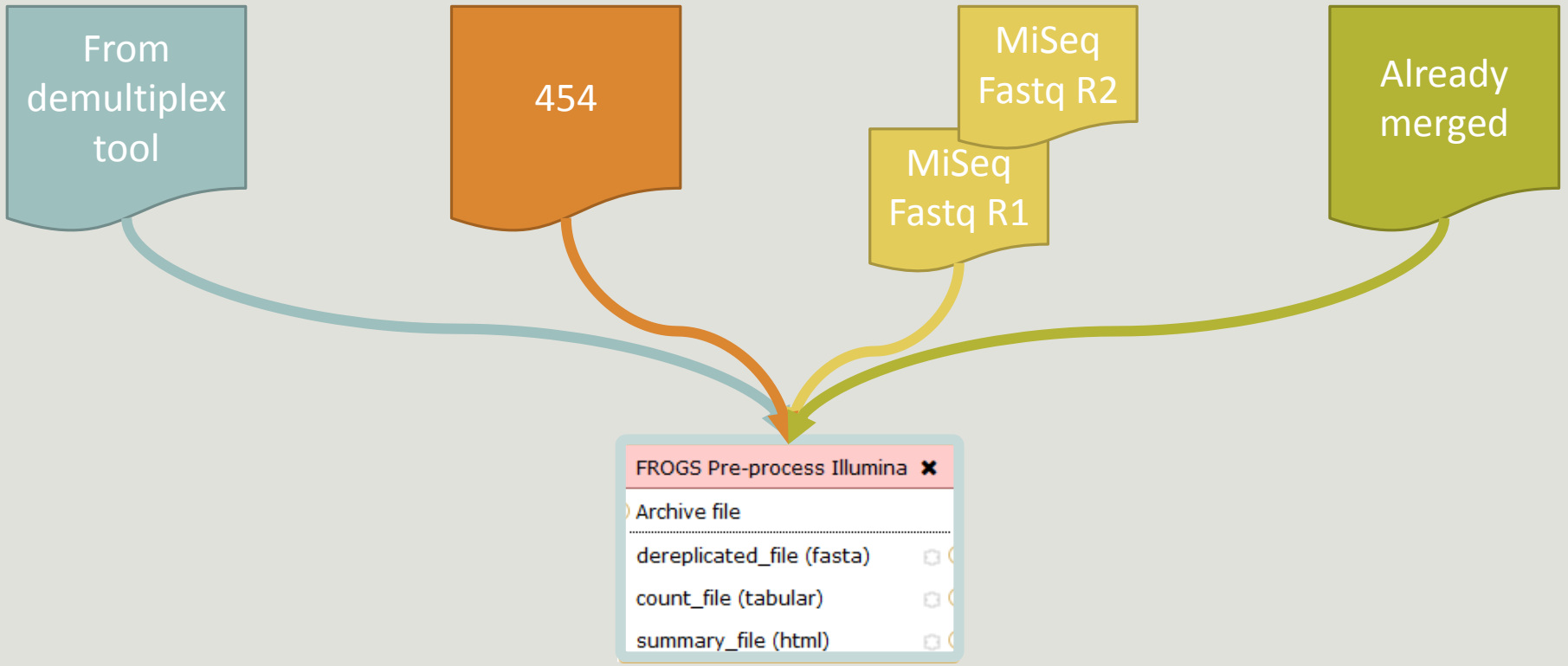
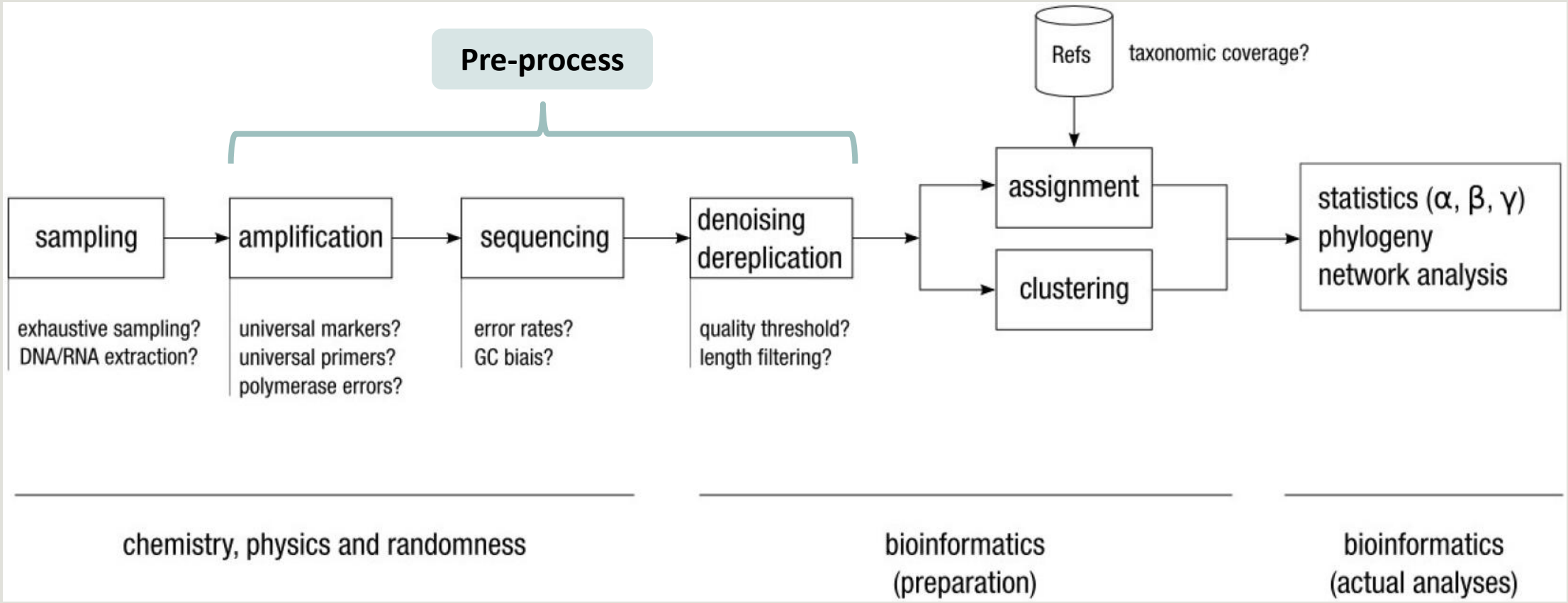
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation


From demultiplex tool
454
MiSeq Fastq R2
MiSeq Fastq R1
Already merged
FROGS Pre-process Illumina
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)

Pre-process

Amplicon-based studies general pipeline



Pre-process

- Delete sequence with not expected lengths
- Delete sequences with ambiguous bases (N)
- Delete sequences do not contain good primers
- Dereplication

- + removing homopolymers (size = 8) for 454 data
- + quality filter for 454 data

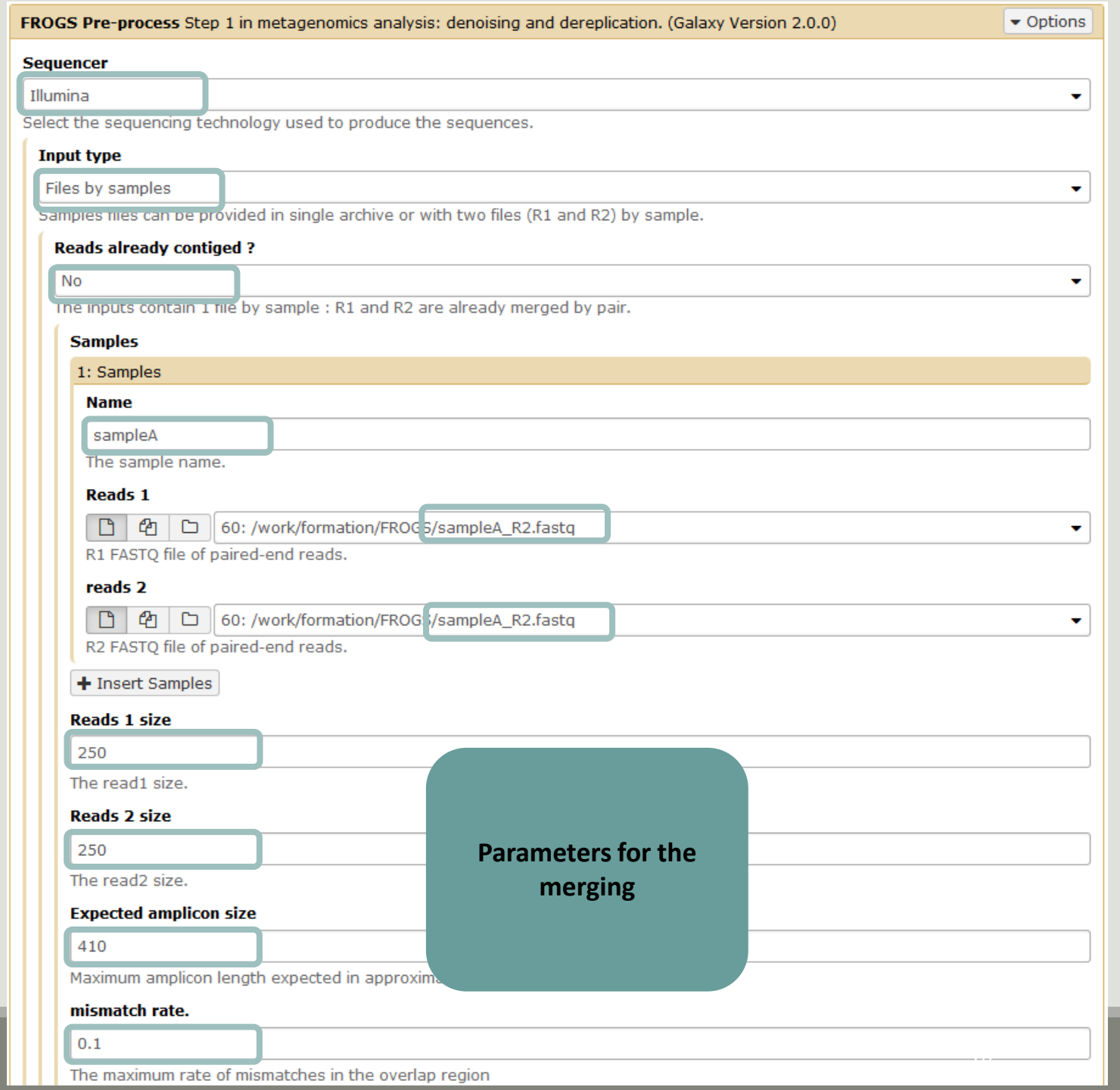
EMBnet Journal, Vol17 no1. doi : 10.14806/ej.17.1.200
Cutadapt removes adapter sequences from high-throughput sequencing reads
Marcel Martin

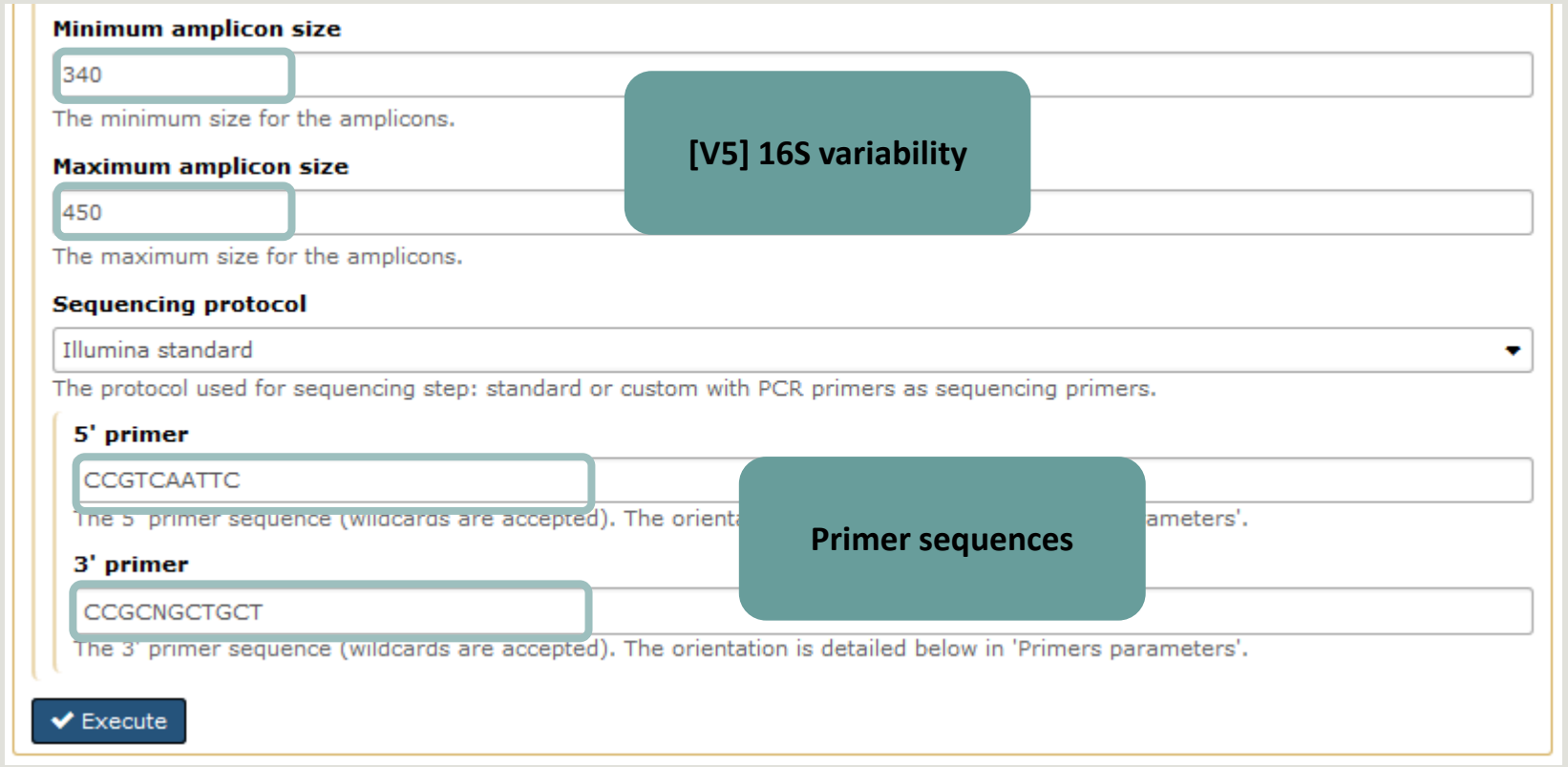
Bioinformatics (2011) 27 (21):2957-2963. doi:10.1093/bioinformatics/btr507
FLASH: fast length adjustment of short reads to improve genome assemblies
TanjaMagoc, Steven L. Salzberg

Example for:

- Illumina MiSeq data
- 1 sample
- Non joined

Pre-process example 1

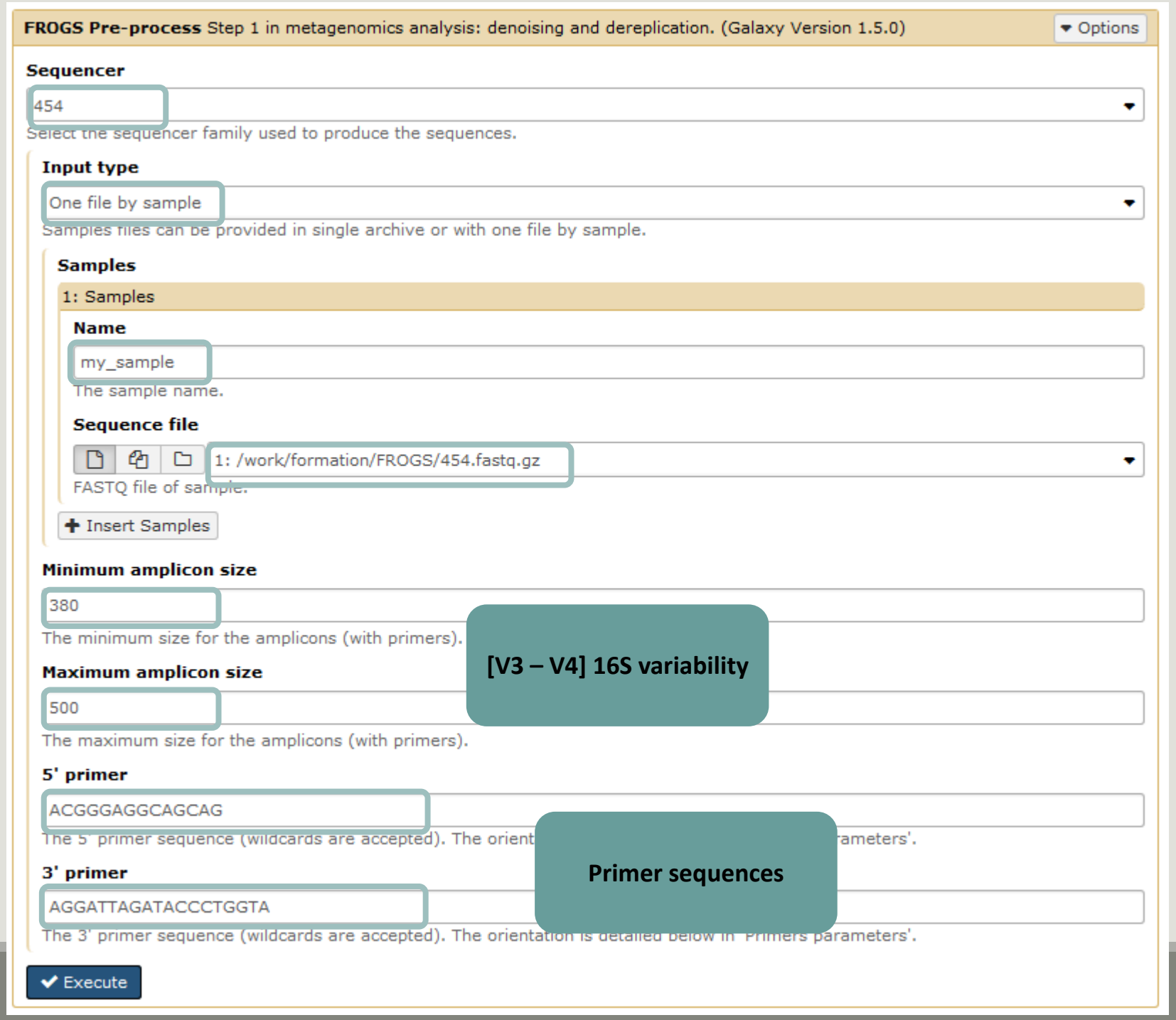




Pre-process example 1

Example for:

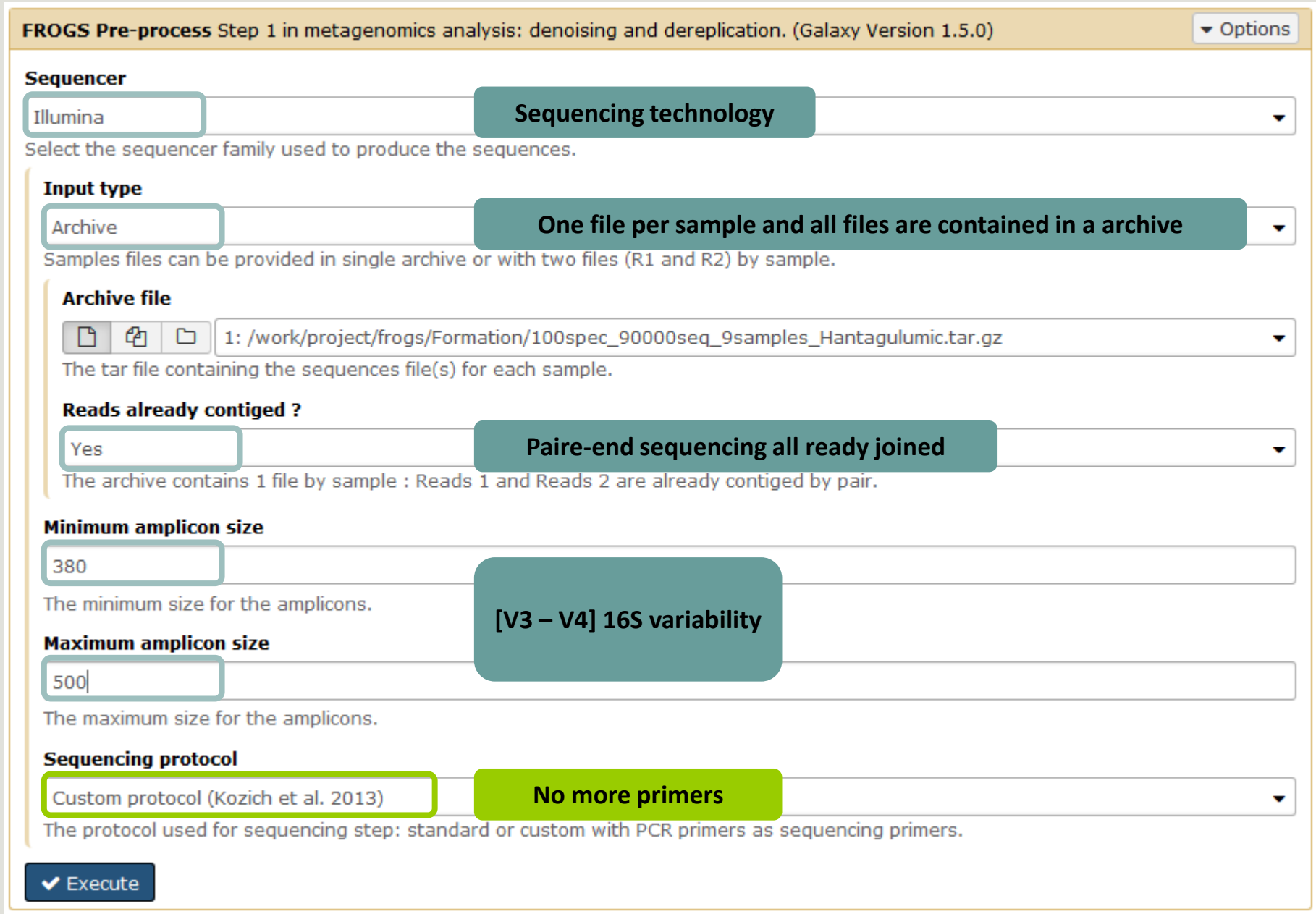
- Sanger 454 data
- 1 sample
- Only one read (454 process)



Pre-process example 2

Example for:

- Illumina MiSeq data
- 9 samples in 1 archive
- Joined
- Without sequenced PCR primers (Kozich protocol)



Pre-process example 3

Your turn! - 3

GO TO EXERCISES 3

454

Exercise 3.1

Go to « 454 » history

Launch the pre-process tool on that data set

→ objective : understand the parameters

1- Test different parameters for « minimum and maximum amplicon size »

2- Enter these primers: Forward: ACGGGAGGCAGCAG Reverse: AGGATTAGATACCCTGGTA

454

FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication. (Galaxy Version 2.0.0) ▾ Options

Sequencer

454

Select the sequencing technology used to produce the sequences.

Input type

One file by sample

Samples files can be provided in single archive or with one file by sample.

Samples

1: Samples

Sample name is required

Name

my_sample

The sample name.

Sequence file

70: /work/formation/FROGS/454.fastq.gz

FASTQ file of sample.

+ Insert Samples

Minimum amplicon size

380

The minimum size for the amplicons (with primers).

Maximum amplicon size

500

The maximum size for the amplicons (with primers).

5' primer

ACGGGAGGCAGCAG

The 5' primer sequence (wildcards are accepted). The orientation is detail

3' primer

AGGATTAGATACCCTGGTA

The 3' primer sequence (wildcards are accepted). The orientation is detail

✔ Execute

Size range of 16S V3-V4:
[380 – 500]

Primers used for sequencing V3-V4:
Forward: ACGGGAGGCAGCAG
Reverse: AGGATTAGATACCCTGGTA

454

Exercise 3.1

What do you understand about amplicon size, which file can help you ?

What is the length of your reads before preprocessing ?

Do you understand how enter your primers ? 

What is the « FROGS Pre-process: dereplicated.fasta » file ? 

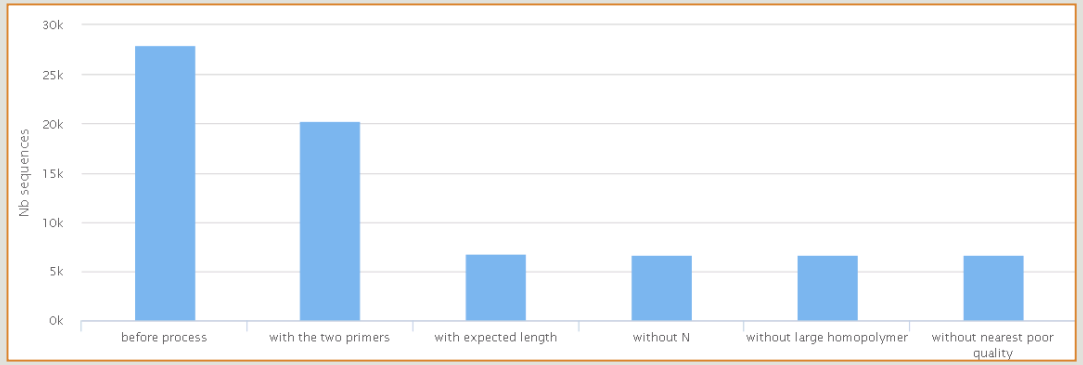
What is the « FROGS Pre-process: count.tsv » file ? 

Explore the file « FROGS Pre-process: report.html »

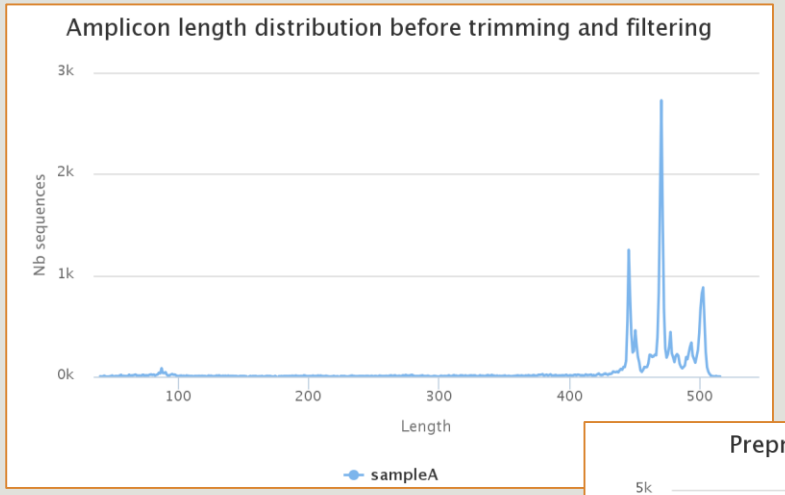
Who loose a lot of sequences ?

454

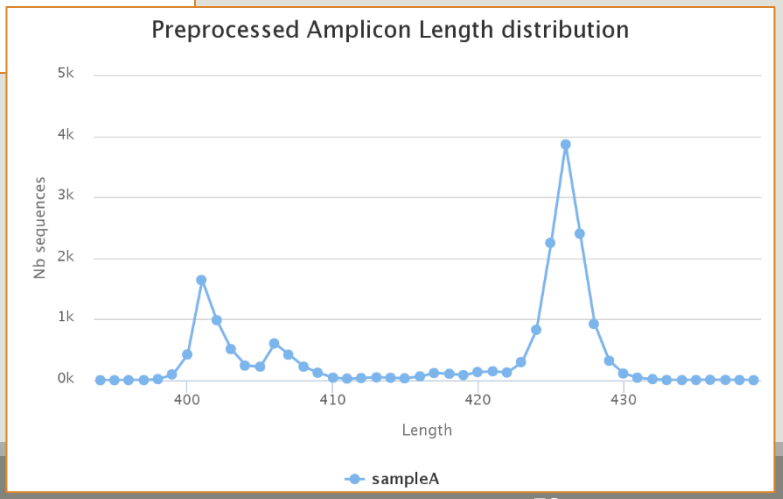
Samples	before process	with the two primers	with expected length	without N	without large homopolymer	without nearest poor quality
sample_454	28,009	20,227	6,806	6,677	6,675	6,672



To be kept, sequences must have the 2 primers



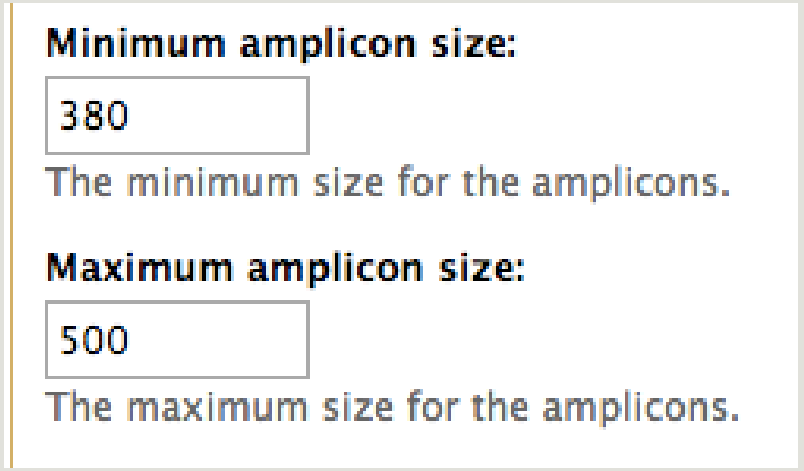
To adjust your filtering, check the distribution of sequence lengths.



454

Cleaning, how it work ?

Filter contig sequence on its length which must be between min-amplicon-size and max-amplicon-size



use cutadapt to search and trim primers sequences with less than 10% differences

454

Cleaning, how it work ?

dereplicate sequences and return one uniq fasta file for all sample and a count table to indicate sequence abundances among sample.

In the HTML report file, you will find for each filter the number of sequences passing it, and a table that details these filters for each sample.

MiSeq
R1 R2

Exercise 3.2

Go to « MiSeq R1 R2 » history

Launch the pre-process tool on that data set

→ objective: understand flash software

The aim of Flash is to merge R1 with R2

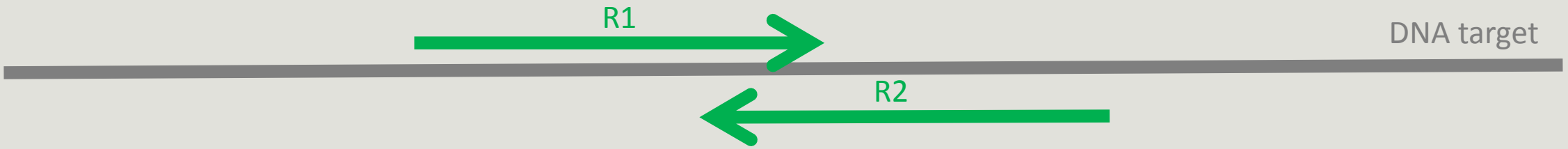
1st case: Impossible to merge

Careful

This case is not yet take in charge by FROGS, but soon available in FROGS V3.0

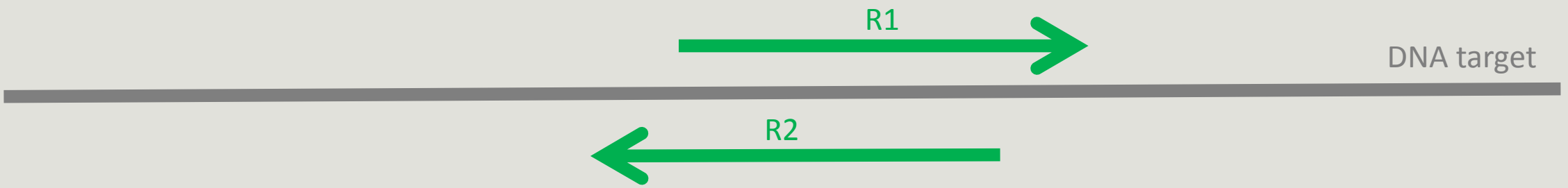
The aim of Flash is to merge R1 with R2

2nd case: flash have to find overlapping region between R1 and R2



The aim of Flash is to merge R1 with R2

3rd case: R1 and R2 cover entirely the target region



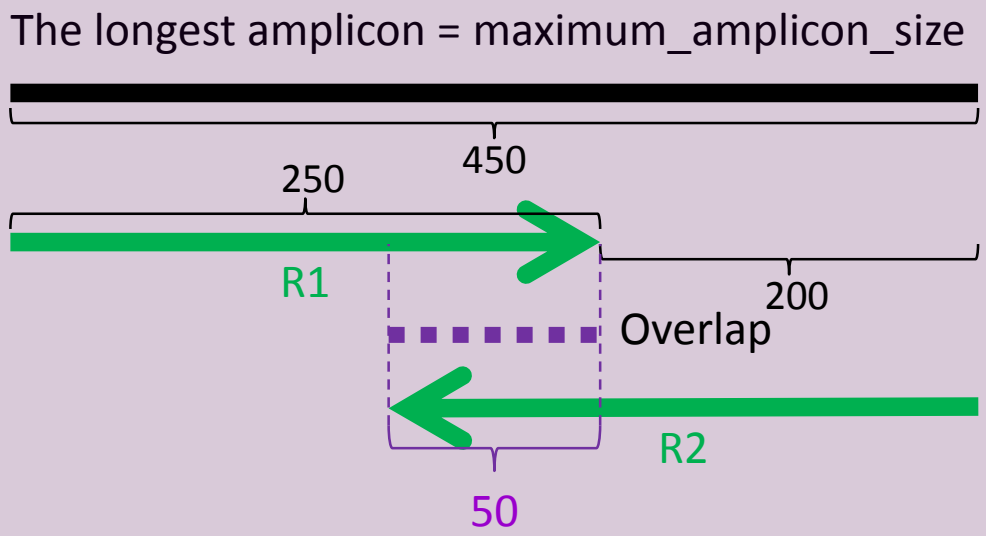
Careful

This case is not treated by FROGS, you must trim your sequences before putting in FROGS.
Ask to a bioinformatician to do it.

Flash, have to determine the overlap size

1 - The Minimum overlap

Representation



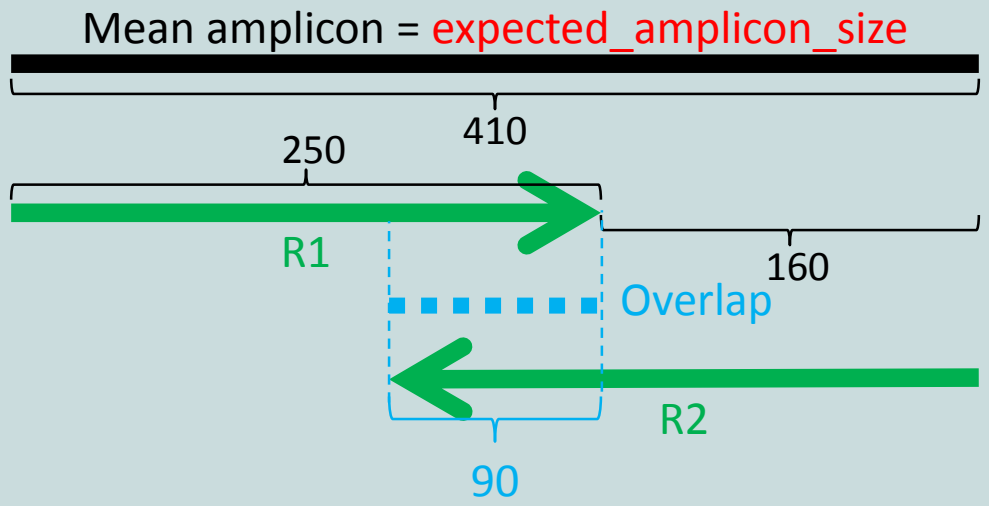
Computation

Min overlap = R1_size + R2_size – maximum_amplicon_size

Min overlap = 250 + 250 – 450 = 50

2 - The Maximum overlap:

Representation



Computation

Expected_overlap = R1_size + R2_size – expected_amplicon_size = 250 + 250 – 410 = 90

Maximum_overlap = Expected_overlap + min(20, (expected_amplicon_size - minimum_amplicon_size)/2)

Maximum_overlap = 90 + min(20, 410 – 340)

Maximum_overlap = 90 + min(20, 35) = 110

The flash maximum_overlap is not the maximum overlap but the overlap for an amplicon size greater than 90% of the set of sizes. This is why we take the expected size (medium amplicon) and add a small correction factor.
Anyway flash is not sensitive to the ten nucleotides.

Waited data

Reads 1 size	→ OK	→ 250
Reads 2 size	→ OK	→ 250
Expected amplicon size	More complex to understand	→ 410
Minimum amplicon size	→ OK	→ 340
Maximum amplicon size	→ OK	→ 450
Sequencing protocol	→ OK	→ standard
5' primer	→ OK	→ CCGTCAATTC
3' primer	→ OK	→ CCGCNGCTGCT

FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication. (Galaxy Ver

Sequencer

Illumina

Select the sequencing technology used to produce the sequences.

Input type

Files by samples

Samples files can be provided in single archive or with two files (R1 and R2) by sample.

Reads already contiged ?

No

The inputs contain 1 file by sample : R1 and R2 are already merged by pair.

Samples

1: Samples

Name

sampleA

The sample name.

Reads 1

59: /work/formation/FROGS/sampleA_R1.fastq

R1 FASTQ file of paired-end reads.

reads 2

60: /work/formation/FROGS/sampleA_R2.fastq

R2 FASTQ file of paired-end reads.

+ Insert Samples

Reads 1 size

250

The read1 size.

Reads 2 size

250

The read2 size.

Size with primers

```
>ERR619083.M00704
CCGTCAATTCATTGAGTTTCAACCTTGCGGCCGTACTTCCCAGGCGGTACGTT
TATCGCGTTAGCTTCGCCAAGCACAGCATCCTGCGCTTAGCCAACGTACATCG
TTTAGGGTGTGGACTACCCGGGTATCTAATCCTGTTCGCTACCCACGCTTTCG
AGCCTCAGCGTCAGTGACAGACCAGAGAGCCGCTTTCGCCACTGGTGTTCCTC
CATATATCTACGCATTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGC
ACTCAAGTCAGACAGTTTCCAGAGCACTCTATGGTTGAGCCATAGCCTTTTAC
TCCAGACTTTCCTGACCGACTGCACTCGCTTTACGCCCAATAAATCCGGACAA
CGCTTGCCACCTACGTATTACCGCNGCTGCT
```

MiSeq
R1 R2

Real 16S sequenced fragment

Expected amplicon size

410

Maximum amplicon length expected in approximately 90% of the amplicons.

mismatch rate.

0.1

The maximum rate of mismatches in the overlap region

Minimum amplicon size

340

The minimum size for the amplicons.

Maximum amplicon size

450

The maximum size for the amplicons.

Sequencing protocol

Illumina standard

The protocol used for sequencing step: standard or custom with PCR primers as sequencing primers.

5' primer

CCGTCAATTC

The 5' primer sequence (w ameters'.

3' primer

CCGCNGCTGCT

The 3' primer sequence (wi rameters'.

Primers used for sequencing V5 region:
Forward: CCGTCAATTC
Reverse: CCGCNGCTGCT
Lecture 5' → 3'

✔ Execute

MiSeq
R1 R2

Exercise 3.2

Interpret « FROGS Pre-process: report.html » file.

MiSeq
R1 R2

Expected amplicon size

410

Maximum amplicon length expected in approximately 90% of the amplicons.

mismatch rate.

0.1

The maximum rate of mismatches in the overlap region

Minimum amplicon size

340

The minimum size for the amplicons.

Maximum amplicon size

450

The maximum size for the amplicons.

Sequencing protocol

Illumina standard

The protocol used for sequencing step: standard or custom with PCR primers as sequencing primers.

5' primer

CCGTCAATTC

The 5' primer sequence (wildcards are accepted). The orientation is detailed below in 'Primers parameters'.

3' primer

CCGCNGCTGCT

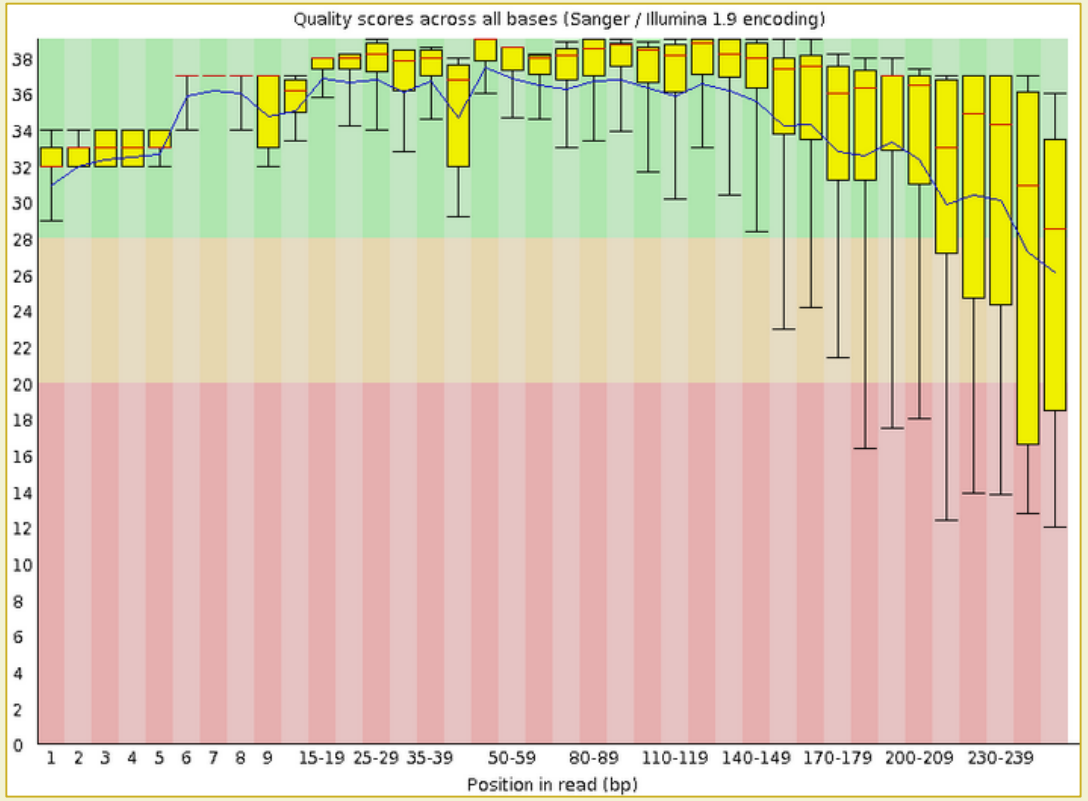
The 3' primer sequence (wildcards are accepted). The orientation is detailed below in 'Primers parameters'.

✔ Execute

To increase if your sequences have low qualities
Use FASTQC to know it!

FastQC: fastq/sam/bam

FastQC:Read QC reports using FastQC



MiSeq merged

Exercise 3.3

Go to« MiSeq merged » history

Launch the pre-process tool on that data set

→ objective: understand output files

MiSeq merged

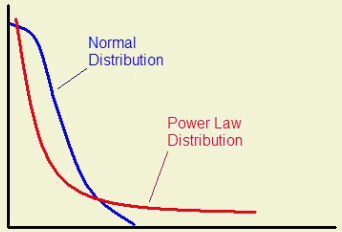
Exercise 3.3

3 samples are **technically replicated** 3 times : 9 samples of 10 000 sequences each.

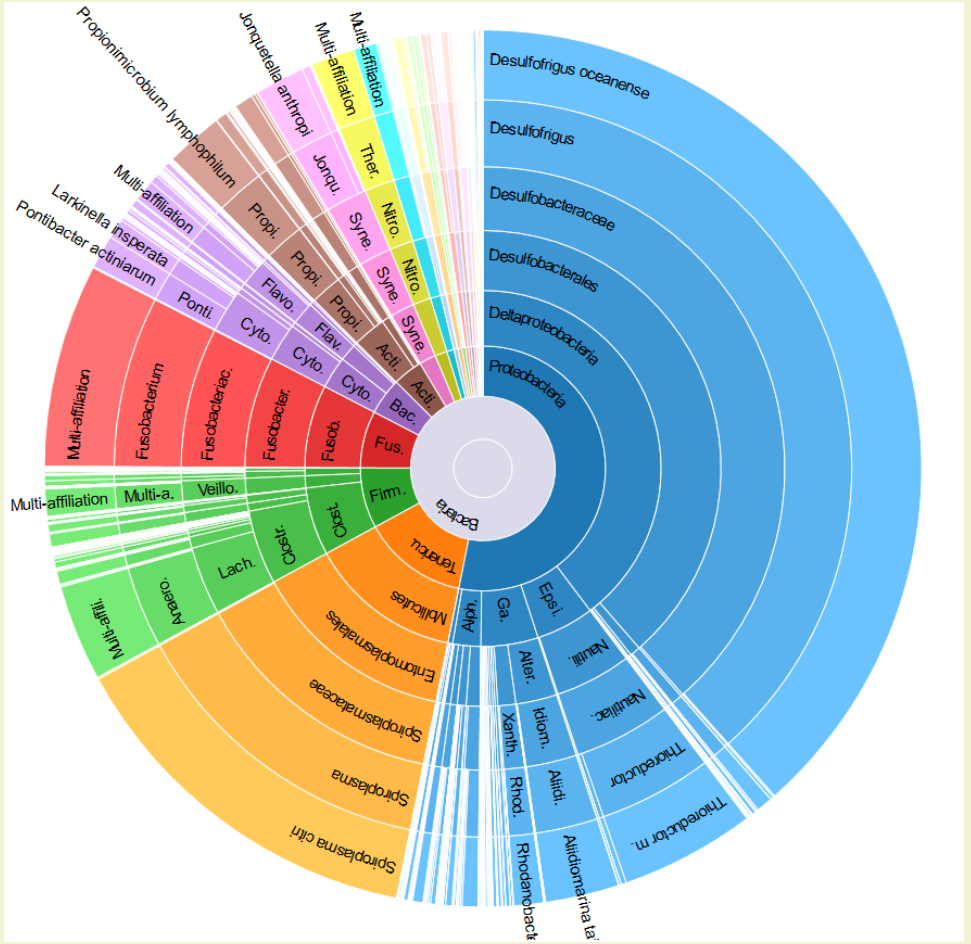
100_10000seq_sampleA1.fastq	100_10000seq_sampleB1.fastq	100_10000seq_sampleC1.fastq
100_10000seq_sampleA2.fastq	100_10000seq_sampleB2.fastq	100_10000seq_sampleC2.fastq
100_10000seq_sampleA3.fastq	100_10000seq_sampleB3.fastq	100_10000seq_sampleC3.fastq

MiSeq merged

Exercise 3.3



- 100 species, covering all bacterial phyla
- Power Law distribution of the species abundances
- Error rate calibrated with real sequencing runs
- 10% chimeras
- 9 samples of 10 000 sequences each (90 000 sequences)



MiSeq merged

Exercise 3.3

"Grinder (v 0.5.3) (Angly et al., 2012) was used to simulate the PCR amplification of full-length (V3-V4) sequences from reference databases. The reference database of size 100 were generated from the LTP SSU bank (version 115) (Yarza et al., 2008) by

(1) filtering out sequences with a N,

(2) keeping only type species

(3) with a match for the forward (ACGGRAGGCAGCAG) and reverse (TACCAGGGTATCTAATCCTA) primers in the V3-V4 region and

(4) maximizing the phylogenetic diversity (PD) for a given database size. The PD was computed from the NJ tree distributed with the LTP."

MiSeq

FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication. (Galaxy Version 2.0.0) ▾ Options

Sequencer

Illumina

Select the sequencing technology used to produce the sequences.

Input type

Archive

Samples files can be provided in single archive or with two files (R1 and R2) by sample.

Archive file

2: /work/formation/FROGS/100spec_90000seq_9samples.tar.gz

The tar file containing the sequences file(s) for each sample.

Reads already contiged ?

Yes

The archive contains 1 file by sample : R1 and R2 are already merged by pair.

Minimum amplicon size

380

The minimum size for the amplicons.

Maximum amplicon size

500

The maximum size for the amplicons.

Sequencing protocol

Illumina standard

The protocol used for sequencing step: standard or custom with PCR primers as sequencing primers.

5' primer

ACGGGAGGCAGCAG

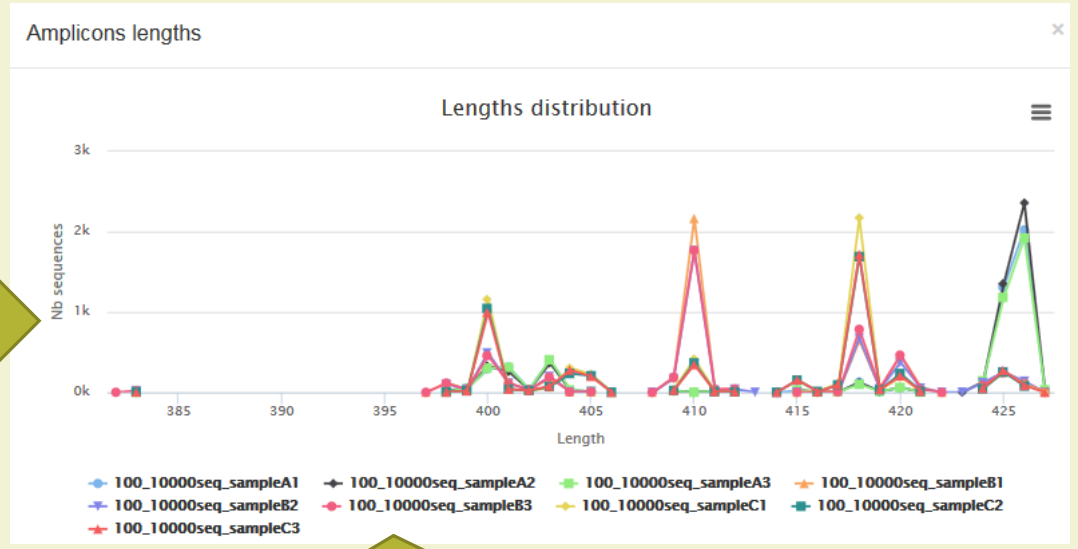
The 5' primer sequence (wildcards are accepted). The orientation is detai

3' primer

TAGGATTAGATACCCTGGTA

The 3' primer sequence (wildcards are accepted). The orientation is detai

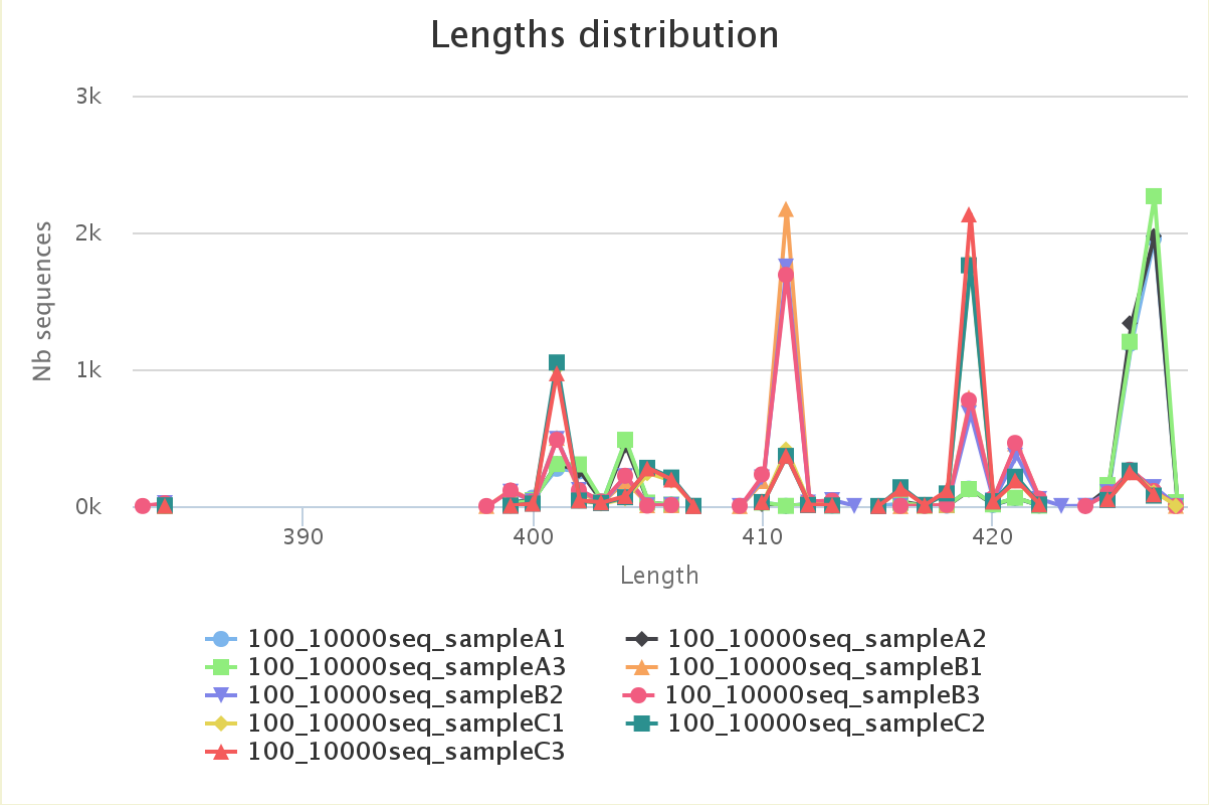
✔ Execute



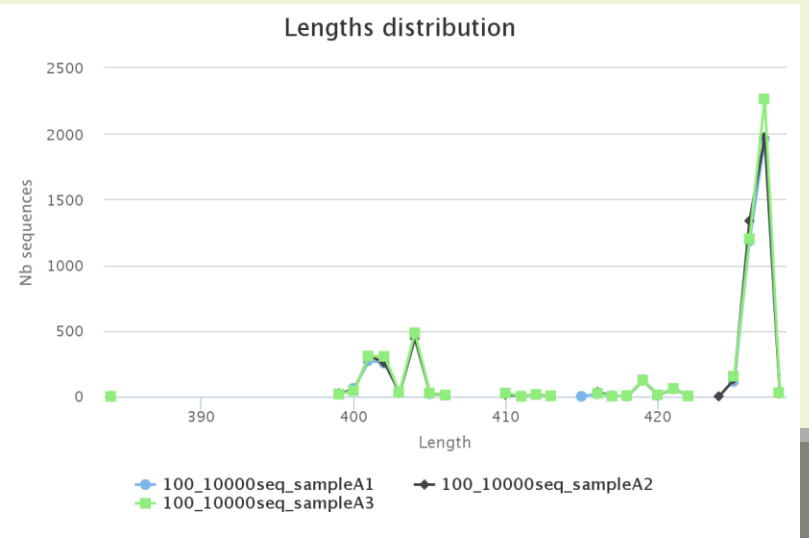
Click on legend

Primers used for this sequencing :
5’ primer: ACGGGAGGCAGCAG
3’ primer: TAGGATTAGATACCCTGGTA
Lecture 5’ → 3’

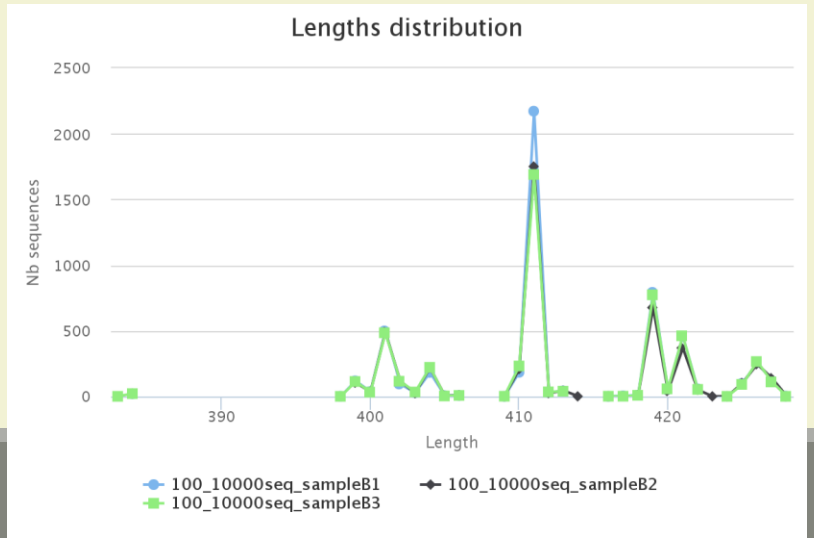
MiSeq merged



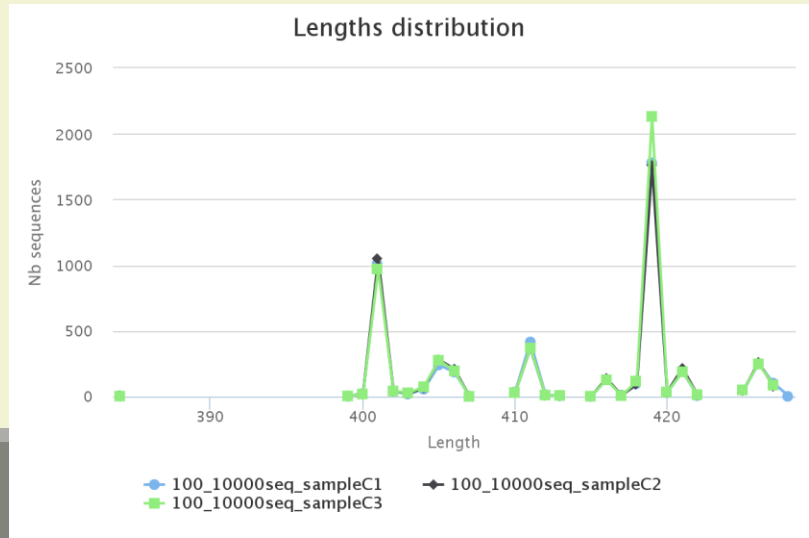
Samples A only



Samples B only



Samples C only



MiSeq merged

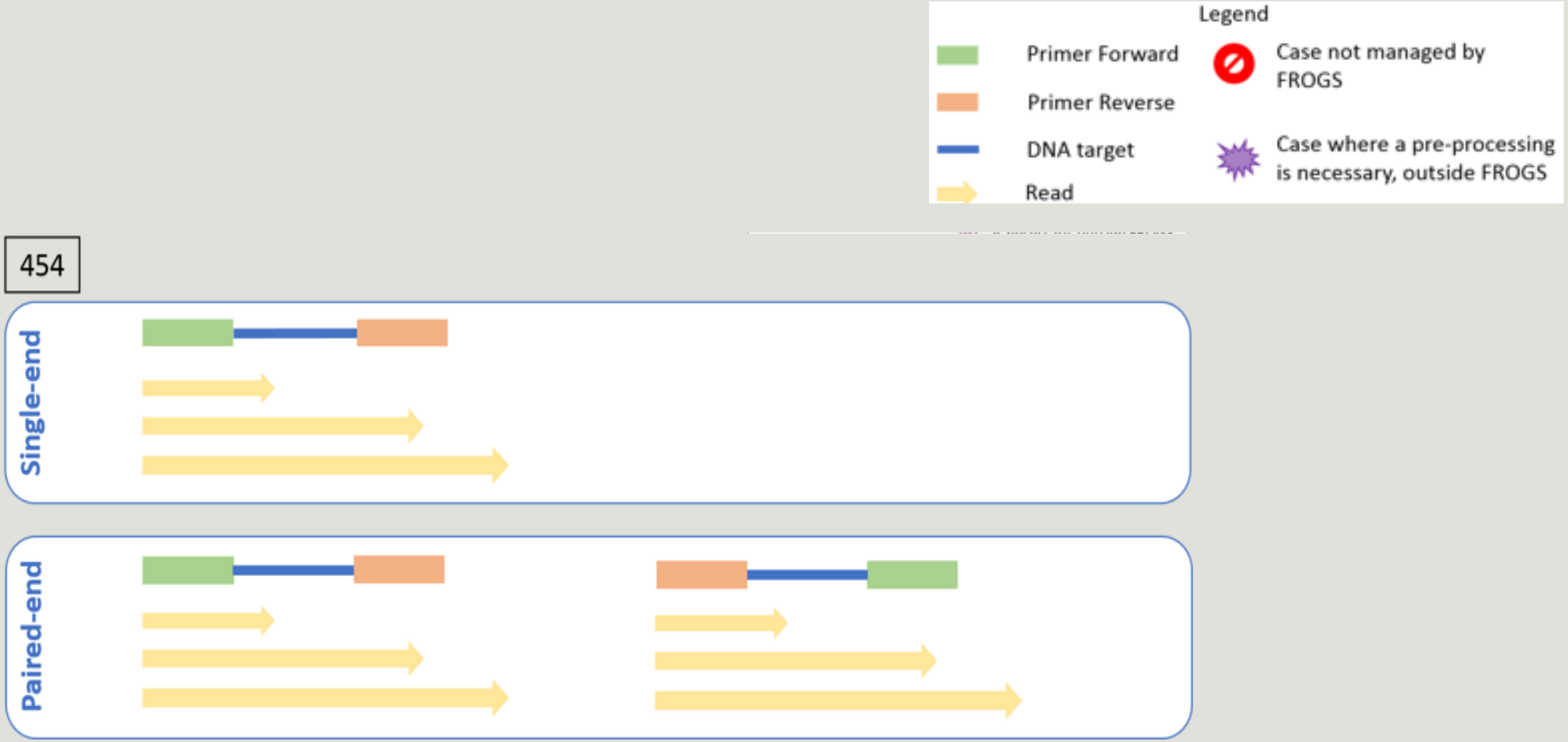
Exercise 3.3 - Questions

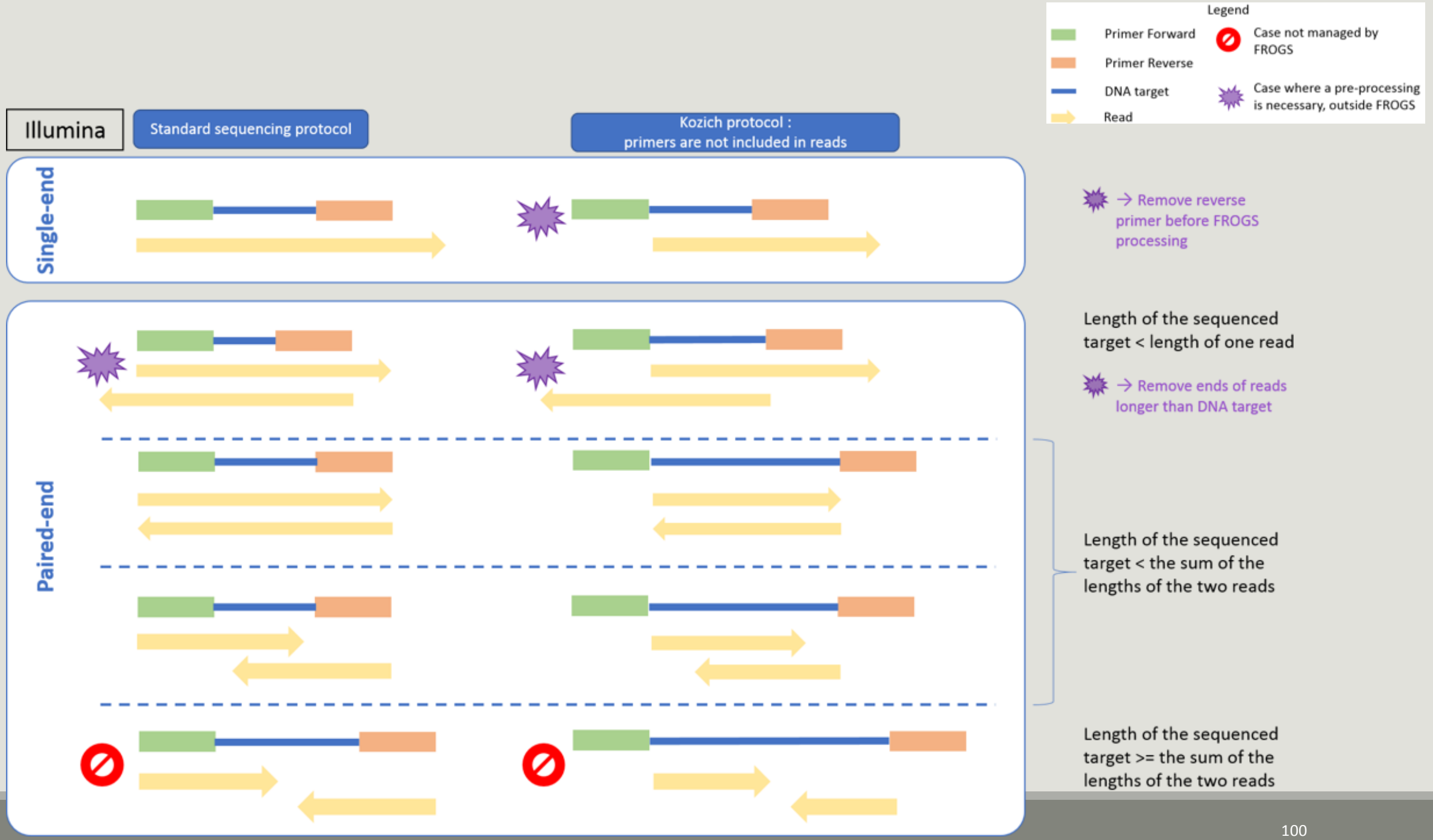
1. How many sequences are there in the input file ?
2. How many sequences did not have the 5’ primer?
3. How many sequences still are after pre-processing the data?
4. How much time did it take to pre-process the data ?
5. What can you tell about the sample based on sequence length distributions ?

Preprocess tool in bref

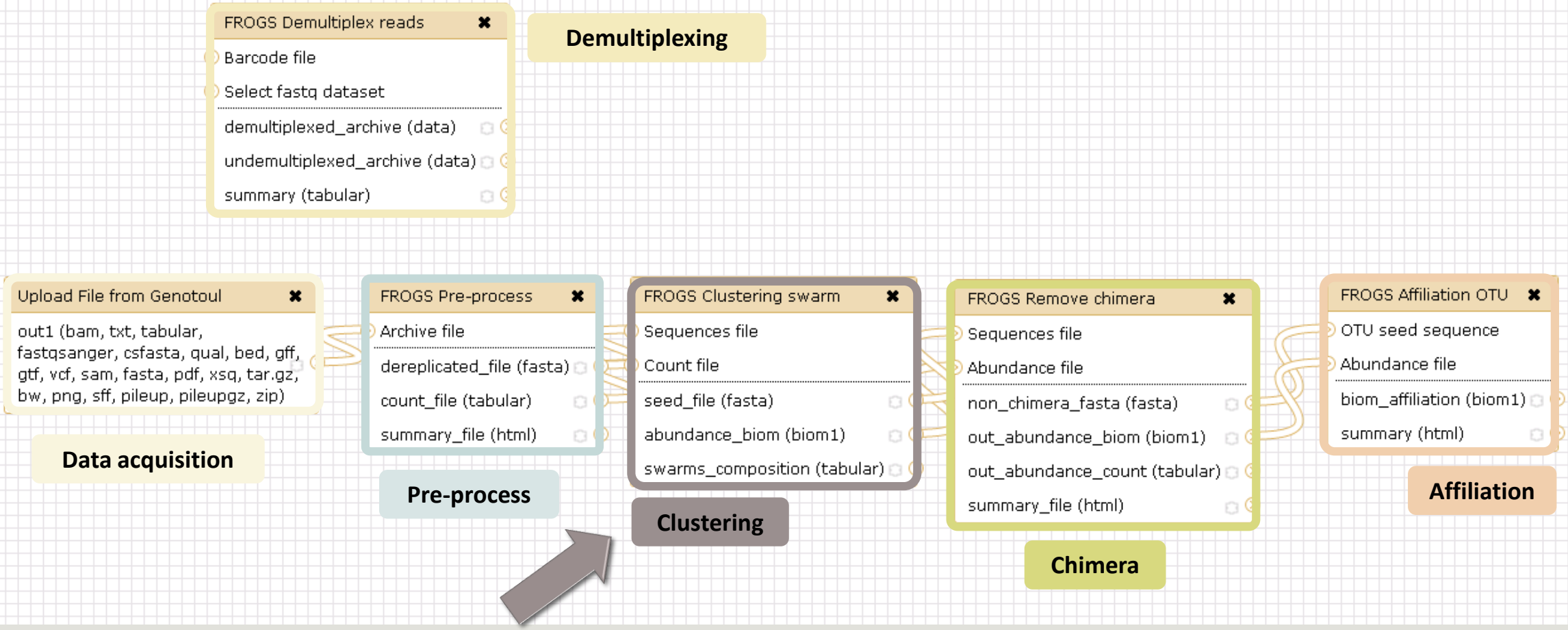
	Take in charge
Illumina	✓
454	✓
Merged data	✓
Not merged data	✓
Without primers	✓
Only R1 or only R2	⊘
Too distant R1 and R2 to be merged	soon
On-overlapping R1 R2	⊘

	Take in charge
Archive .tar.gz	✓
Fastq	✓
Fasta	⊘
With only 1 primer	⊘
Multiplexed data	⊘
Demultiplexed data	✓


Legend
Primer Forward
Primer Reverse
DNA target
Read
Case not managed by FROGS
Case where a pre-processing is necessary, outside FROGS
454
Single-end
Paired-end

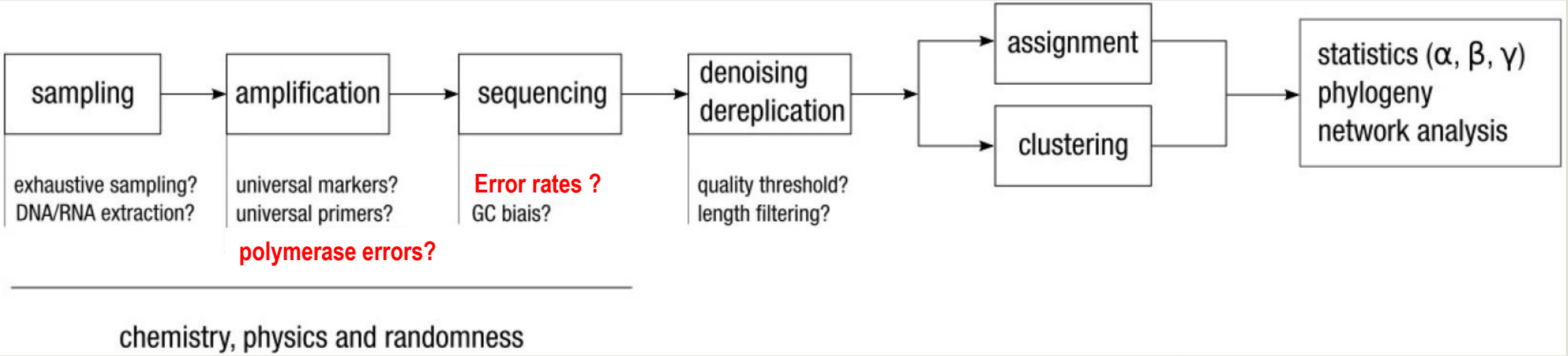

Legend
Primer Forward
Primer Reverse
DNA target
Read
Case not managed by FROGS
Case where a pre-processing is necessary, outside FROGS
Illumina
Standard sequencing protocol
Kozich protocol : primers are not included in reads
Single-end
→ Remove reverse primer before FROGS processing
Paired-end
Length of the sequenced target < length of one read
→ Remove ends of reads longer than DNA target
Length of the sequenced target < the sum of the lengths of the two reads
Length of the sequenced target >= the sum of the lengths of the two reads

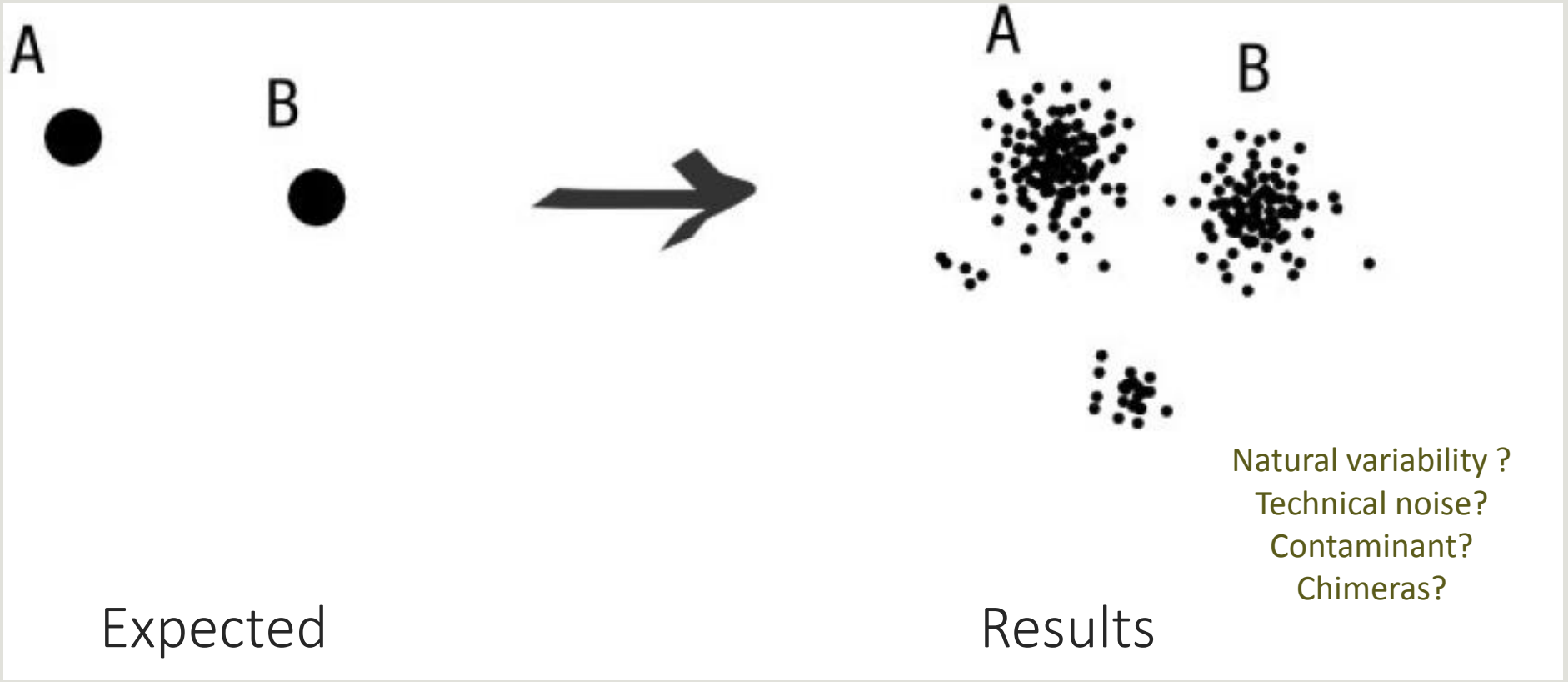
Clustering tool

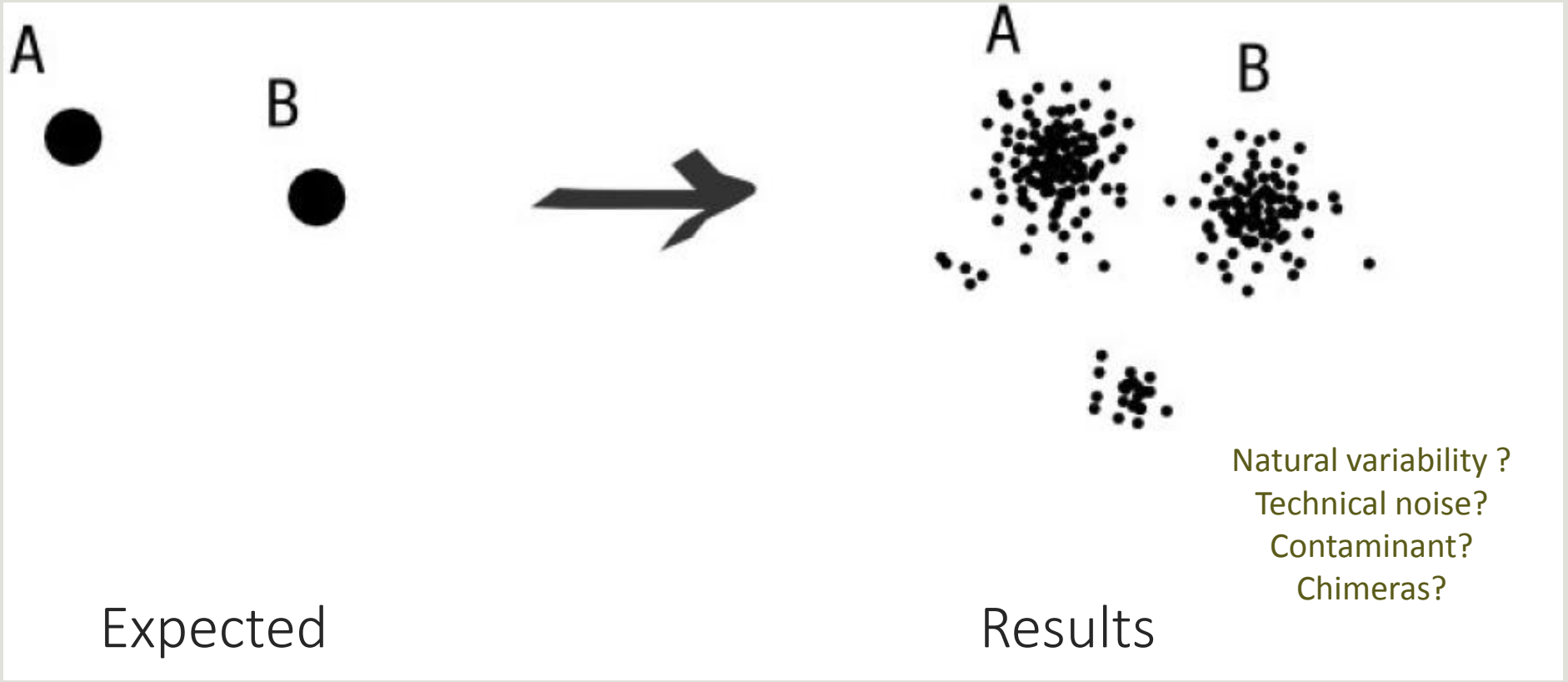

FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation

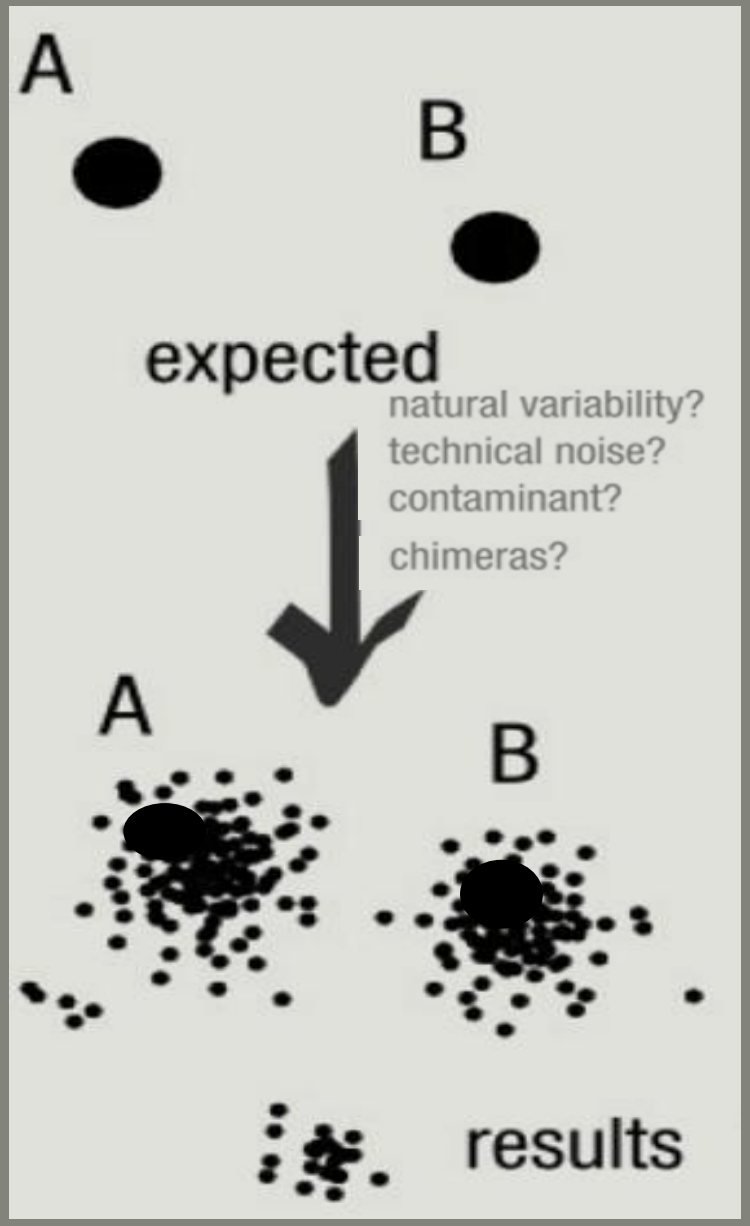
Why do we need clustering ?

Amplication and sequencing and are not perfect processes




A
B
A
B
Natural variability ?
Technical noise?
Contaminant?
Chimeras?
Expected
Results


A
B
A
B
Natural variability ?
Technical noise?
Contaminant?
Chimeras?
Expected
Results



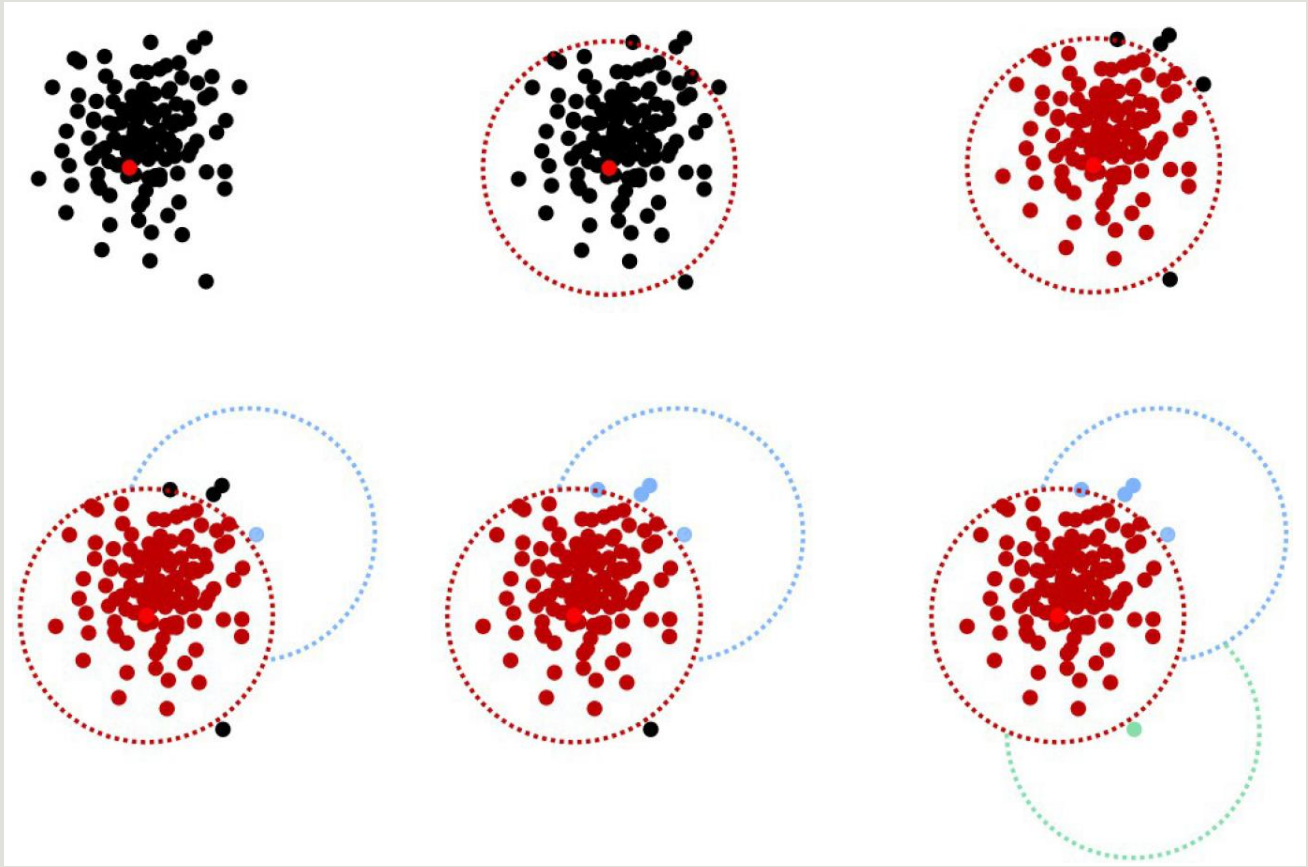
To have the best accuracy:

Method: All against all

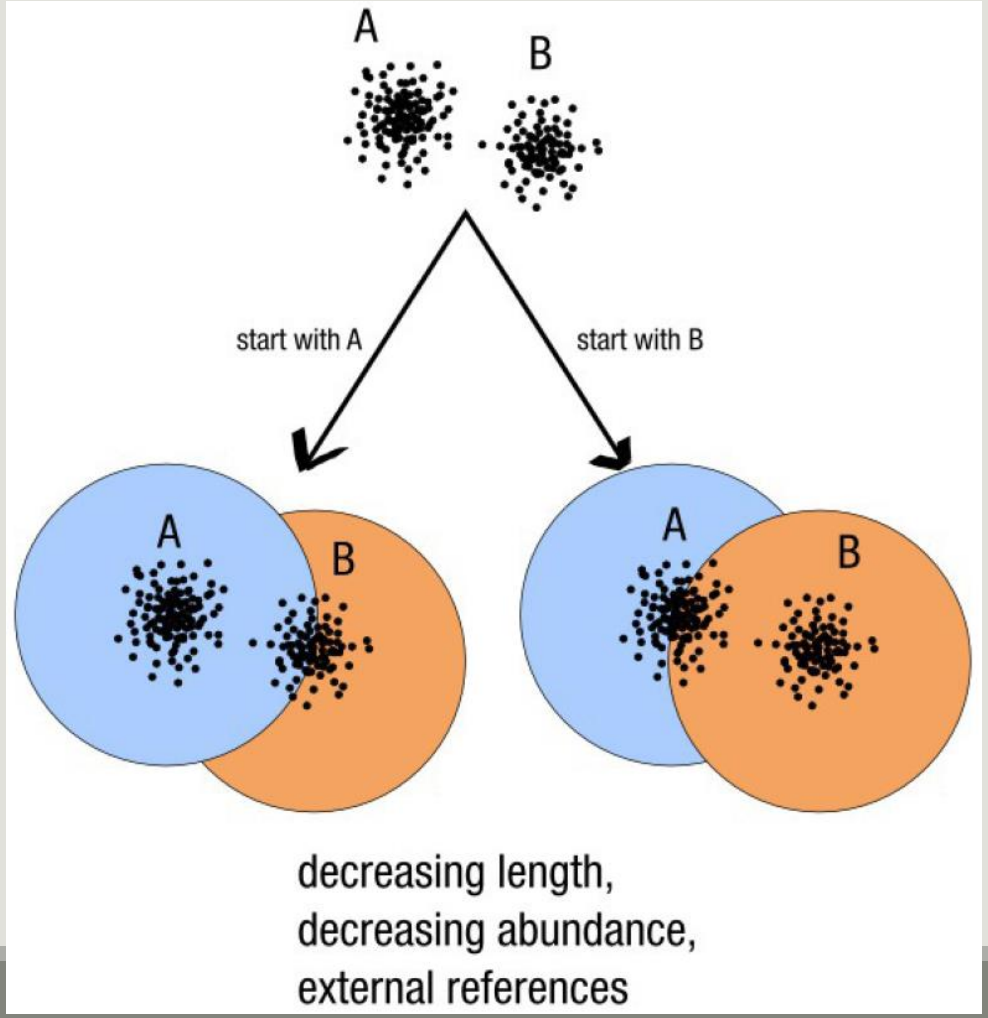
- Very accurate
- Requires a lot of memory and/or time

=> Impossible on very large datasets without strong filtering or sampling

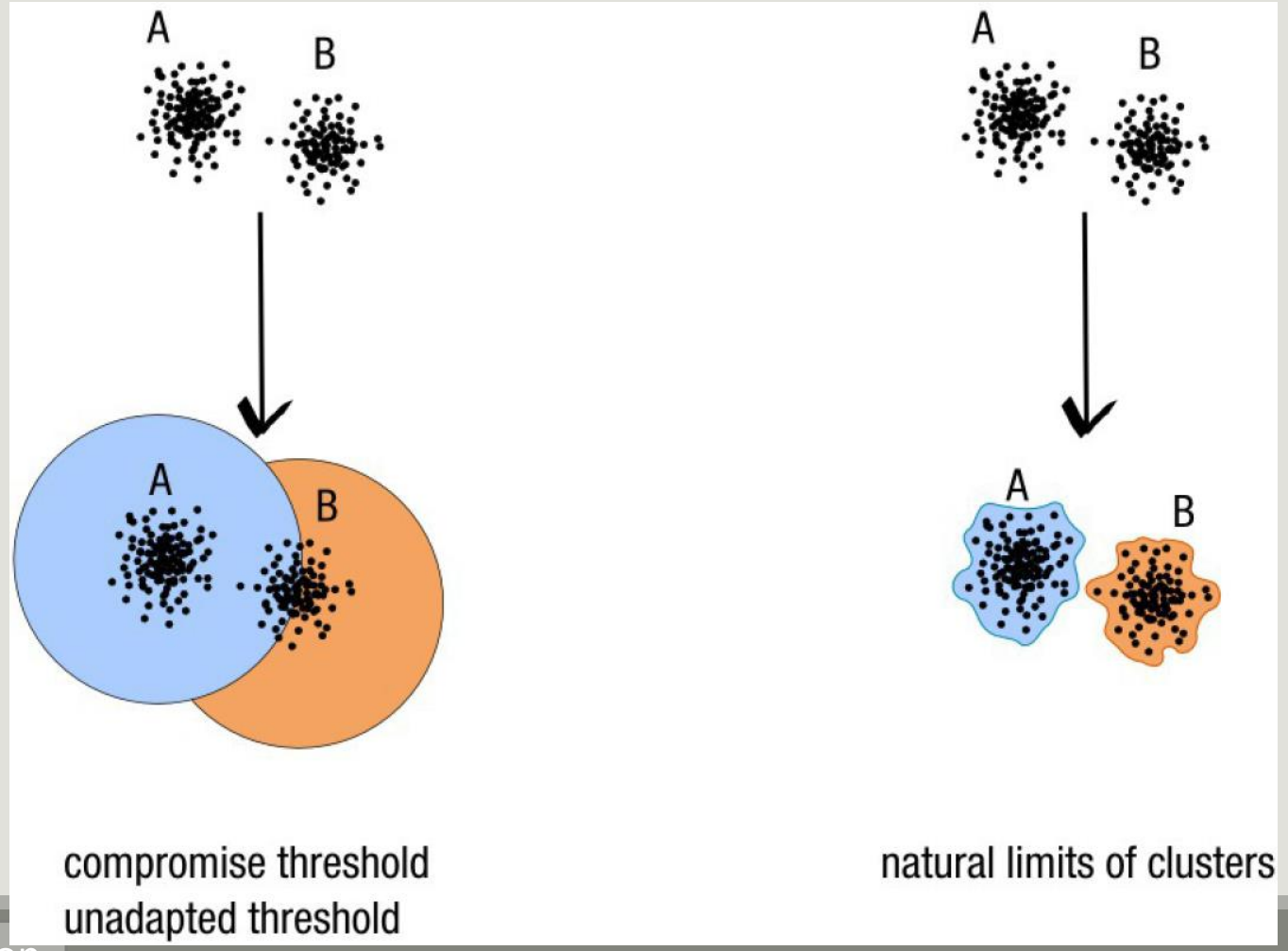
How traditional clustering works ?



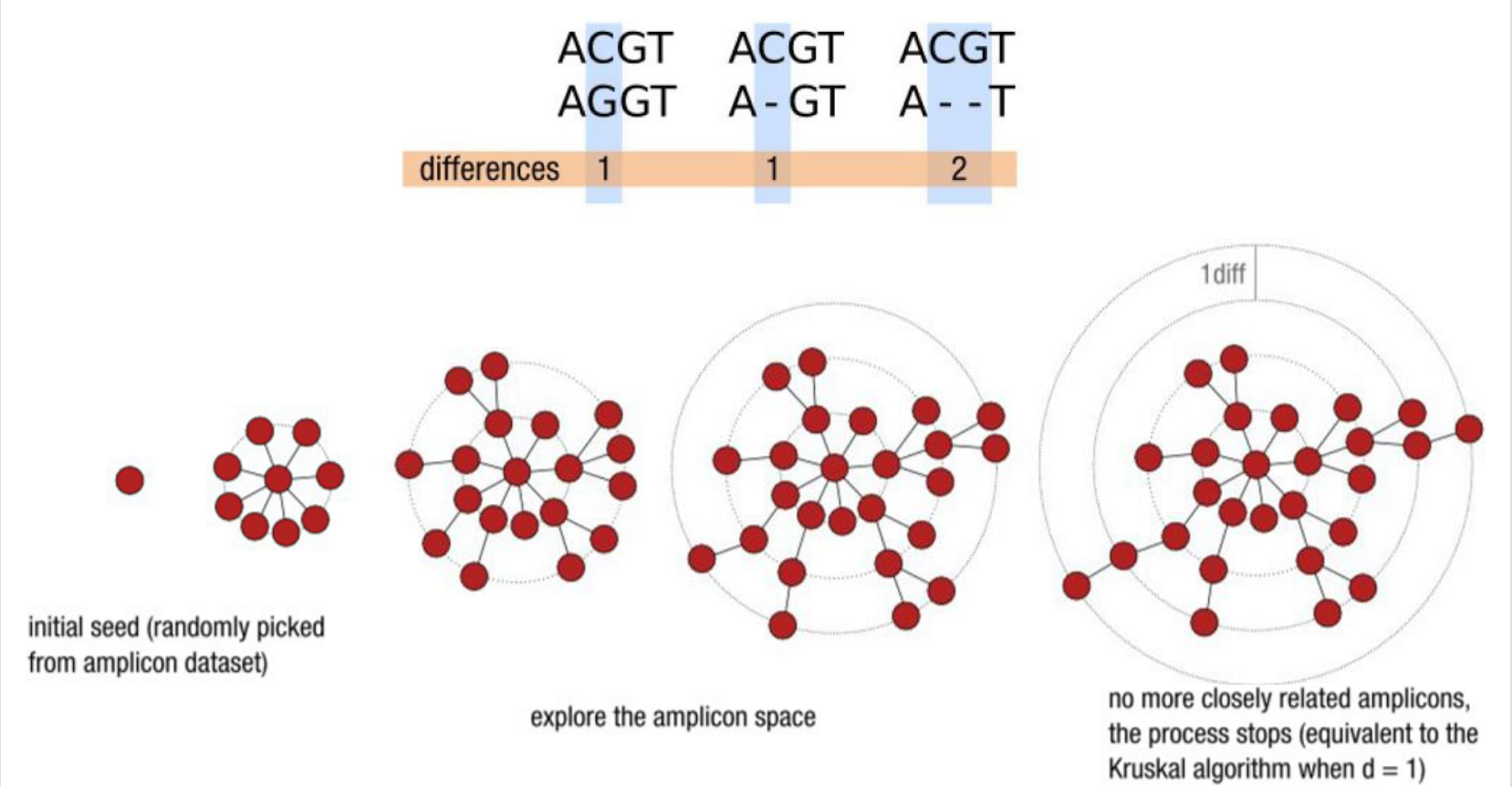
Input order dependent results



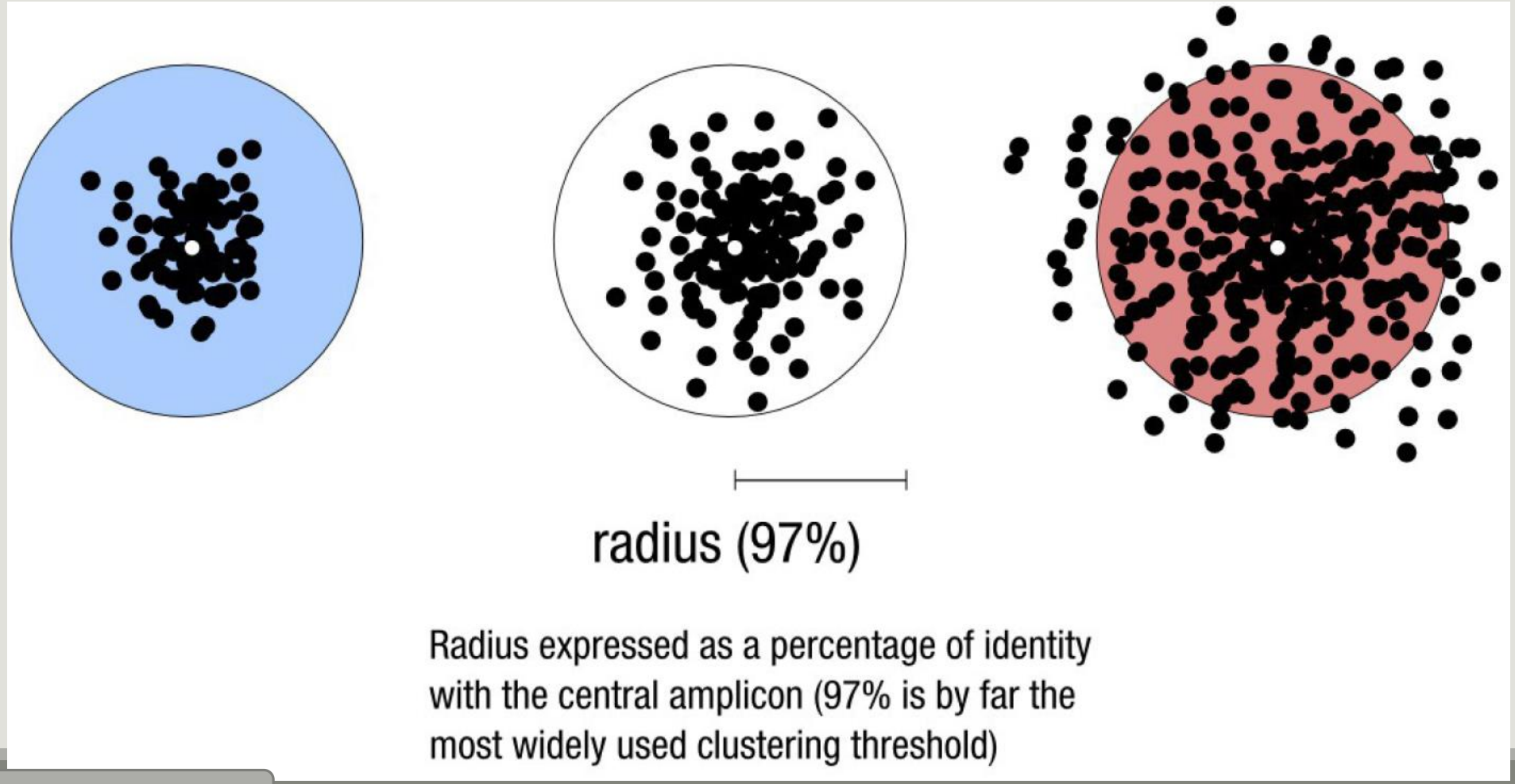
Single a priori clustering threshold



Swarm clustering method

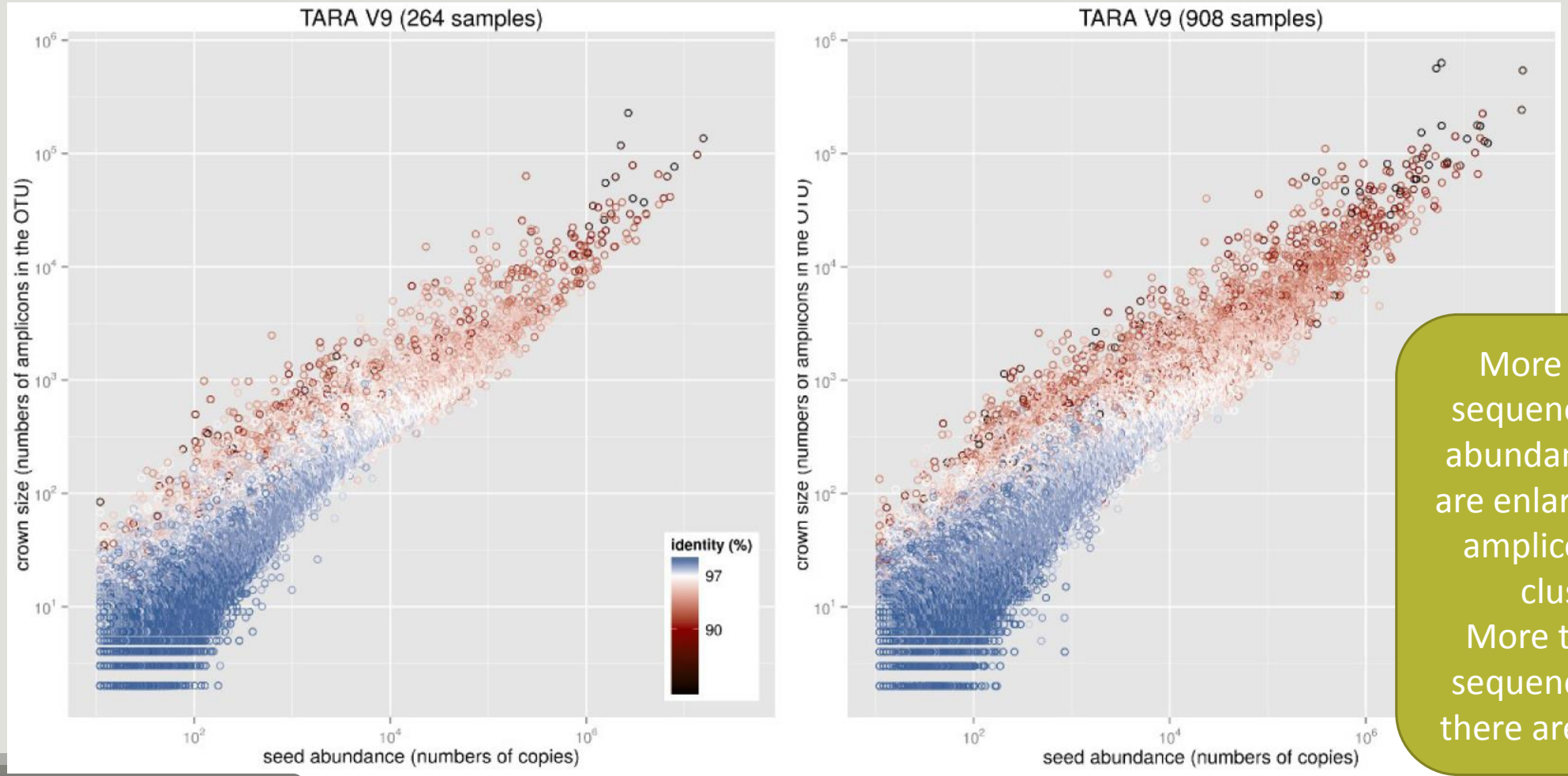


Comparison Swarm and 3% clusterings



Radius expressed as a percentage of identity with the central amplicon (97% is by far the most widely used clustering threshold)

Comparison Swarm and 3% clusterings



clusters produced with swarm using d = 1

More there is sequences, more abundant clusters are enlarged (more amplicon in the cluster).
More there are sequences, more there are artefacts

SWARM

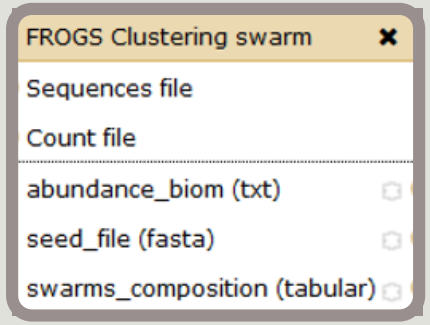
A robust and fast clustering method for amplicon-based studies.

The purpose of **swarm** is to provide a novel clustering algorithm to handle large sets of amplicons.

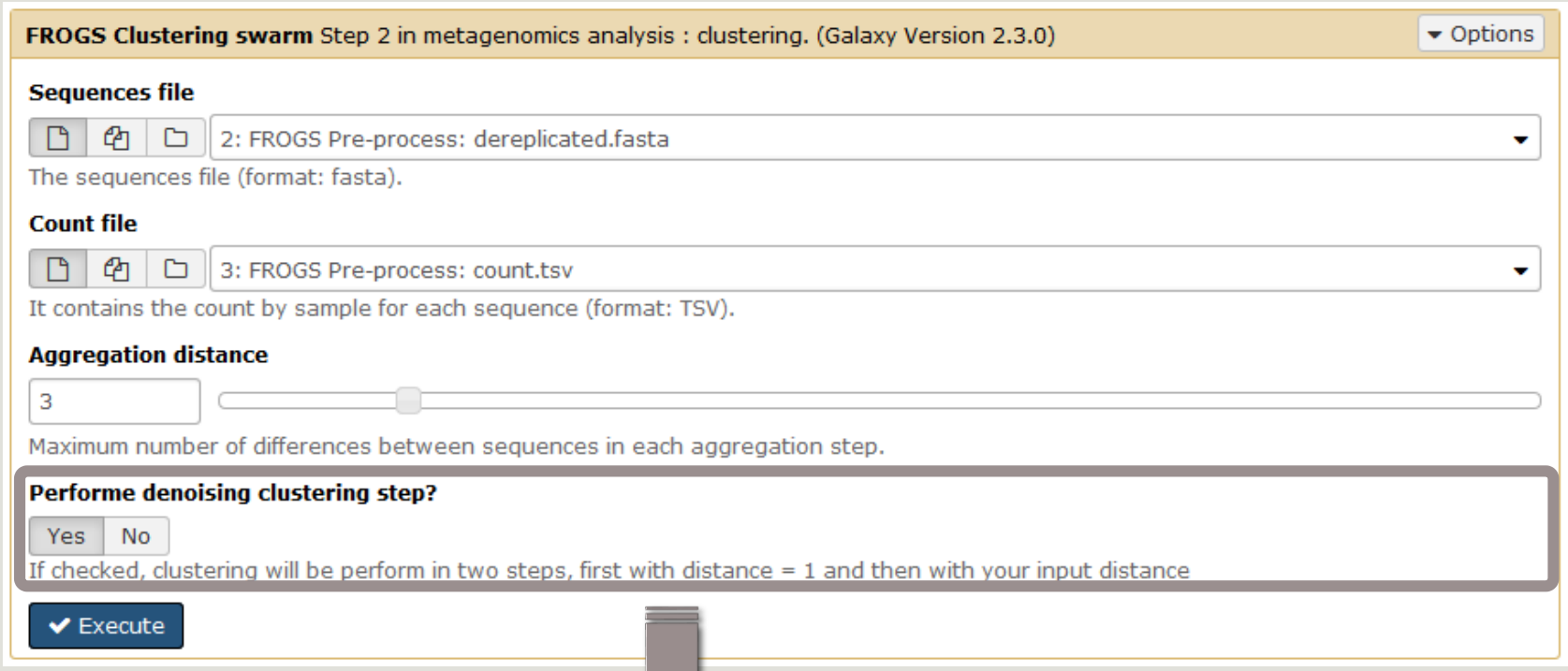
swarm results are resilient to input-order changes and rely on a small **local** linking threshold *d*, the maximum number of differences between two amplicons.

swarm forms stable high-resolution clusters, with a high yield of biological information.

Swarm: robust and fast clustering method for amplicon-based studies.
Mahé F, Rognes T, Quince C, de Vargas C, Dunthorn M.
PeerJ. 2014 Sep 25;2:e593. doi: 10.7717/peerj.593. eCollection 2014.
PMID:25276506



Clustering



<u>1st run for denoising:</u>
Swarm with d = 1 -> high clusters definition
linear complexity

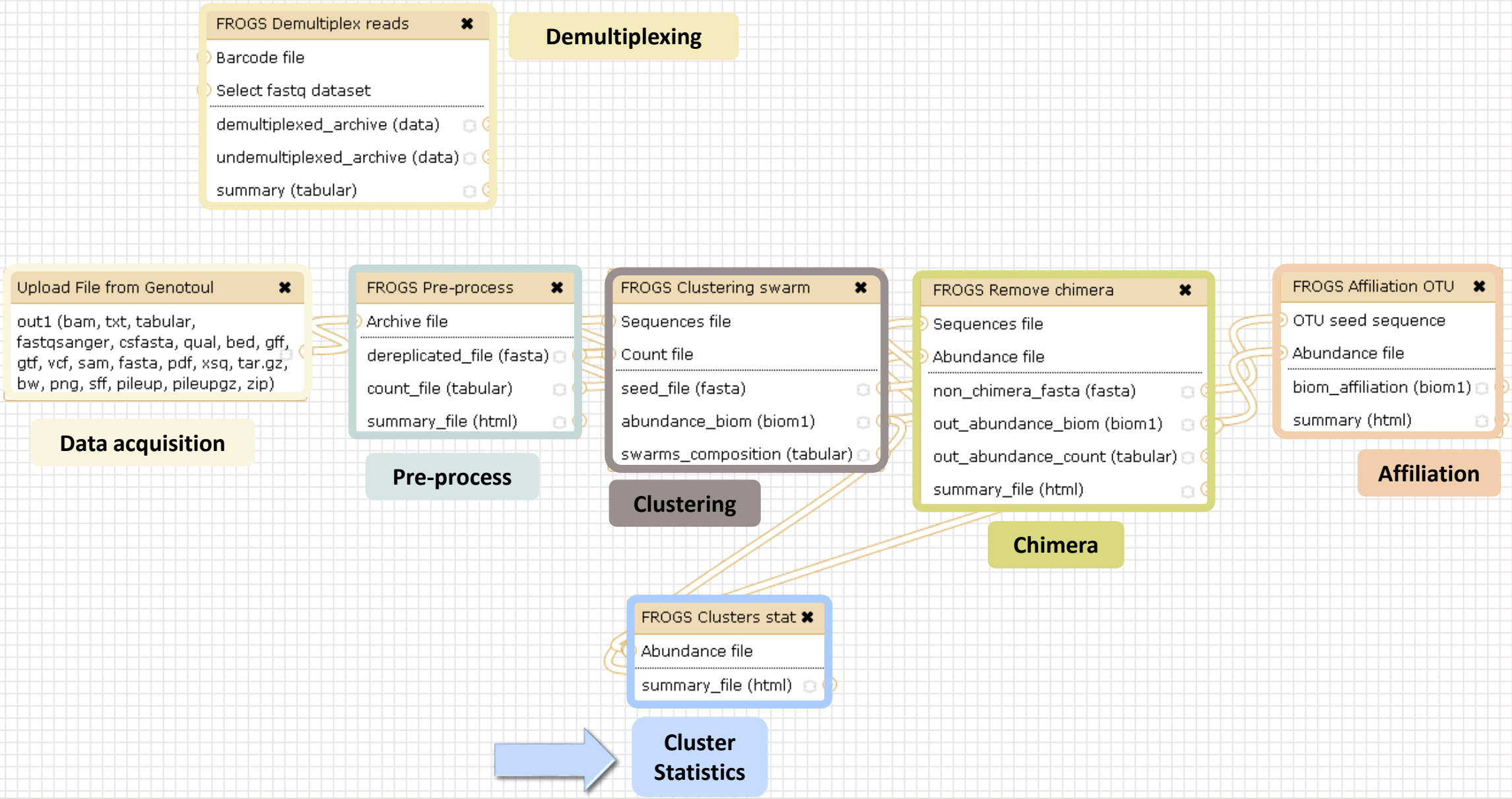
<u>2nd run for clustering:</u>
Swarm with d = 3 on the seeds of first Swarm
quadratic complexity

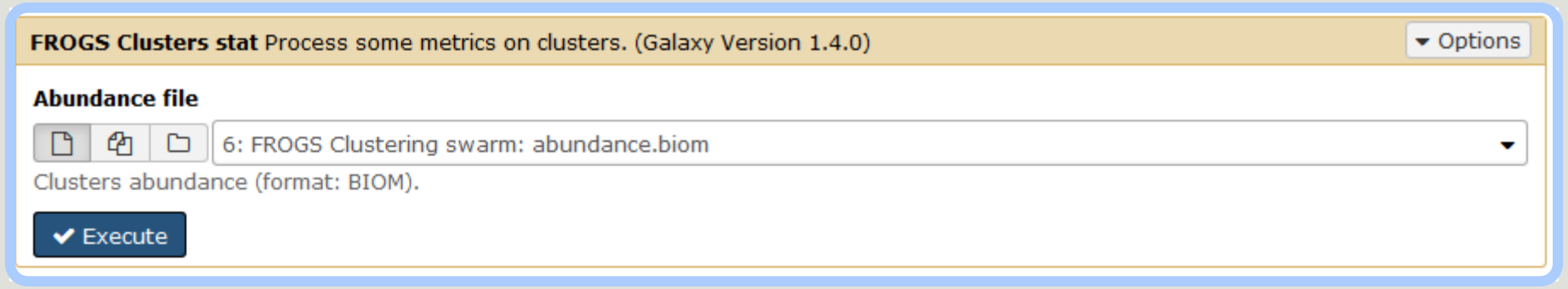
Gain time !

Remove false positives !

PeerJ PrePrints 2:e386v1. 2014. doi: 10.7287/peerj.preprints.386v1
Swarm: robust and fast clustering method for amplicon-based studies.
Mahé F, Rognes T, Quince C, de Vargas C, Dunthorn M.

Cluster stat tool


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics


FROGS Clusters stat Process some metrics on clusters. (Galaxy Version 1.4.0)
Options
Abundance file
6: FROGS Clustering swarm: abundance.biom
Clusters abundance (format: BIOM).
Execute

Your Turn! - 4

LAUNCH CLUSTERING AND CLUSTERSTAT TOOLS

MiSeq merged

Exercise 4

Go to « MiSeq merged » history

Launch the Clustering SWARM tool on that data set with aggregation distance = 3 and the denoising

→ objectives :

- understand the denoising efficiency
- understand the ClusterStat utility

MiSeq merged

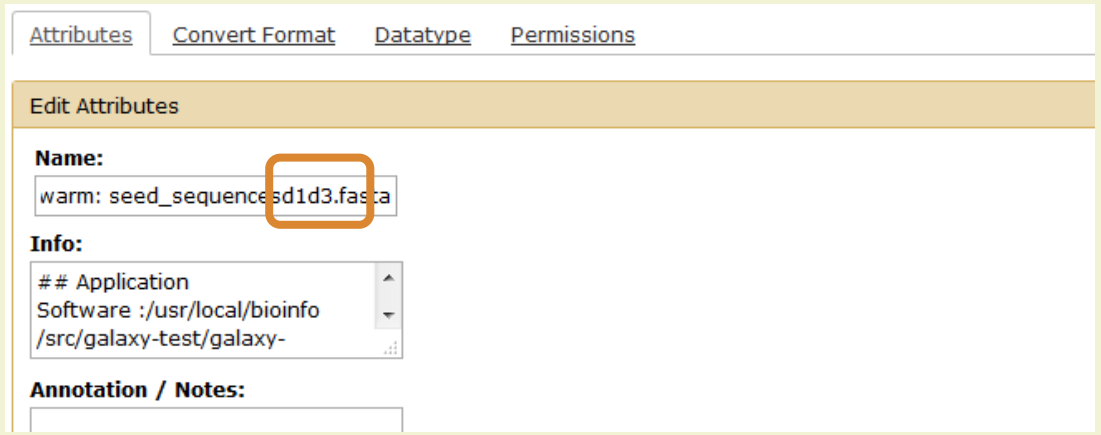
Exercise 4

1. How much time does it take to finish?
2. How many clusters do you get ?

MiSeq merged

Exercise 4

3. Edit the biom and fasta output dataset by adding d1d3



FROGS Clusters stat Process some metrics on clusters.

4. Launch FROGS Cluster Stat tools on the previous abundance biom file

MiSeq merged

Exercise 4

5. Interpret the boxplot: **Clusters size summary**
6. Interpret the table: **Clusters size details**
7. What can we say by observing the **sequence distribution**?
8. How many clusters share “sampleB3” with at least one other sample?
9. How many clusters could we expect to be shared ?
10. How many sequences represent the 550 specific clusters of “sampleC2”?
11. This represents what proportion of “sampleC2”?
12. What do you think about it?
13. How do you interpret the « Hierarchical clustering » ?

The « Hierachical clustering » is established with a Bray Curtis distance particularly well adapted to abundance table of very heterogenous values (very big and very small figures).

Sigenae - Welcome mbernard | Analyze Data | Workflow | Shared Data | Visualization | Admin | Help | User | Using 5%

Tools

deepTools

FROGS - FIND RAPIDLY OTU WITH GALAXY SOLUTION

FROGS pipeline

- FROGS Upload archive from your computer
- FROGS Demultiplex reads Split by samples the reads in function of inner barcode.
- FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication.
- FROGS Clustering swarm Step 2 in metagenomics analysis : clustering.
- FROGS Remove chimera Step 3 in metagenomics analysis : Remove PCR chimera in each sample.
- FROGS Filters Filters OTUs on several criteria.
- FROGS Affiliation OTU Step 4 in metagenomics analysis : Taxonomic affiliation of each OTU's seed by RDPtools and BLAST
- FROGS BIOM to TSV Converts a BIOM file in TSV file.
- FROGS Clusters stat Process some metrics on clusters.
- FROGS Affiliations stat Process some metrics on taxonomies.
- FROGS BIOM to std BIOM Converts a FROGS BIOM in fully compatible BIOM.
- FROGS Abundance normalisation

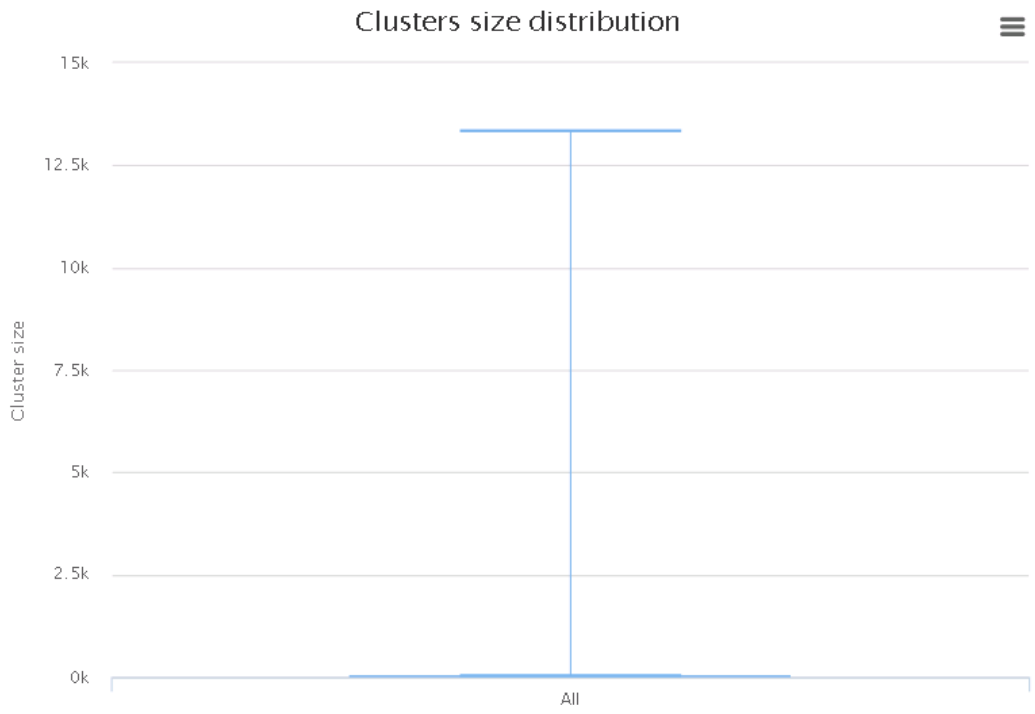
Clusters distribution | Sequences distribution | Samples distribution

Clusters: 5,945

Sequences: 89,721

Most of clusters are singletons

Clusters size summary



Clusters size distribution (decile)

Decile	Value
Min	1
1	1
2	1
3	1
4	1
Median	1
6	1
7	1
8	2
9	2
Max	13,337

History

15: FROGS Filters: sequences.fasta

14: FROGS Remove chimera: report.html

13: FROGS Remove chimera: non_chimera_abundance.biom

12: FROGS Remove chimera: non_chimera.fasta

11: FROGS Clusters stat: summary_swarm_d1d3.html

format: html, database: ?
Application Software :/usr/local/bioinfo/src/galaxy-dev/galaxy-dist/tools/FROGS/tools/clusters_stat.py (version : 1.1.0)
Command : /usr/local/bioinfo/src/galaxy-dev/galaxy-dist/tools/FROGS/tools/clusters_stat.py --input-biom /galaxydata/database/file

HTML file

10: FROGS Clustering swarm: swarms_composition_d1d3.tsv

9: FROGS Clustering swarm: abundance_d1d3.biom

8: FROGS Clustering swarm: seed_sequences_d1d3.fasta

7: FROGS Pre-process: report.html

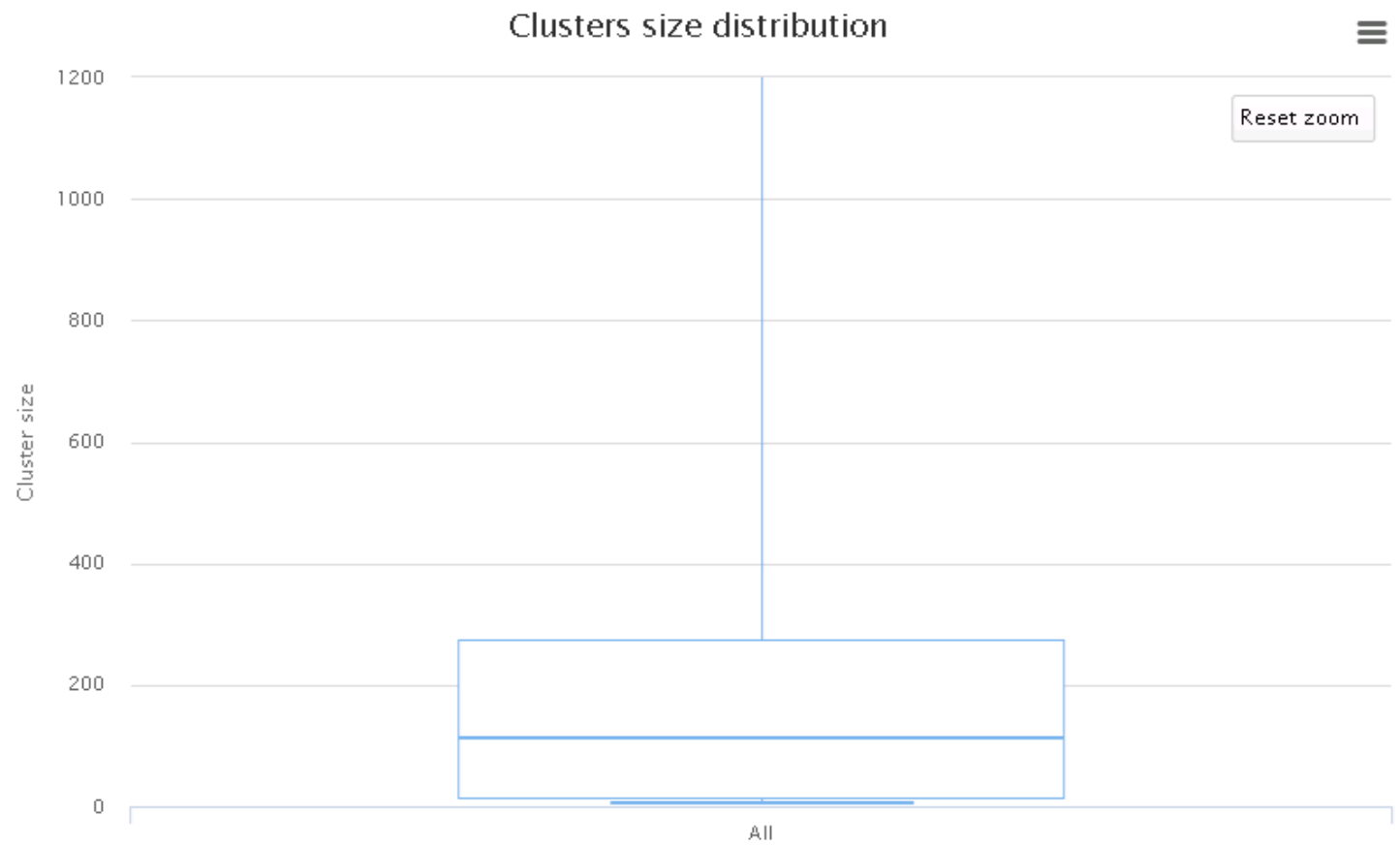
Clusters distribution | Sequences distribution | Samples distribution

Clusters
141

Sequences
81,838

Clusters size summary

After filtering little clusters



Clusters size distribution (decile)

Decile	Value
Min	5
1	6
2	8
3	30
4	70
Median	112
6	145
7	225
8	412
9	994
Max	13,337

Clusters size details

Most of clusters are singletons

CSV

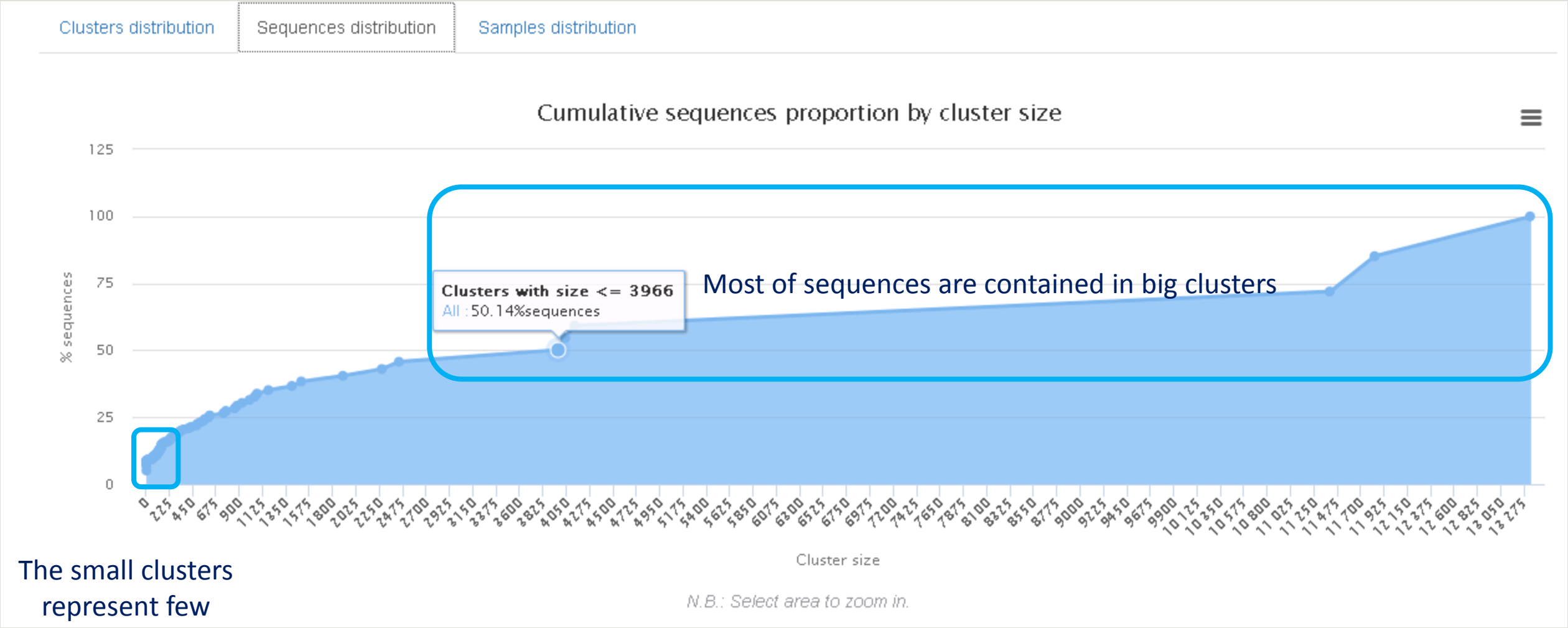
Show 10 entries

Search:

Clusters size

Cluster size	Number of cluster	% of all clusters
1	4,595	77.36
2	866	14.58
3	155	2.61
4	83	1.40
5	42	0.71
6	29	0.49
7	22	0.37
8	13	0.22
9	6	0.10
10	6	0.10

After clustering



The small clusters represent few sequences

Sequences

367 clusters of sampleA1 are common at least once with another sample

58 % of the specific clusters of sampleA1 represent around 5% of sequences
Could be interesting to remove if individual variability is not the concern of user

CSV

Show 10 entries

Samples information

Sample	Shared clusters	Own clusters	Shared sequences	Own sequences
100_10000seq_sampleA1	367	513	9,447	528
100_10000seq_sampleA2	365	490	9,476	503
100_10000seq_sampleA3	384	483	9,478	494
100_10000seq_sampleB1	395	548	9,397	572
100_10000seq_sampleB2	375	508	9,455	515
100_10000seq_sampleB3	376	562	9,388	579
100_10000seq_sampleC1	372	539	9,413	552
100_10000seq_sampleC2	389	550	9,408	567
100_10000seq_sampleC3	361	516	9,442	525

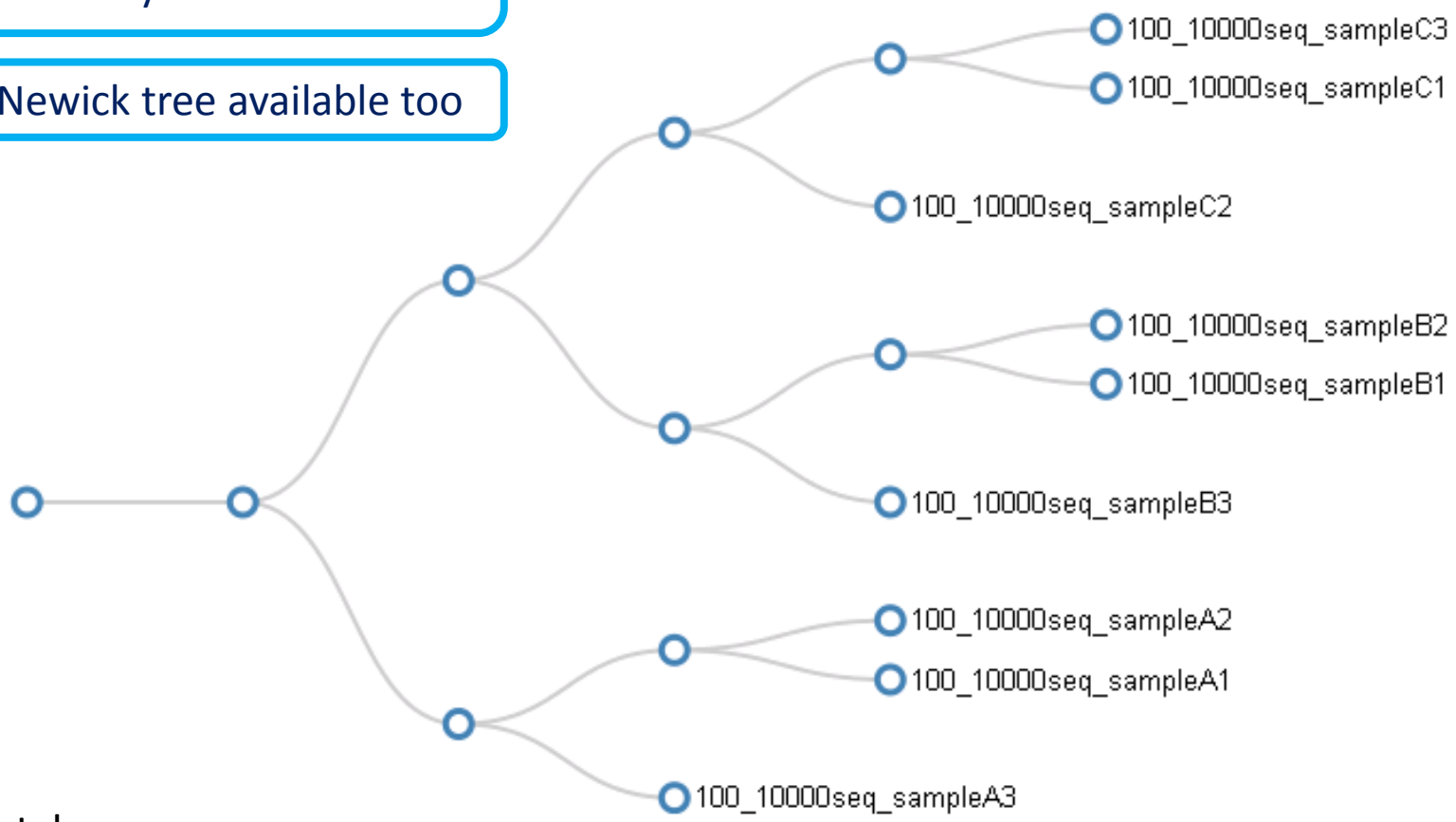
Showing 1 to 9 of 9 entries

Previous 1 Next

Hierachical clustering

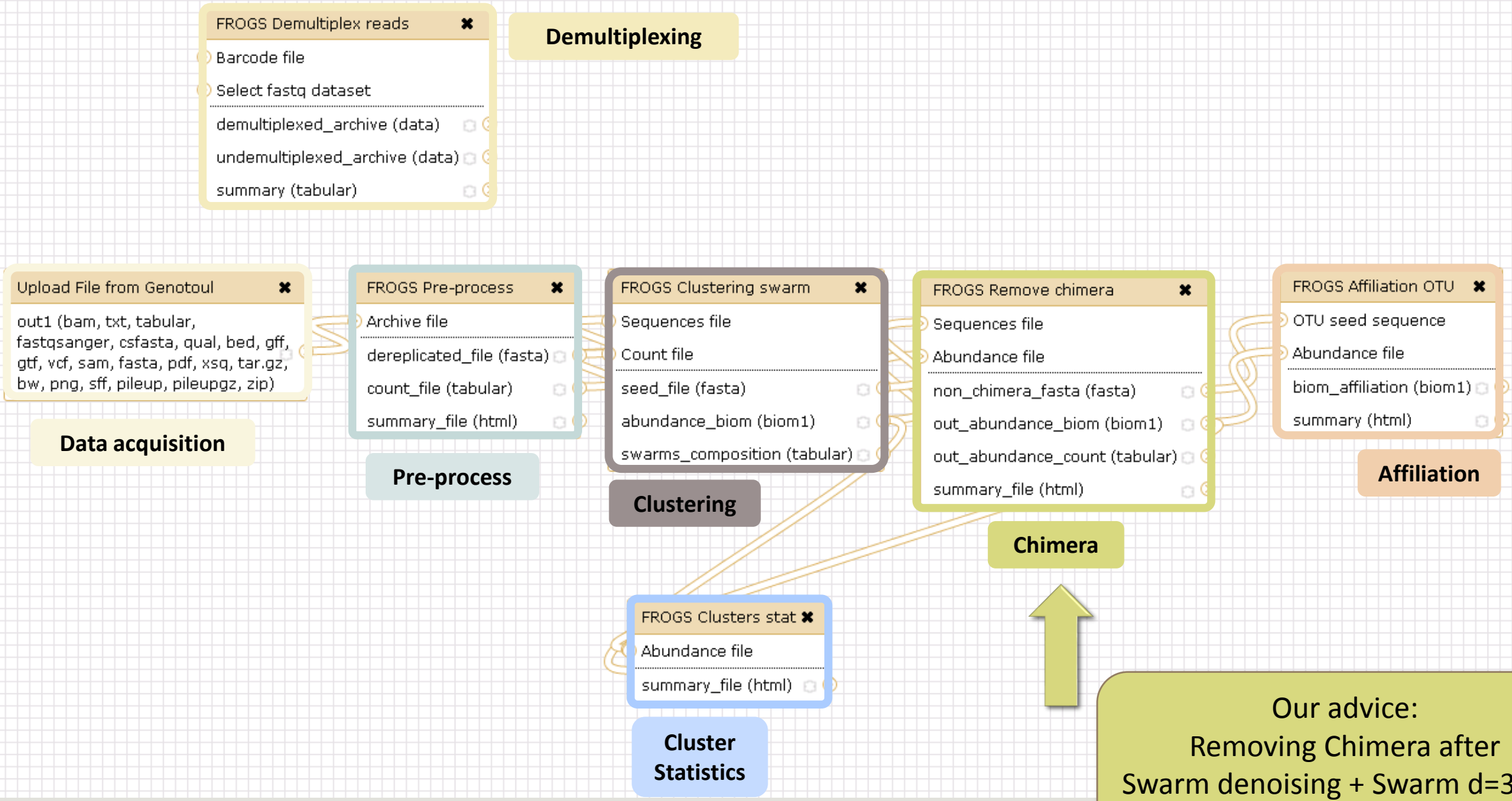
Hierarchical classification on Bray Curtis distance

Newick tree available too



Samples distribution tab

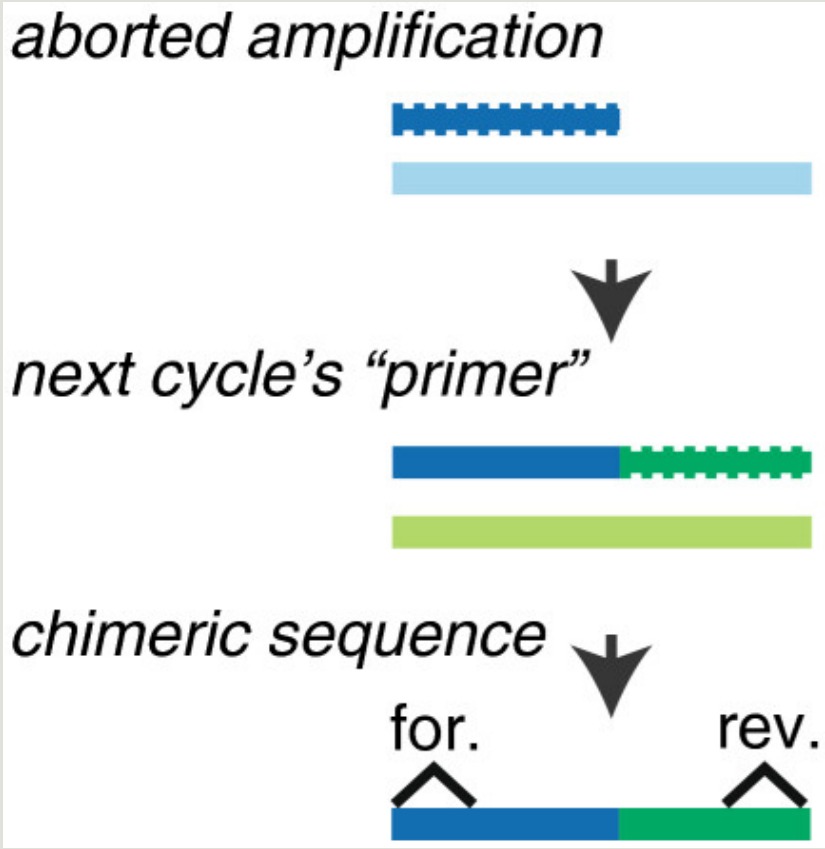
Chimera removal tool


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
Our advice:
Removing Chimera after
Swarm denoising + Swarm d=3, for
saving time without sensitivity loss

What is chimera ?

PCR-generated chimeras are typically created when an aborted amplicon acts as a primer for a heterologous template. Subsequent chimeras are about the same length as the non-chimeric amplicon and contain the forward (for.) and reverse (rev.) primer sequence at each end of the amplicon.

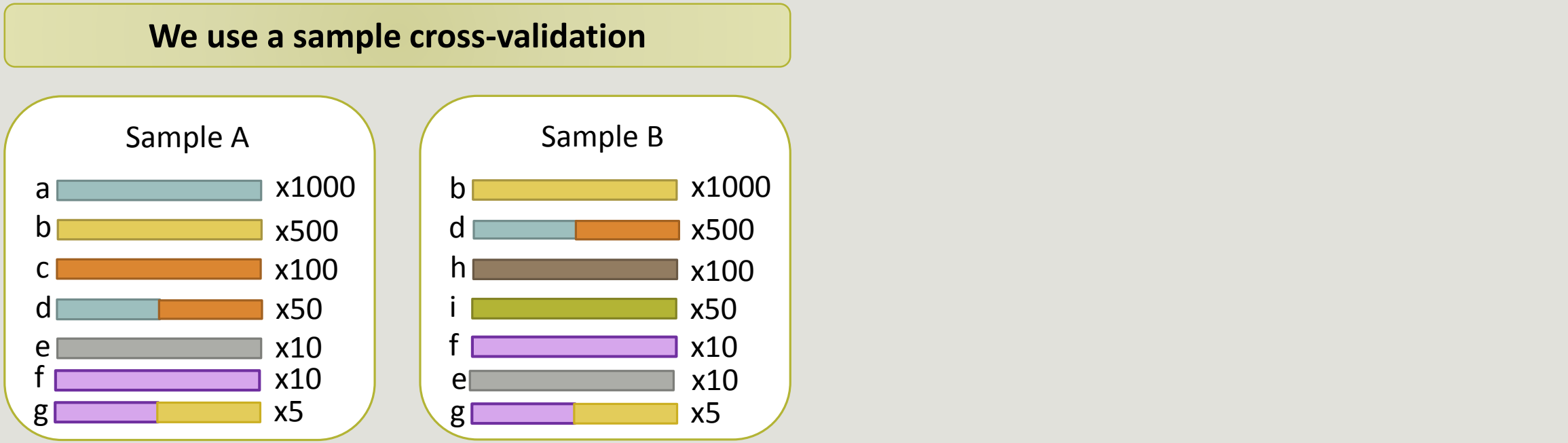
Chimera: from 5 to 45% of reads (Schloss 2011)



Fichot and Norman *Microbiome* 2013 **1**:10
doi:10.1186/2049-2618-1-10

A smart removal chimera to be accurate

We use a sample cross-validation



“ **d** ” is view as chimera by Vsearch
Its “ parents ” are presents

“ **d** ” is view as normal sequence by Vsearch
Its “ parents ” are absents

⇒ For FROGS “d” is not a chimera
⇒ For FROGS “g” is a chimera, “g” is removed
⇒ FROGS increases the detection specificity

Your Turn! - 5

LAUNCH THE REMOVE CHIMERA TOOL

MiSeq merged

Exercise 5

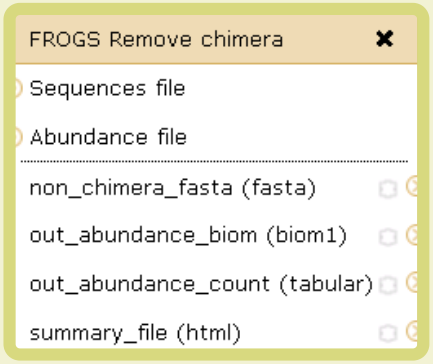
Go to « MiSeq merged » history

Launch the « FROGS Remove Chimera » tool

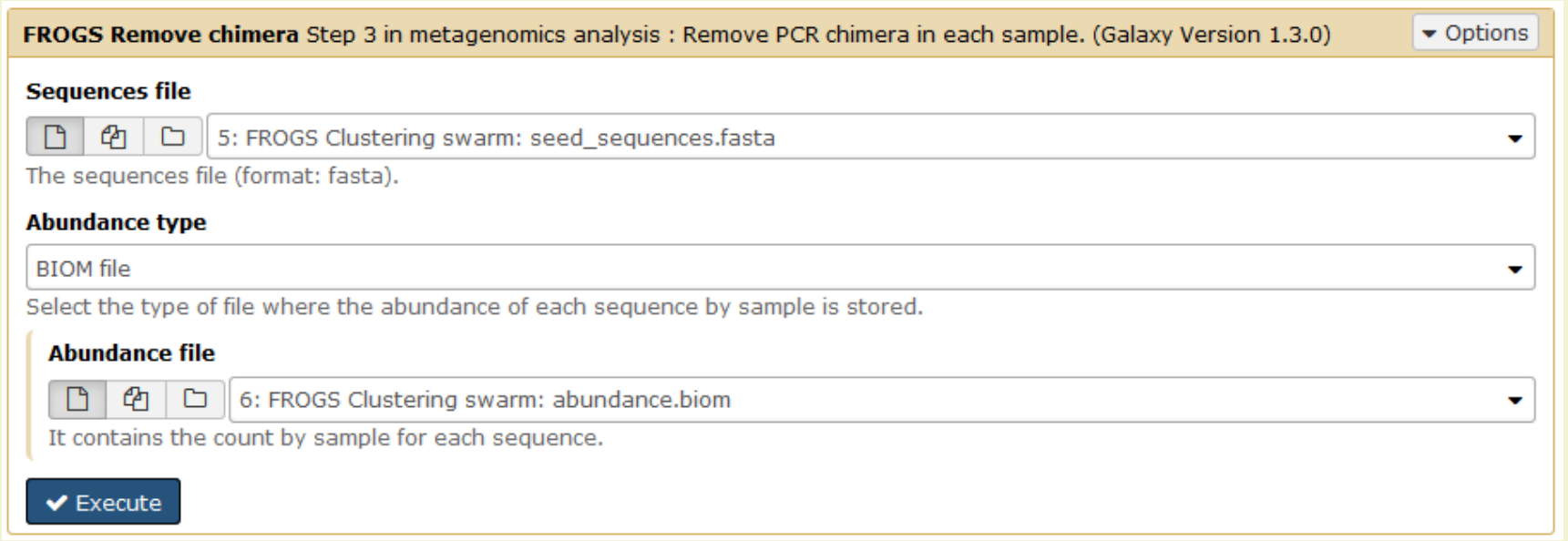
Follow by the « FROGS ClusterStat » tool on the swarm d1d3 non chimera abundance biom

→ objectives :

- understand the efficiency of the chimera removal
- make links between small abundant OTUs and chimeras


FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)

Chimera


FROGS Remove chimera Step 3 in metagenomics analysis : Remove PCR chimera in each sample. (Galaxy Version 1.3.0)
Options
Sequences file
5: FROGS Clustering swarm: seed_sequences.fasta
The sequences file (format: fasta).
Abundance type
BIOM file
Select the type of file where the abundance of each sequence by sample is stored.
Abundance file
6: FROGS Clustering swarm: abundance.biom
It contains the count by sample for each sequence.
Execute

MiSeq merged

Exercise 5

1. Understand the « FROGS remove chimera : report.html»
   a. How many clusters are kept after chimera removal?
   b. How many sequences that represent ? So what abundance?
   c. What do you conclude ?

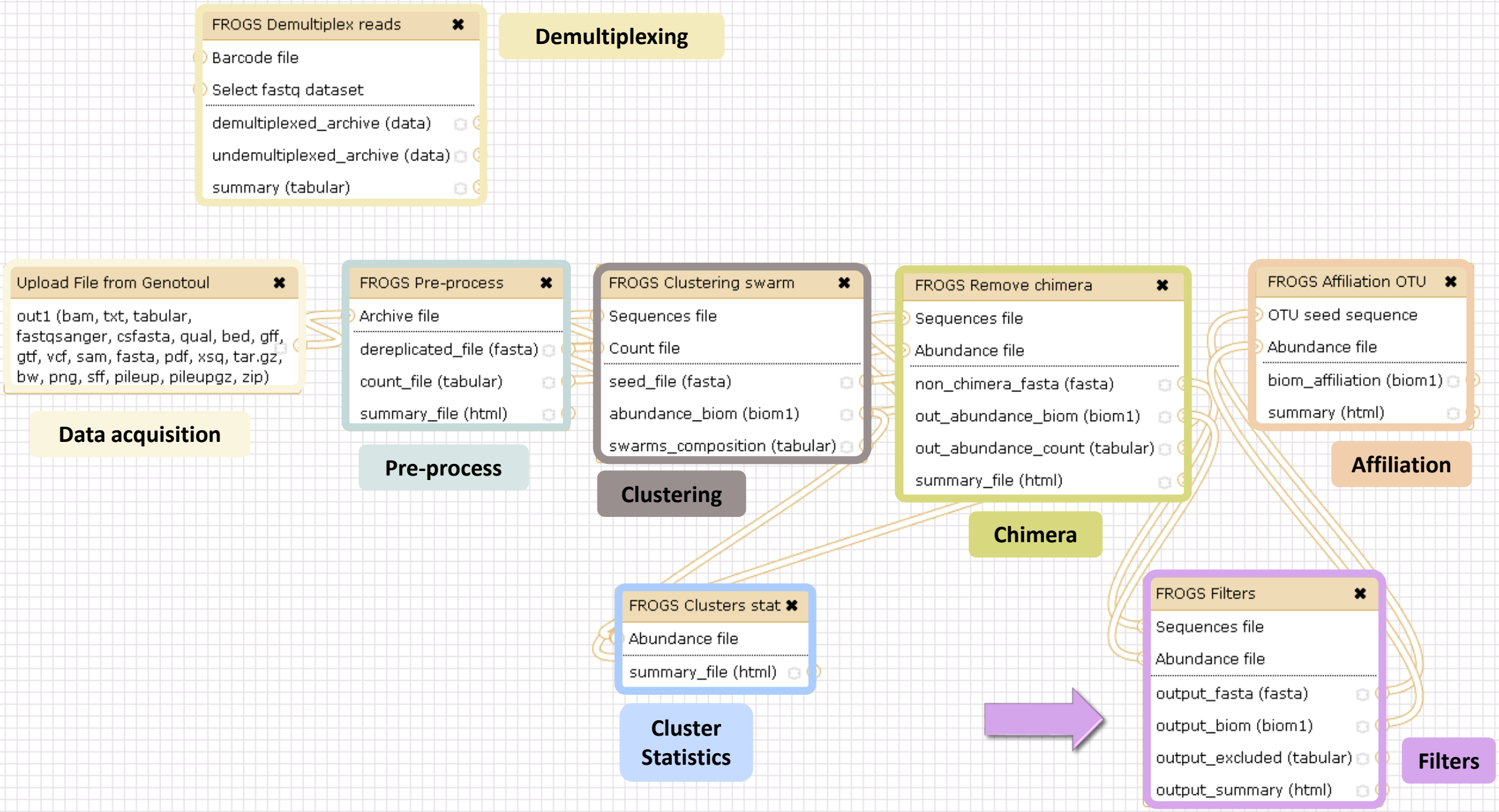
MiSeq merged

Exercise 5

2. Launch « FROGS ClusterStat » tool on non_chimera_abundanced1d3.biom
3. Rename output in summary_nonchimera_d1d3.html
4. Compare the HTML files
   a. Of what are mainly composed singleton ? (compare with precedent summary.html)
   b. What are their abundance?
   c. What do you conclude ?

The weakly abundant Clusters are mainly false positives, our data would be much more exact if we remove them

Filters tool


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters

Affiliation runs long time

Advise:

Apply filters between “Chimera Removal ” and “Affiliation”.
Remove OTUs with weak abundance and non redundant before affiliation.

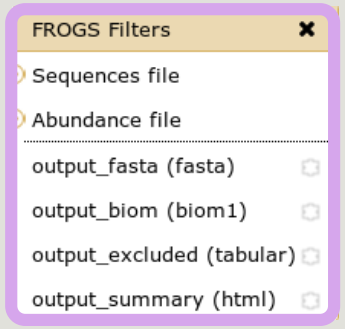
You will gain time !

Filters

Filters allows to filter the result thanks to different criteria et may be used after different steps of pipeline :

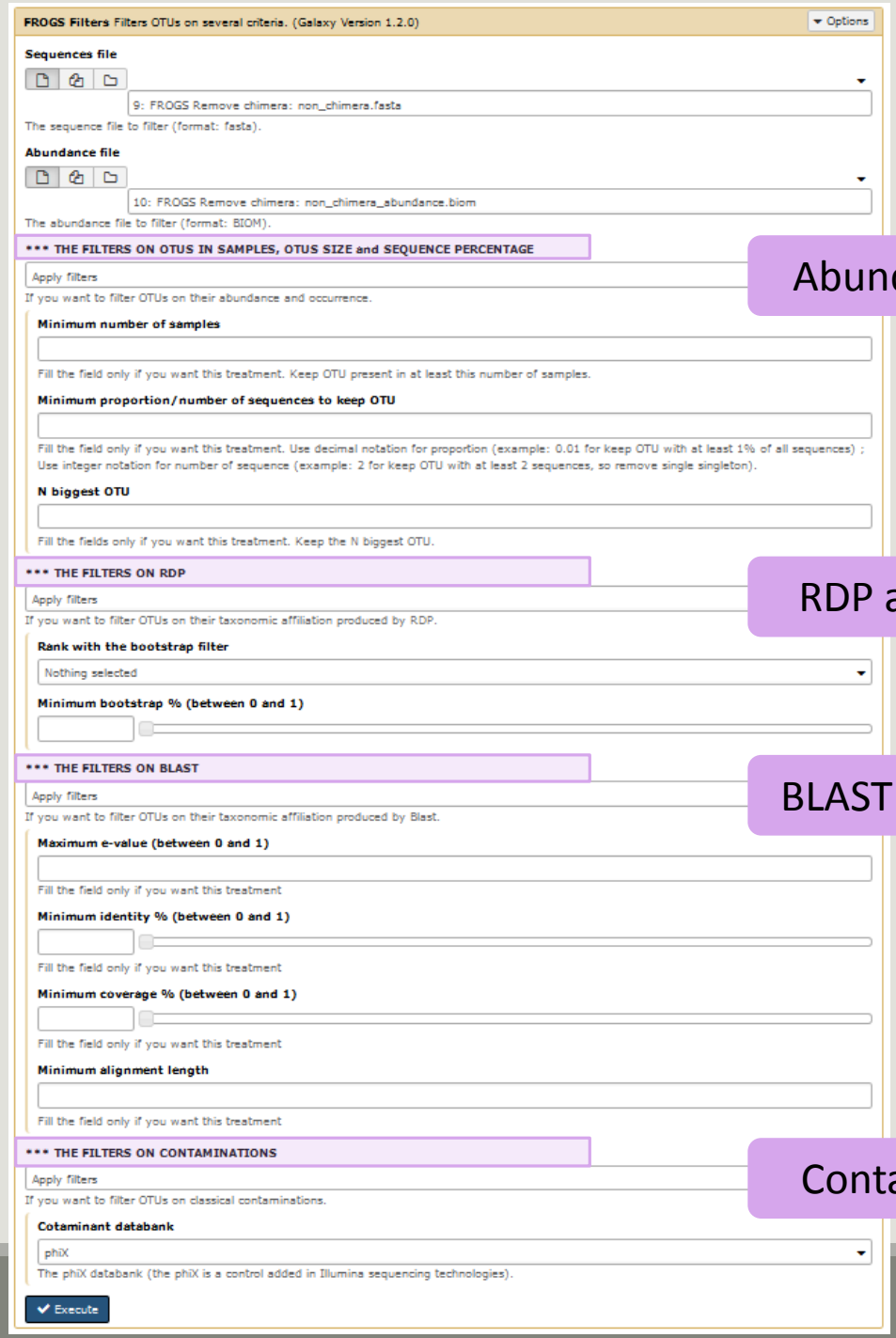
- On the abundance
- On RDP affiliation
- On Blast affiliation
- On phix contaminant

After Affiliation tool



Filters

4 filter sections



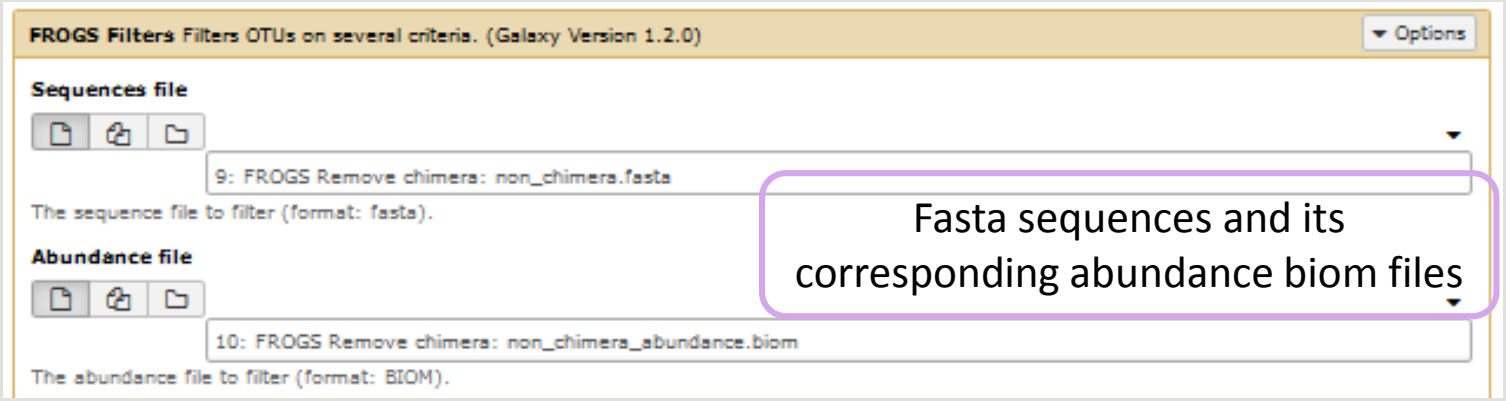
Abundance filters

RDP affiliation filters

BLAST affiliation filters

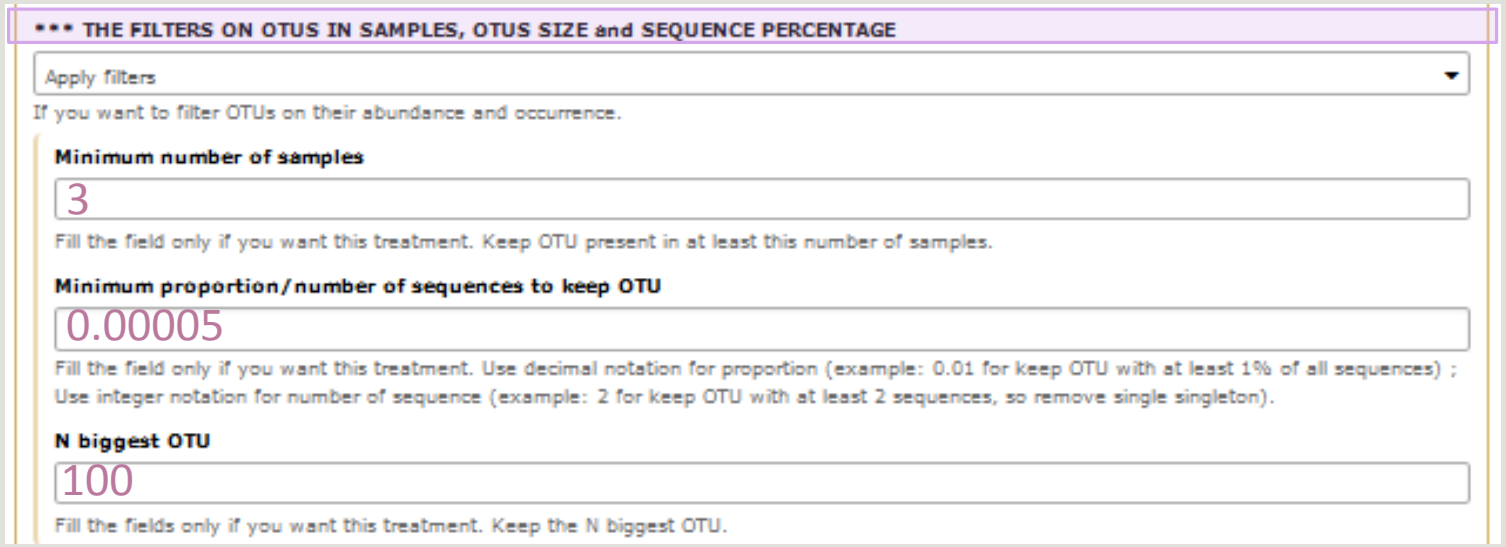
Contamination filter

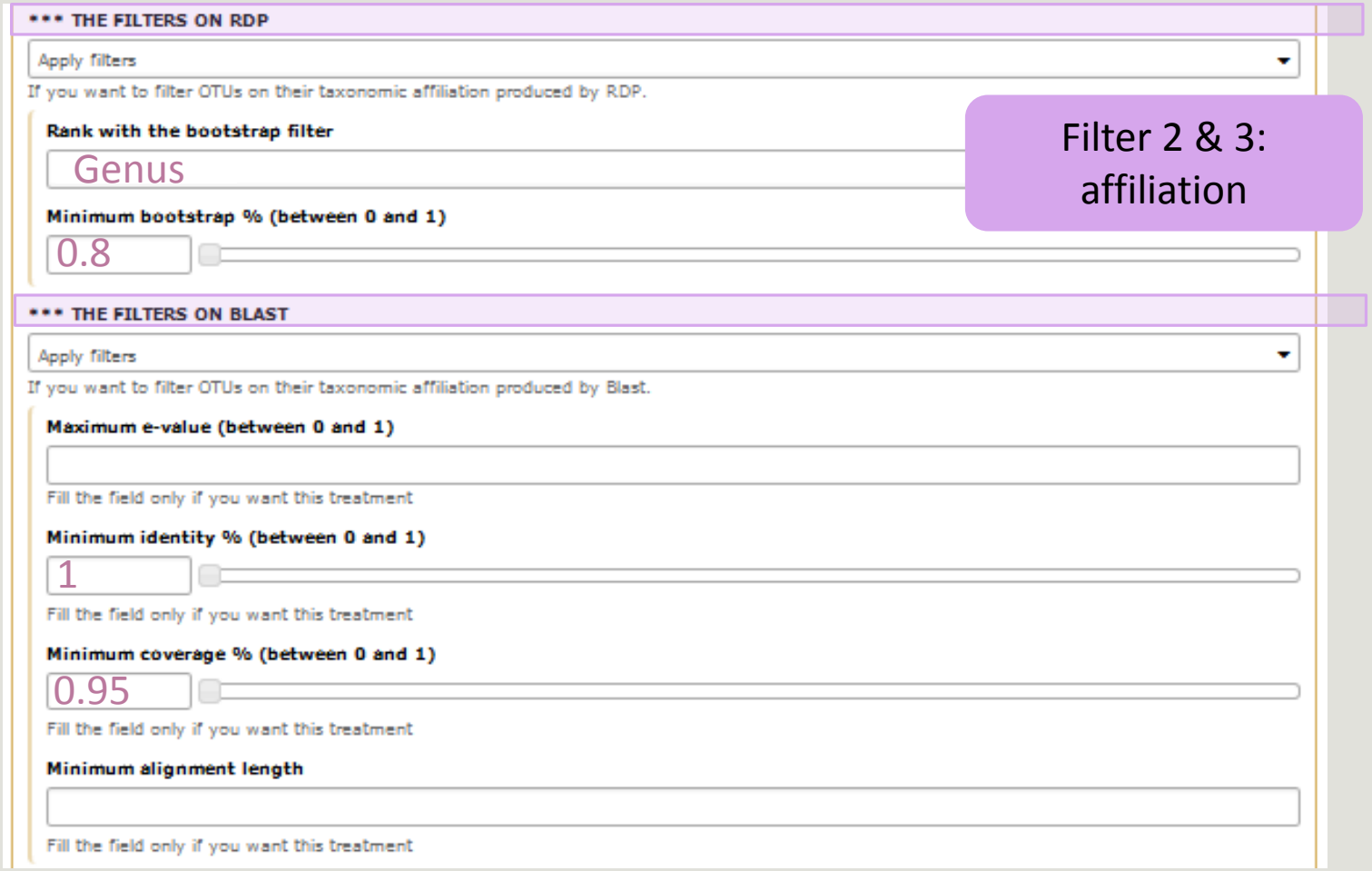
Input



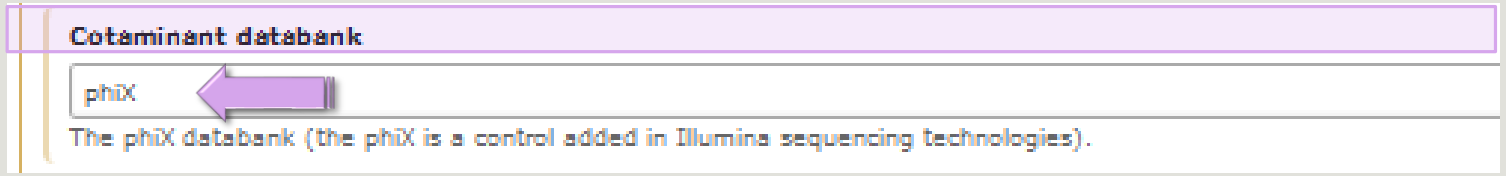
Fasta sequences and its corresponding abundance biom files

Filter 1 : abundance




*** THE FILTERS ON RDP
Apply filters
If you want to filter OTUs on their taxonomic affiliation produced by RDP.
Rank with the bootstrap filter
Genus
Minimum bootstrap % (between 0 and 1)
0.8
*** THE FILTERS ON BLAST
Apply filters
If you want to filter OTUs on their taxonomic affiliation produced by Blast.
Maximum e-value (between 0 and 1)
Fill the field only if you want this treatment
Minimum identity % (between 0 and 1)
1
Fill the field only if you want this treatment
Minimum coverage % (between 0 and 1)
0.95
Fill the field only if you want this treatment
Minimum alignment length
Fill the field only if you want this treatment
Filter 2 & 3: affiliation

Filter 4 :
contamination



Soon, several contaminant banks

Your Turn! - 6

LAUNCH DE LA TOOL FILTERS

MiSeq merged

Exercise 6

Go to history « MiSeq merged »

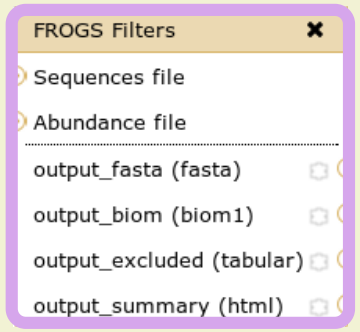
Launch « Filters » tool with non_chimera_abundanced1d3.biom, non_chimerad1d3.fasta

Apply 2 filters :

- Minimum proportion/number of sequences to keep OTU: 0.00005*
- Minimum number of samples: 3

→ objective : play with filters, understand their impacts on falses-positives OTUs

*Nat Methods. 2013 Jan;10(1):57-9. doi: 10.1038/nmeth.2276. Epub 2012 Dec 2.
Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing.
Bokulich NA1, Subramanian S, Faith JJ, Gevers D, Gordon JI, Knight R, Mills DA, Caporaso JG.



Filters

FROGS Filters Filters OTUs on several criteria. (Galaxy Version 1.2.0) — Options

Sequences file

9: FROGS Remove chimera: non_chimera.fasta

The sequence file to filter (format: fasta).

Abundance file

10: FROGS Remove chimera: non_chimera_abundance.biom

The abundance file to filter (format: BIOM).

***** THE FILTERS ON OTUS IN SAMPLES, OTUS SIZE and SEQUENCE PERCENTAGE**

Apply filters

If you want to filter OTUs on their abundance and occurrence.

Minimum number of samples

3

Fill the field only if you want this treatment. Keep OTU present in at least this number of samples.

Minimum proportion/number of sequences to keep OTU

0.00005

Fill the field only if you want this treatment. Use decimal notation for proportion (example: 0.01 for keep OTU with at least 1% of all sequences) ; Use integer notation for number of sequence (example: 2 for keep OTU with at least 2 sequences, so remove single singleton).

N biggest OTU

Fill the fields only if you want this treatment. Keep the N biggest OTU.

***** THE FILTERS ON RDP**

No filters

If you want to filter OTUs on their taxonomic affiliation produced by RDP.

***** THE FILTERS ON BLAST**

No filters

If you want to filter OTUs on their taxonomic affiliation produced by Blast.

***** THE FILTERS ON CONTAMINATIONS**

No filters

If you want to filter OTUs on classical contaminations.

Execute

Output

92: FROGS Filters: report.html

91: FROGS Filters: excluded.tsv

90: FROGS Filters: abundance.biom

89: FROGS Filters: sequences.fasta

If Filters fields are « Apply » so you have to fill at one field. Otherwise, galaxy become red !

MiSeq merged

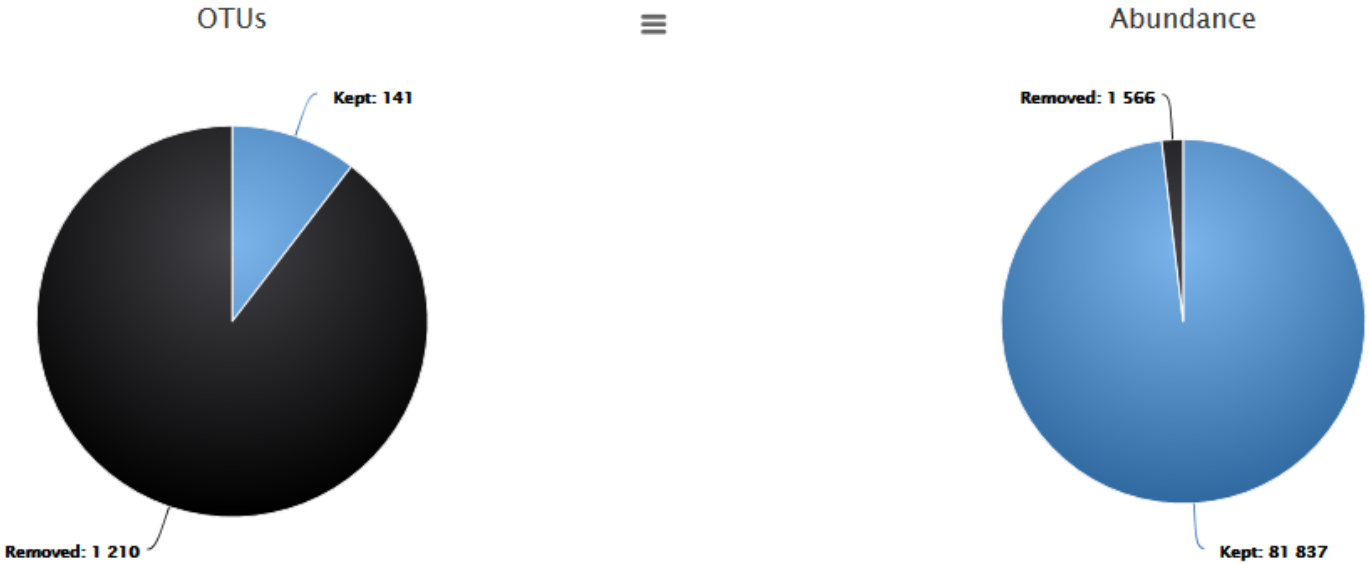
Exercise 6

1. What are the output files of “Filters” ?
2. Explore “FROGS Filter : report.html” file.
3. How many OTUs have you removed ?
4. Build the Venn diagram on the two filters.
5. How many OTUs have you removed with each filter “abundance > 0.005% ”, “Remove OTUs that are not present at least in 3 samples”?
6. How many OTUs do they remain ?
7. Is there a sample more impacted than the others ?
8. To characterize these new OTUs, do not forget to launch “FROGS Cluster Stat” tool, and rename the output HTML file.

Filters by OTUs | Filters by samples

Configuration tabs

Filters summary

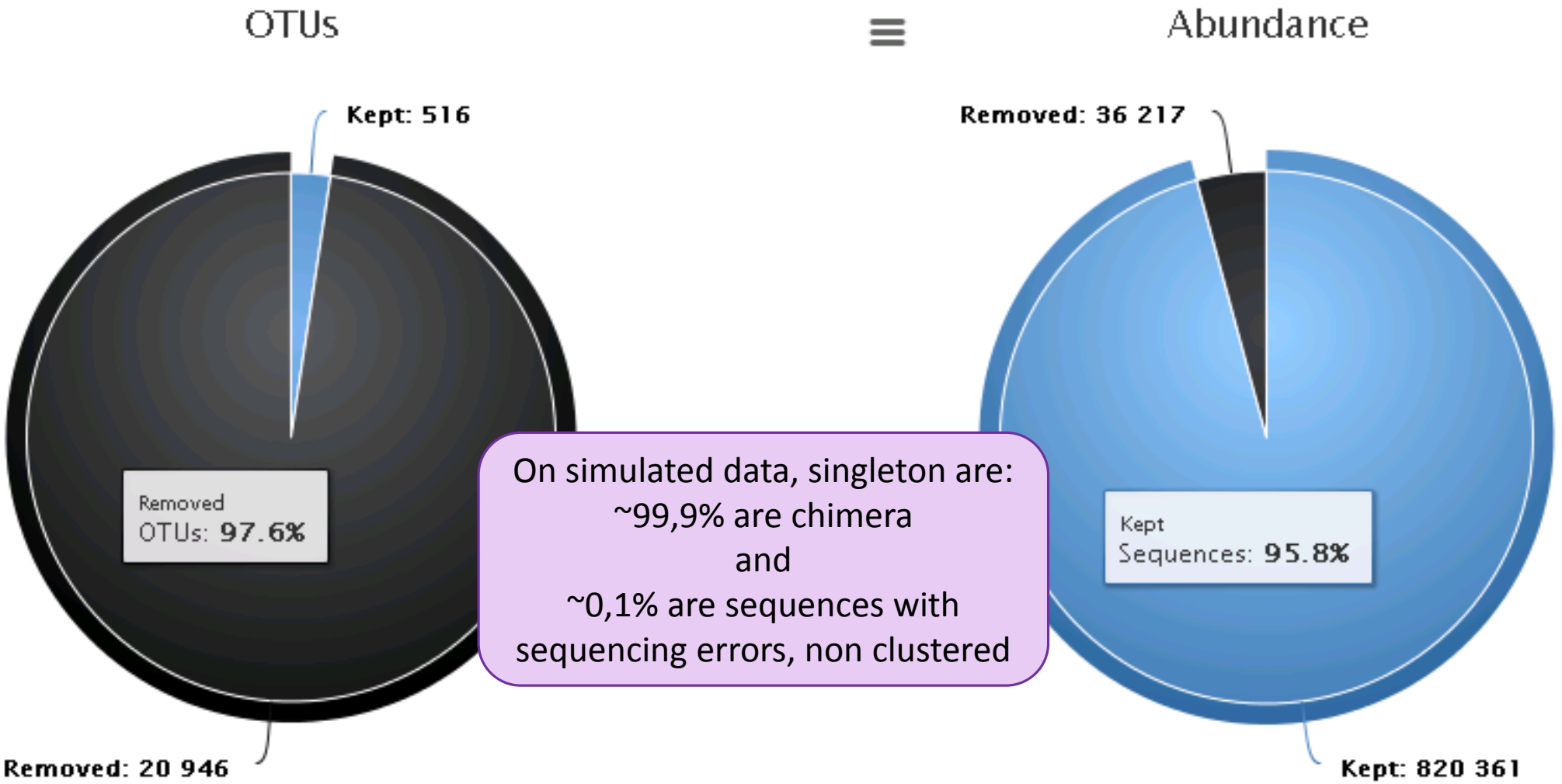


Filters intersections

Draw a Venn to see which OTUs had been deleted by the filters chosen (Maximum 6 options):

- [ ] Present in minus of 3 samples
- [ ] Abundance < 5e-05

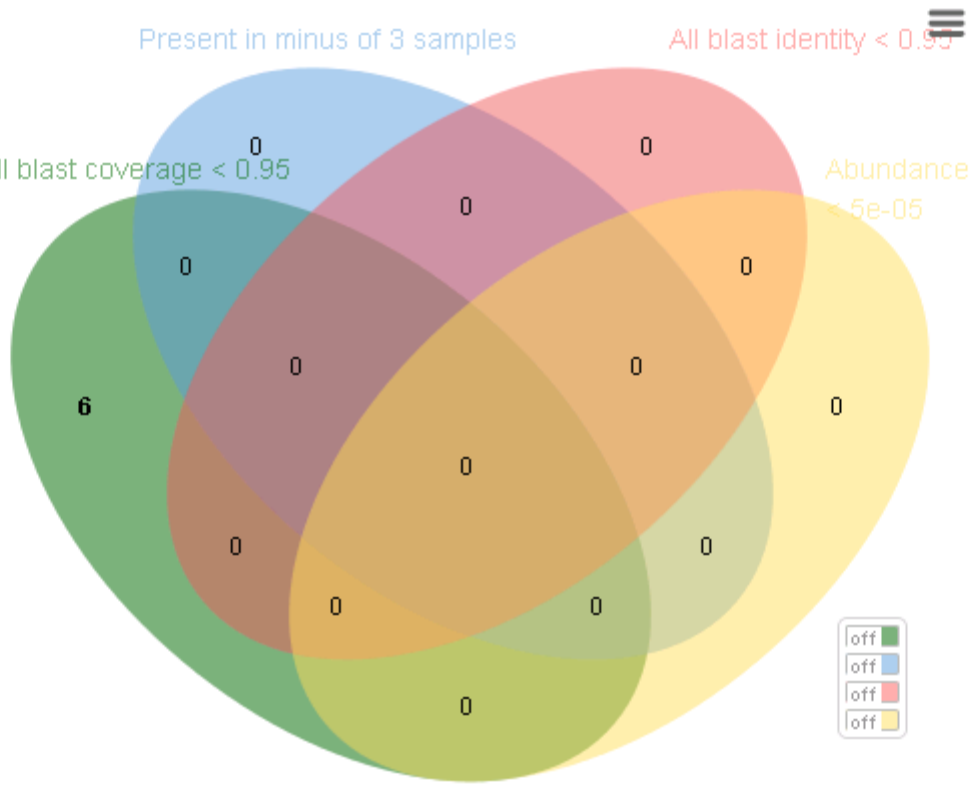
Venn



On simulated data, singleton are:
~99,9% are chimera
and
~0,1% are sequences with sequencing errors, non clustered

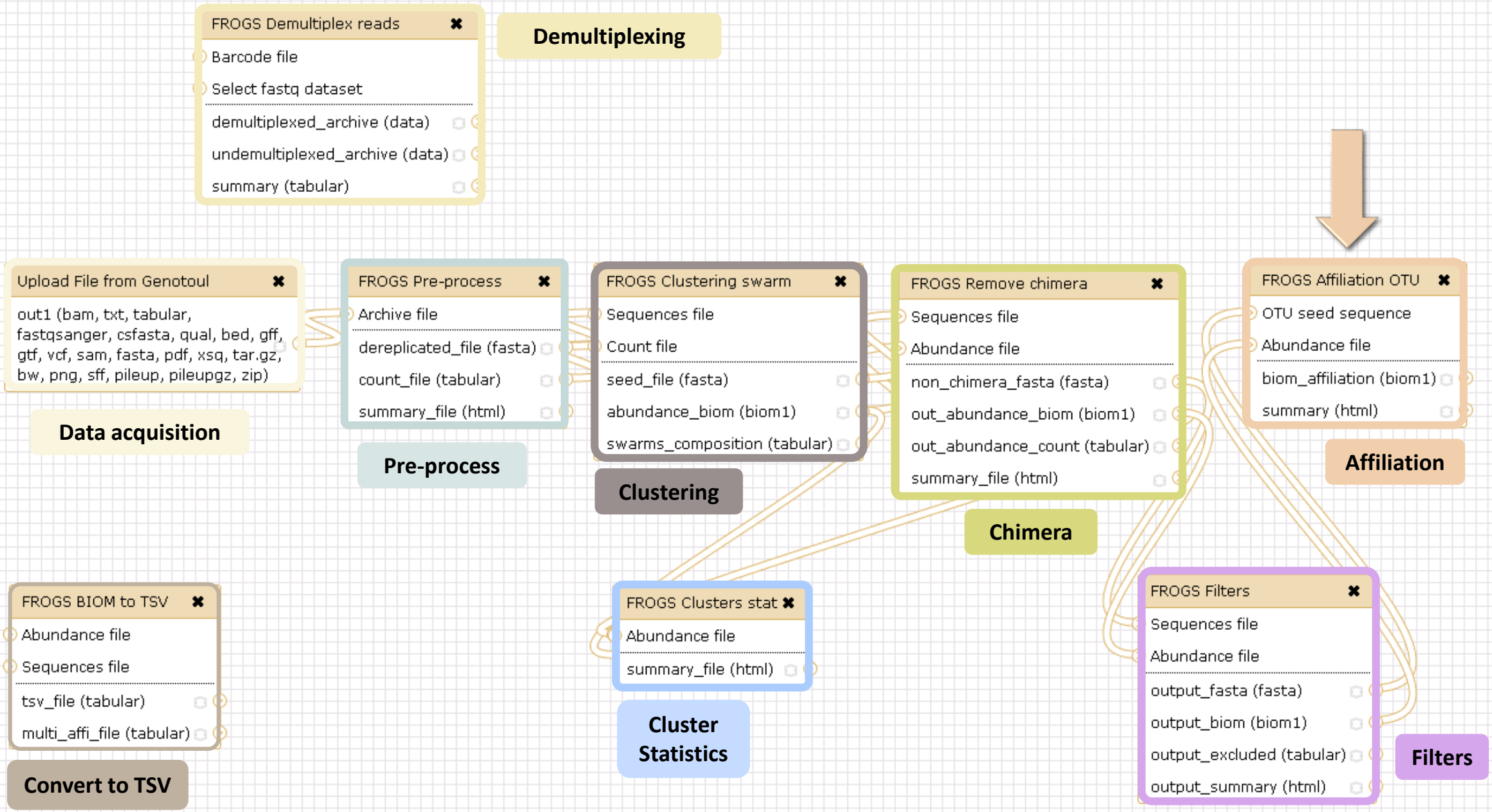
Removing little OTUs (conservation rate =0.005%) and non shared OTU (in less than 2 samples)

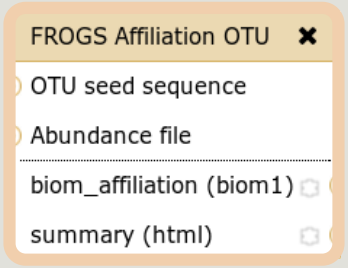
Venn on removed OTUs



Close

Affiliation tool


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
Convert to TSV
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters



Affiliation

FROGS Affiliation OTU Step 4 in metagenomics analysis : Taxonomic affiliation of each OTU's seed by RDPtools and BLAST (Galaxy Version 0.8.0)

Options

Using reference database

silva123 16S

Select reference from the list

OR

- silva128 16S
- silva128 18S
- silva128 23S
- silva123 16S
- silva123 23S
- silva123 18S
- greengenes13_5
- midas_S123_2.1.3
- midas_S119_1.20
- pr2_gb203_4.5

Also perform RDP assignation?

Yes | No

Optional

Taxonomy affiliation will be perform thanks to Blast. This o … erform it also with RDP classifier (default No)

OTU seed sequence

17: FROGS Filters: sequences.fasta

OTU sequences (format: fasta).

Abundance file

18: FROGS Filters: abundance.biom

OTU abundances (format: BIOM).

Execute

1 Cluster = 2 affiliations

Double Affiliation vs SILVA 123 (for 16S, 18S or 23S), SILVA 119 (for 18S) or Greengenes **with :**

1. RDPClassifier* (Ribosomal Database Project): one affiliation with bootstrap, on each taxonomic subdivision.

Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Lachnospiraceae(100);Pseudobutyrivibrio(80); Pseudobutyrivibrio xylanivorans (80)

2. NCBI Blastn+** : all identical Best Hits with identity %, coverage %, e-value, alignment length and a special tag "**Multi-affiliation".**

Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Pseudobutyrivibrio;Pseudobutyrivibrio ruminis; Pseudobutyrivibrio xylanivorans

Identity: 100% and Coverage: 100%

* Appl. Environ. Microbiol. August 2007 vol. 73 no. 16 5261-5267. doi : 10.1128/AEM.00062-07
Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy.
Qiong Wang, George M.Garrity, James M. Tiedje and James R. Cole

** BMC Bioinformatics 2009, 10:421. doi:10.1186/1471-2105-10-421
BLAST+: architecture and applications
Christiam Camacho, George Coulouris, Vahram Avagyan, Ning Ma, Jason Papadopoulos,Kevin Bealer and Thomas L Madden

Affiliation Strategy of FROGS

Blastn+ with "**Multi-affiliation**" management

V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S unknown species
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S Butyrivibrio fibrisolvens
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S rumen bacterium 8|9293-9
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S Pseudobutyrivibrio xylanivorans
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S Pseudobutyrivibrio ruminis

5 identical blast best hits on SILVA 123 databank

Affiliation Strategy of FROGS

Blastn+ with “**Multi-affiliation**” management

V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S unknown species
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S Butyrivibrio fibrisolvens
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S rumen bacterium 8|9293-9
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S Pseudobutyrivibrio xylanivorans
V3 – V4	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|16S Pseudobutyrivibrio ruminis

FROGS Affiliation:	Bacteria|Firmicutes|Clostridia|Clostridiales|Lachnospiraceae|Pseudobutyrivibrio|**Multi-affiliation**

Your Turn! – 7

LAUNCH THE « FROGS AFFILIATION » TOOL

MiSeq merged

Exercise 7.1

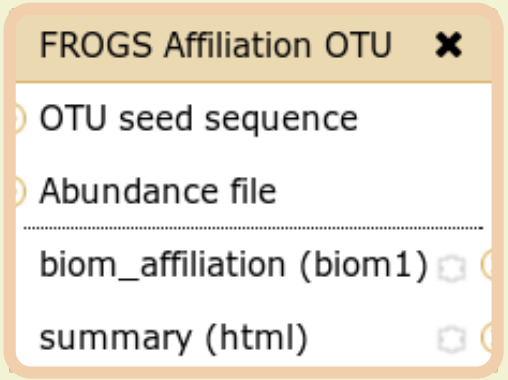
Go to « MiSeq merged » history

Launch the « FROGS Affiliation » tool with

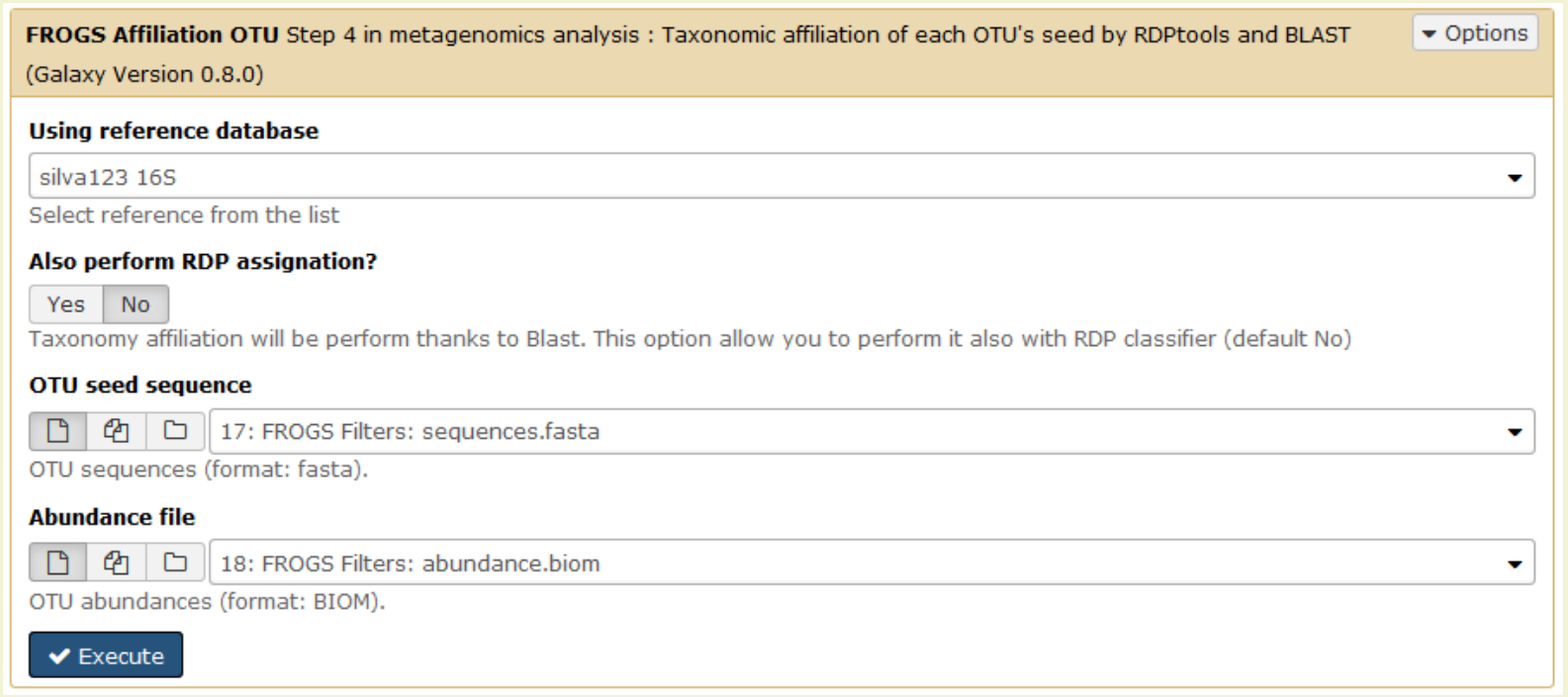
- SILVA 123 or 128 16S database
- FROGS Filters abundance biom and fasta files (after swarm d1d3, remove chimera and filter low abundances)

→ objectives :

- understand abundance tables columns
- understand the BLAST affiliation



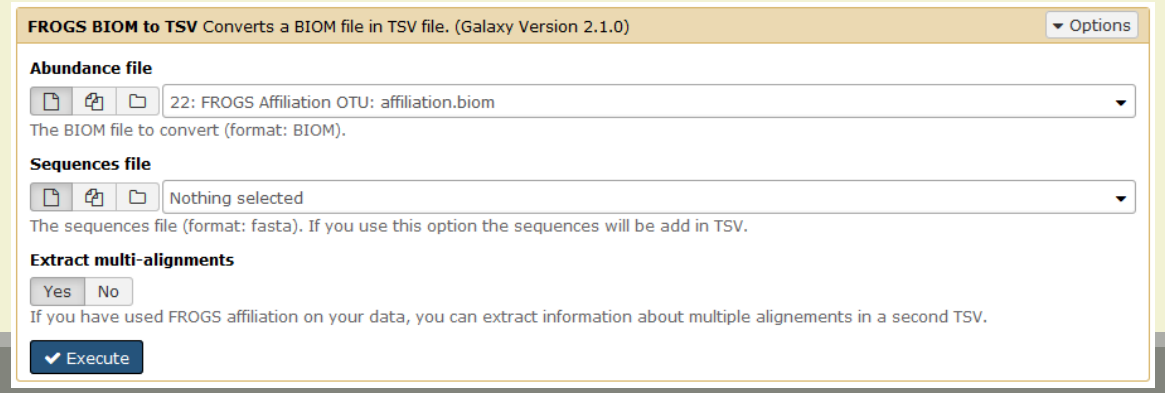
Affiliation

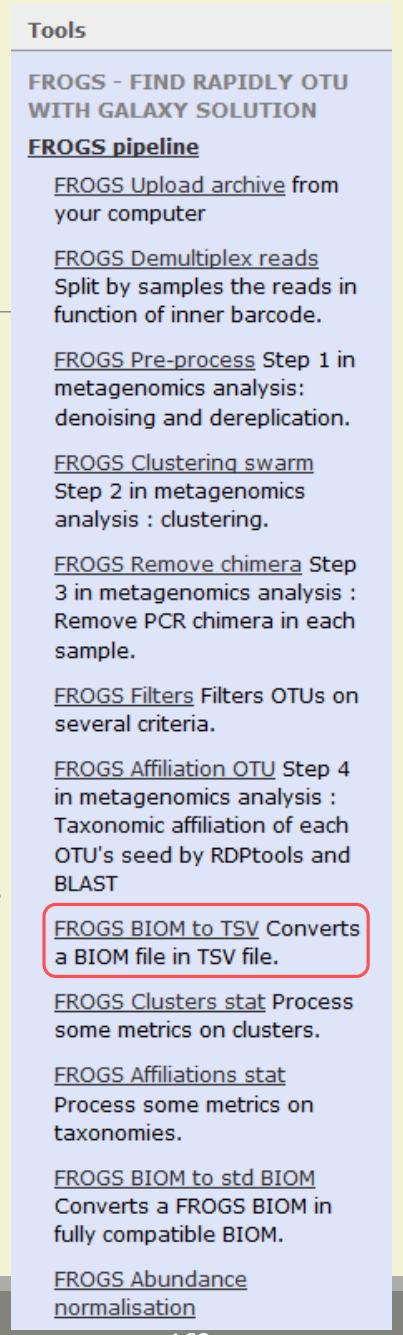


MiSeq merged

Exercise 7.1

1. What are the « FROGS Affiliation » output files ?
2. How many sequences are affiliated by BLAST ?
3. Click on the « eye » button on the BIOM output file, what do you understand ?
4. Use the Biom_to_TSV tool on this last file and click again on the ”eye” on the new output generated.
   What do the columns ?
   What is the difference if we click on case or not ? What consequence about weight of your file ?





MiSeq merged

Exercise 7.1

5. Understand Blast affiliations - Cluster_2388 (affiliation from silva 123)

blast_subject	blast_evalue	blast_len	blast_perc_query_coverage	blast_perc_identity	blast_taxonomy
JN880417.1.1422	0.0	360	88.88	99.44	Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Planctomycetaceae;Telmatocola;Telmatocola sphagniphila

Blast JN880417.1.1422 vs our OTU

OTU length : 405

Excellent blast but no matches at the beginning of OTU.

Telmatocola sphagniphila strain SP2 16S ribosomal RNA gene, partial sequence

Sequence ID: ref|NR_118328.1 Length: 1422 Number of Matches: 1

Range 1: 375 to 734 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
654 bits(354)	0.0	358/360(99%)	0/360(0%)	Plus/Plus

```
Query  46   CGCGTGCGCGATGAAGGCCTTCGGGTTGTAAAGCGCGAAAGAGGTAATAAAGGGAAACCT  105
Sbjct  375  CGCGTGCGCGATGAAGGCCTTCGGGTTGTAAAGCGCGAAAGAGGSAATAAAGGGAAACTT  434

Query  106  GATTGAACCTCAGTAAGCTCGGGCTAAGTTTGTGCCAGCAGCCGCGGTAAGACGAACCGA  165
Sbjct  435  GATTGAACCTCAGTAAGCTCGGGCTAAGTTTGTGCCAGCAGCCGCGGTAAGACGAACCGA  494

Query  166  GCGAACGTTGTTCGGAATCACTGGGCATAAAGGGCGCGTAGGCGGGTTTCTAAGTCCGTG  225
Sbjct  495  GCGAACGTTGTTCGGAATCACTGGGCATAAAGGGCGCGTAGGCGGGTTTCTAAGTCCGTG  554

Query  226  GTGAAATACTTCAGCTCAACTGGAGAACTGCCTCGGATACTGGGAATCTCGAGTAATGTA  285
Sbjct  555  GTGAAATACTTCAGCTCAACTGGAGAACTGCCTCGGATACTGGGAATCTCGAGTAATGTA  614

Query  286  GGGGCACGTGGAACGGCTGGTGGAGCGGTGAAATGCGTTGATATCAGTCGGAACTCCGGT  345
Sbjct  615  GGGGCACGTGGAACGGCTGGTGGAGCGGTGAAATGCGTTGATATCAGTCGGAACTCCGGT  674

Query  346  GGCGAAGGCGATGTGCTGGACATTTACTGACGCTGAGGCGCGAAAGCCAGGGGAGCAAAC  405
Sbjct  675  GGCGAAGGCGATGTGCTGGACATTTACTGACGCTGAGGCGCGAAAGCCAGGGGAGCAAAC  734
```

Telmatocola sphagniphila strain SP2 16S ribosomal RNA gene, partial sequence

NCBI Reference Sequence: NR_118328.1

FASTA Graphics

Go to:

```
LOCUS       NR_118328              1422 bp    rRNA    linear   BCT 03-FEB-2015
DEFINITION  Telmatocola sphagniphila strain SP2 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   NR_118328
VERSION     NR_118328.1  GI:645321338
DBLINK      Project: 33175
            BioProject: PRJNA33175
KEYWORDS    RefSeq.
SOURCE      Telmatocola sphagniphila
  ORGANISM  Telmatocola sphagniphila
            Bacteria; Planctomycetes; Planctomycetia; Planctomycetales;
            Planctomycetaceae.
REFERENCE   1  (bases 1 to 1422)
  AUTHORS   Kulichevskaya,I.S., Serkebaeva,Y.M., Kim,Y., Rijpstra,W.I.,
            Damste,J.S., Liesack,W. and Dedysh,S.N.
  TITLE     Telmatocola sphagniphila gen. nov., sp. nov., a novel dendriform
            planctomycete from northern wetlands
  JOURNAL   Front Microbiol 3, 146 (2012)
   PUBMED   22529844
  REMARK    Publication Status: Online-Only
REFERENCE   2  (bases 1 to 1422)
  CONSRTM   NCBI RefSeq Targeted Loci Project
  TITLE     Direct Submission
  JOURNAL   Submitted (28-APR-2014) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   3  (bases 1 to 1422)
  AUTHORS   Dedysh,S.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-2011) Winogradsky Institute of Microbiology RAS,
            Prospect 60-Letya Octyabrya 7/2, Moscow 117312, Russia
COMMENT     REVIEWED REFSEQ: This record has b[illegible] NCBI staff. The
            reference sequence is identical to JN880417:1-1422.
```

Blast columns

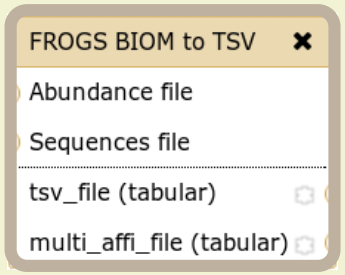
OTU_2 seed has a best BLAST hit with the reference sequence AJ496032.1.1410

The reference sequence taxonomic affiliation is this one.

#blast_taxonomy	blast_subject	blast_perc_identity	blast_perc_query_coverage	blast_evalue	blast_aln_length
Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Metascardovia;Multi-affiliation	multi-subject	100.0	100.0	0.0	411
Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;Fibrobacter;Fibrobacter succinogenes	AJ496032.1.1410	100.0	100.0	0.0	419
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Nosocomiicoccus;Nosocomiicoccus ampullae	EU240886.1.1502	100.0	100.0	0.0	427
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter;Psychrobacter immobilis	U39399.1.1477	100.0	100.0	0.0	426
Bacteria;Thermotogae;Thermotogae;Thermotogales;Thermotogaceae;Petrotoga;Petrotoga miotherma	FR733705.1.1499	100.0	100.0	0.0	419
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Pseudahrensia;Pseudahrensia aquimaris	GU575117.1.1441	100.0	100.0	0.0	401
Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Persicitalea;Persicitalea jodogahamensis	multi-subject	100.0	100.0	0.0	421
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio;Multi-affiliation	multi-subject	100.0	100.0	0.0	404

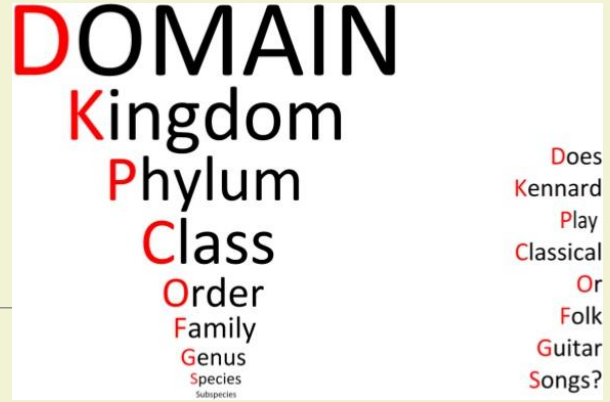
Evaluation variables of BLAST

Convert to TSV



Focus on “Multi-”

(affiliation from silva 123)



Observe line of Cluster 1 inside abundance.tsv and multi_hit.tsv files, what do you conclude ?

#blast_taxonomy	blast_subject	blast_perc_identity	blast_perc_query_coverage	blast_evalue	blast_aln_length
Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Metascardovia;Multi-affiliation	multi-subject	100.0	100.0	0.0	411
Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;Fibrobacter;Fibrobacter succinogenes	AJ496032.1.1410	100.0	100.0	0.0	419
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Nosocomiicoccus;Nosocomiicoccus ampullae	EU240886.1.1502	100.0	100.0	0.0	427
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter;Psychrobacter immobilis	U39399.1.1477	100.0	100.0	0.0	426
Bacteria;Thermotogae;Thermotogae;Thermotogales;Thermotogaceae;Petrotoga;Petrotoga miotherma	FR733705.1.1499	100.0	100.0	0.0	419
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Pseudahrensia;Pseudahrensia aquimaris	GU575117.1.1441	100.0	100.0	0.0	401
Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Persicitalea;Persicitalea jodogahamensis	multi-subject	100.0	100.0	0.0	421
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio;Multi-affiliation	multi-subject	100.0	100.0	0.0	404

Cluster_1 has 5 identical blast hits, with different taxonomies as the species level

Focus on “Multi-”

(affiliation from silva 123)

Observe line of Cluster 11 inside abundance.tsv and multi_hit.tsv files, what do you conclude ?

Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;Henriciella;Henriciella marina	multi-subject	100.0	100.0

Cluster_11 has 2 identical blast hits, with identical species but with different strains (strains are not written in our data)

Focus on “Multi-”

(affiliation from silva 123)

Observe line of Cluster 43 inside abundance.tsv and multi_hit.tsv files, what do you conclude ?

Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Multi-affiliation;Multi-affiliation		multi-subject	99.3	100.0

Cluster_43	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Selenomonas 3;unknown species	JQ447821.1.1420
Cluster_43	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Centipeda;Centipeda periodontii	AJ010963.1.1494

Cluster_43 has 2 identical blast hits, with different taxonomies at the genus level

Back on Blast parameters

#blast_taxonomy	blast_subject	blast_perc_identity	blast_perc_query_coverage	blast_evalue	blast_aln_length
Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Metascardovia;Multi-affiliation	multi-subject	100.0	100.0	0.0	411
Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;Fibrobacter;Fibrobacter succinogenes	AJ496032.1.1410	100.0	100.0	0.0	419
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Nosocomiicoccus;Nosocomiicoccus ampullae	EU240886.1.1502	100.0	100.0	0.0	427
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter;Psychrobacter immobilis	U39399.1.1477	100.0	100.0	0.0	426
Bacteria;Thermotogae;Thermotogae;Thermotogales;Thermotogaceae;Petrotoga;Petrotoga miotherma	FR733705.1.1499	100.0	100.0	0.0	419
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Pseudahrensia;Pseudahrensia aquimaris	GU575117.1.1441	100.0	100.0	0.0	401
Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Persicitalea;Persicitalea jodogahamensis	multi-subject	100.0	100.0	0.0	421
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio;Multi-affiliation	multi-subject	100.0	100.0	0.0	404

Evaluation variables of BLAST

Blast variables : e-value

The Expect value (E) is a parameter that describes the number of hits one can "expect" to see by chance when searching a database of a particular size.

The lower the E-value, or the closer it is to zero, the more "significant" the match is.

Blast variables : blast_perc_identity

Identity percentage between the Query (OTU) and the subject in the alignment (length subject = 1455 bases)

Score	Expect	Identities	Gaps	Strand
760 bits(411)	0.0	411/411(100%)	0/411(0%)	Plus/Plus

```
Query  1    TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCGACGCCGCGTGCGGGATGACGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCGACGCCGCGTGCGGGATGACGG  390

Query  61   CCTTCGGGTTGTAAACCGCTTTTAATTGGGAGCAAGCAGTTTTACTGTGAGTGTACTTTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  CCTTCGGGTTGTAAACCGCTTTTAATTGGGAGCAAGCAGTTTTACTGTGAGTGTACTTTT  450

Query  121  TGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  451  TGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT  510

Query  181  GTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGGTGTGAAAGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  511  GTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGGTGTGAAAGTC  570

Query  241  CATCGCTTAACGGTGGATTTGCGCTGGGTACGGGCAGGCTAGAGTGTAGTAGGGGAGACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  571  CATCGCTTAACGGTGGATTTGCGCTGGGTACGGGCAGGCTAGAGTGTAGTAGGGGAGACT  630

Query  301  GGAATTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  631  GGAATTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGC  690

Query  361  AGGTCTCTGGGCTATGACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC  411
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  691  AGGTCTCTGGGCTATGACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC  741
```

Query length = 411
Alignment length = 411
0 mismatch
-> 100% identity

Blast variables : blast_perc_identity

Identity percentage between the Query (OTU) and the subject in the alignment (length subject = 1455 bases)

Score	Expect	Identities	Gaps	Strand
614 bits(332)	5e-172	385/411(94%)	5/411(1%)	Plus/Plus

```
Query  1       TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCGACGCCGCGTGCGGGATGACGG  60
Sbjct  140728  TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGCGGGATGACGG  140787

Query  61      CCTTCGGGTTGTAAACCGCTTTTAATTGGGAGCAAGCAGTTTTACTGTGAGTGTACTTTT  120
Sbjct  140788  CCTTCGGGTTGTAAACCGCTTTTGATTGGGAGCAAGC-G----AGAGTGAGTGTACCTTT  140842

Query  121     TGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT  180
Sbjct  140843  CGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT  140902

Query  181     GTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGGTGTGAAAGTC  240
Sbjct  140903  ATCCGGAATTATTGGGCGTAAAGRGCTCGTAGGCGGTTCGTCGCGTCTGGTGTGAAAGTC  140962

Query  241     CATCGCTTAACGGTGGATTTGCGCTGGGTACGGGCAGGCTAGAGTGTAGTAGGGGAGACT  300
Sbjct  140963  CATCGCTTAACGGTGGATCTGCGCCGGGTACGGGCGGRCTGGAGTGCGGTAGGGGAGACT  141022

Query  301     GGAATTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGC  360
Sbjct  141023  GGAATTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGC  141082

Query  361     AGGTCTCTGGGCTATGACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC  411
Sbjct  141083  AGGTCTCTGGGCCGTTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC  141133
```

Query length = 411
Alignment length = 411
26 mismatches (gaps included)
-> 94% identity

Blast variables : blast_perc_query_coverage

Coverage percentage of alignment on query (OTU)

Score	Expect	Identities	Gaps	Strand
760 bits(411)	0.0	411/411(100%)	0/411(0%)	Plus/Plus

```
Query  1    TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCGACGCCGCGTGCGGGATGACGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAGCGACGCCGCGTGCGGGATGACGG  390

Query  61   CCTTCGGGTTGTAAACCGCTTTTAATTGGGAGCAAGCAGTTTTACTGTGAGTGTACTTTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  CCTTCGGGTTGTAAACCGCTTTTAATTGGGAGCAAGCAGTTTTACTGTGAGTGTACTTTT  450

Query  121  TGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  451  TGAATAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTT  510

Query  181  GTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGGTGTGAAAGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  511  GTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGGTGTGAAAGTC  570

Query  241  CATCGCTTAACGGTGGATTTGCGCTGGGTACGGGCAGGCTAGAGTGTAGTAGGGGAGACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  571  CATCGCTTAACGGTGGATTTGCGCTGGGTACGGGCAGGCTAGAGTGTAGTAGGGGAGACT  630

Query  301  GGAATTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  631  GGAATTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGC  690

Query  361  AGGTCTCTGGGCTATGACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC  411
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  691  AGGTCTCTGGGCTATGACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC  741
```

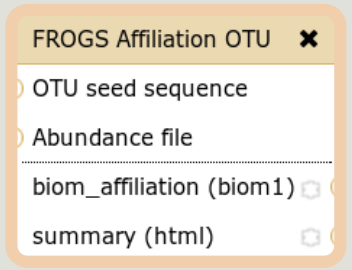
Query length = 411
100% coverage

Blast variables : blast-length

Length of alignment between the OTUs = “Query” and “subject” sequence of database

	Coverage %	Identity %	Length alignment
OTU1	100	98	400
OTU2	100	98	500

More mismatches/gaps



Affiliation

FROGS Affiliation OTU Step 4 in metagenomics analysis : Taxonomic affiliation of each OTU's seed by RDPtools and BLAST (Galaxy Version 0.8.0)

Options

Using reference database

silva123 16S

Select reference from the list

Also perform RDP assignation?

Yes | No

Optional and not in our guideline

Taxonomy affiliation will be perform thanks to Blast. This option allow you to perform it also with RDP classifier (default No)

OTU seed sequence

17: FROGS Filters: sequences.fasta

OTU sequences (format: fasta).

Abundance file

18: FROGS Filters: abundance.biom

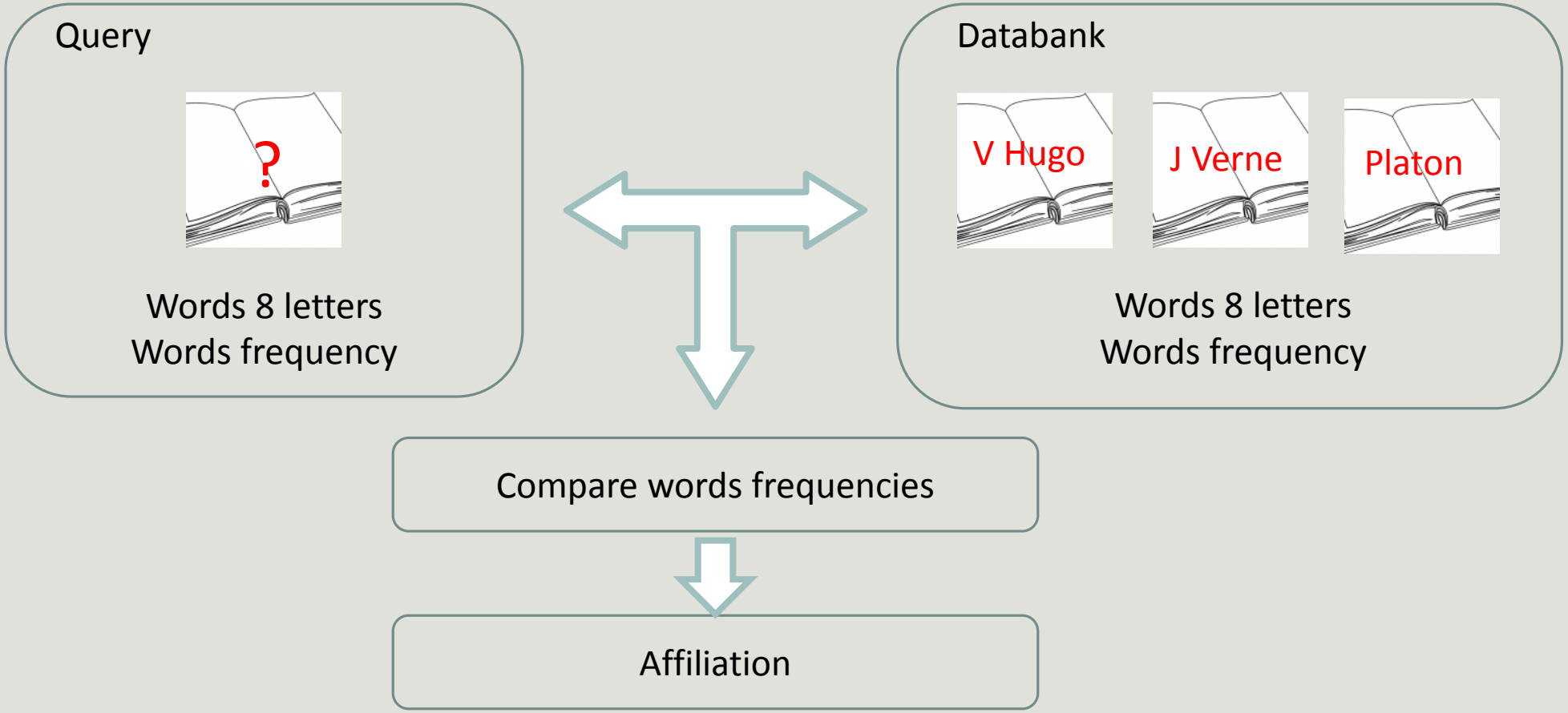
OTU abundances (format: BIOM).

Execute

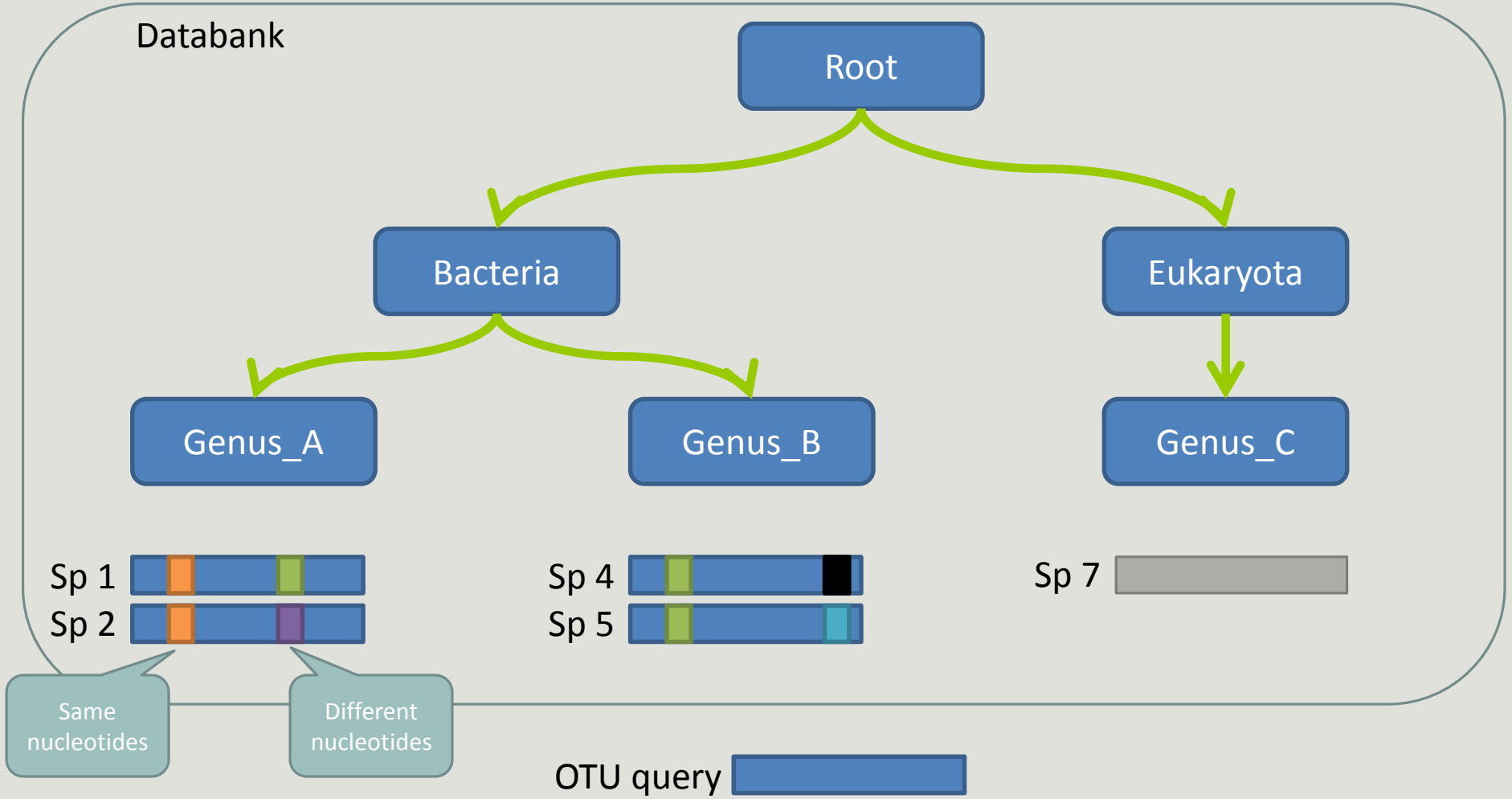
Who have already used RDP previously ?

Escape RDP explanation

How works RDP ?

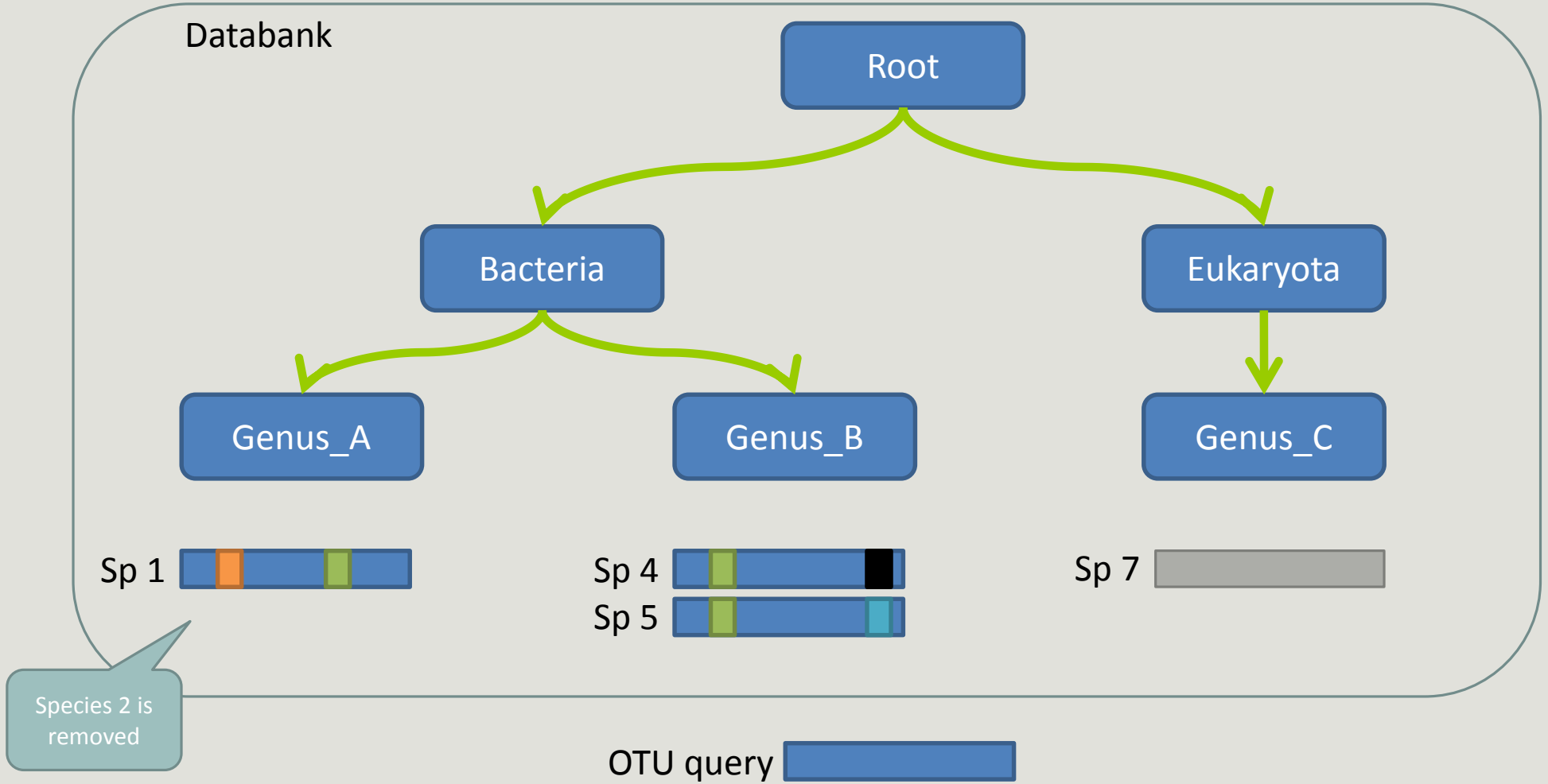


How works RDP ?



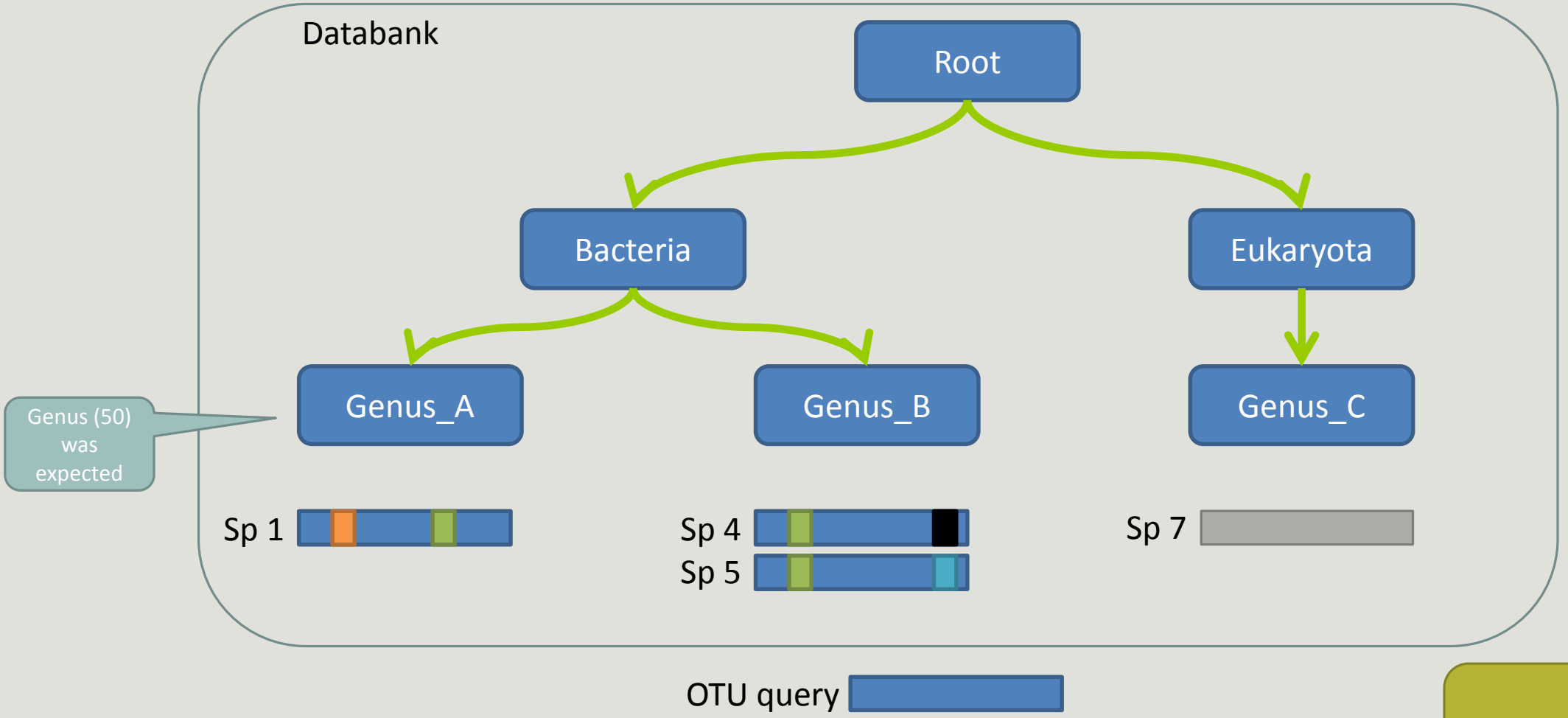
Result:
Bacteria(100) ; Genus_A(50) ; Sp1(25)

The dysfunctions of RDP ?



Result:
?

The dysfunctions of RDP n°1 ?

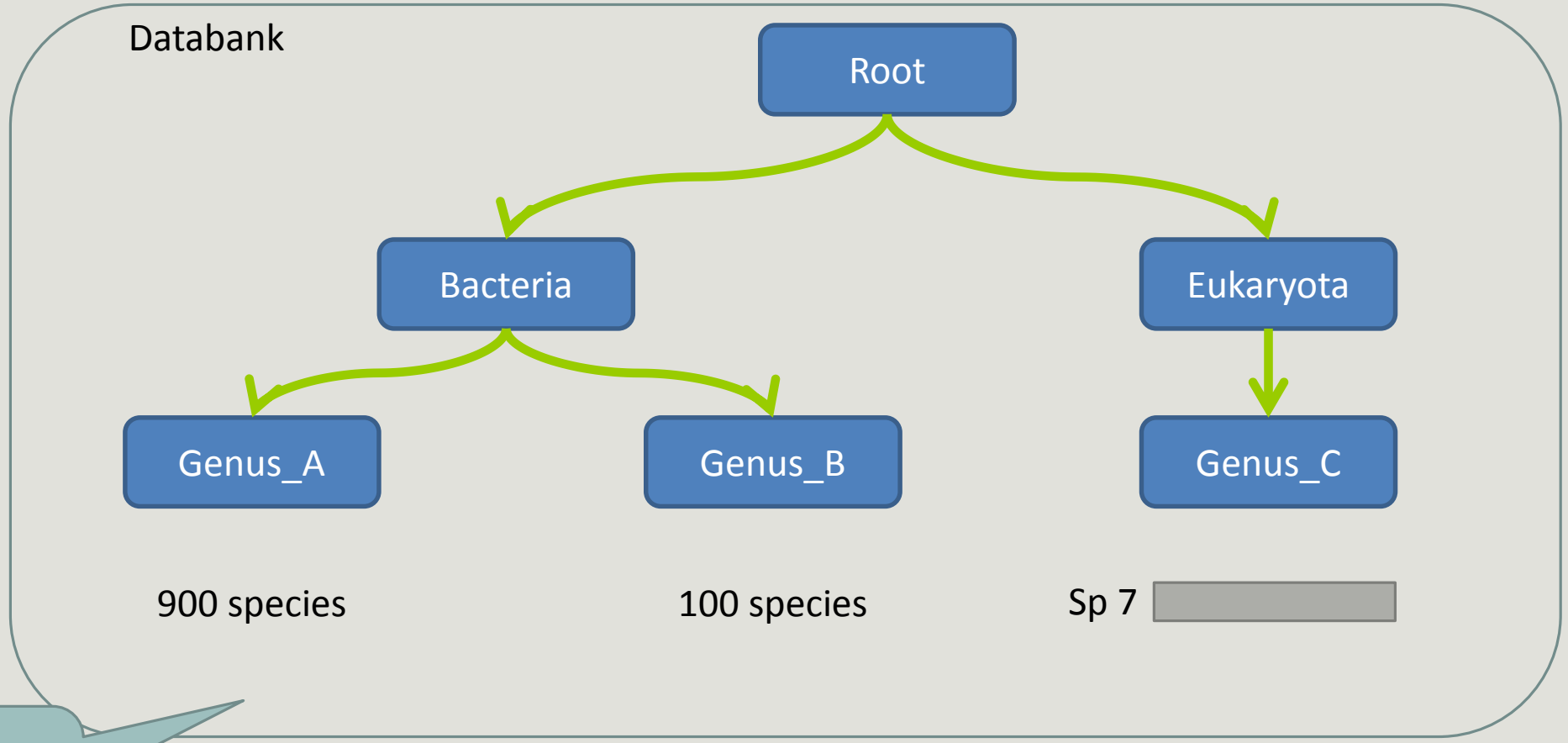


Order dependent

Genus (50) was expected.
If seq order was inversed in banks, so we got the second statistics.

Result:
Bacteria(100); Genus_A(33); sp1(33) OR Bacteria(100); Genus_B(66); sp5(33)

The dysfunctions of RDP n°2 ?



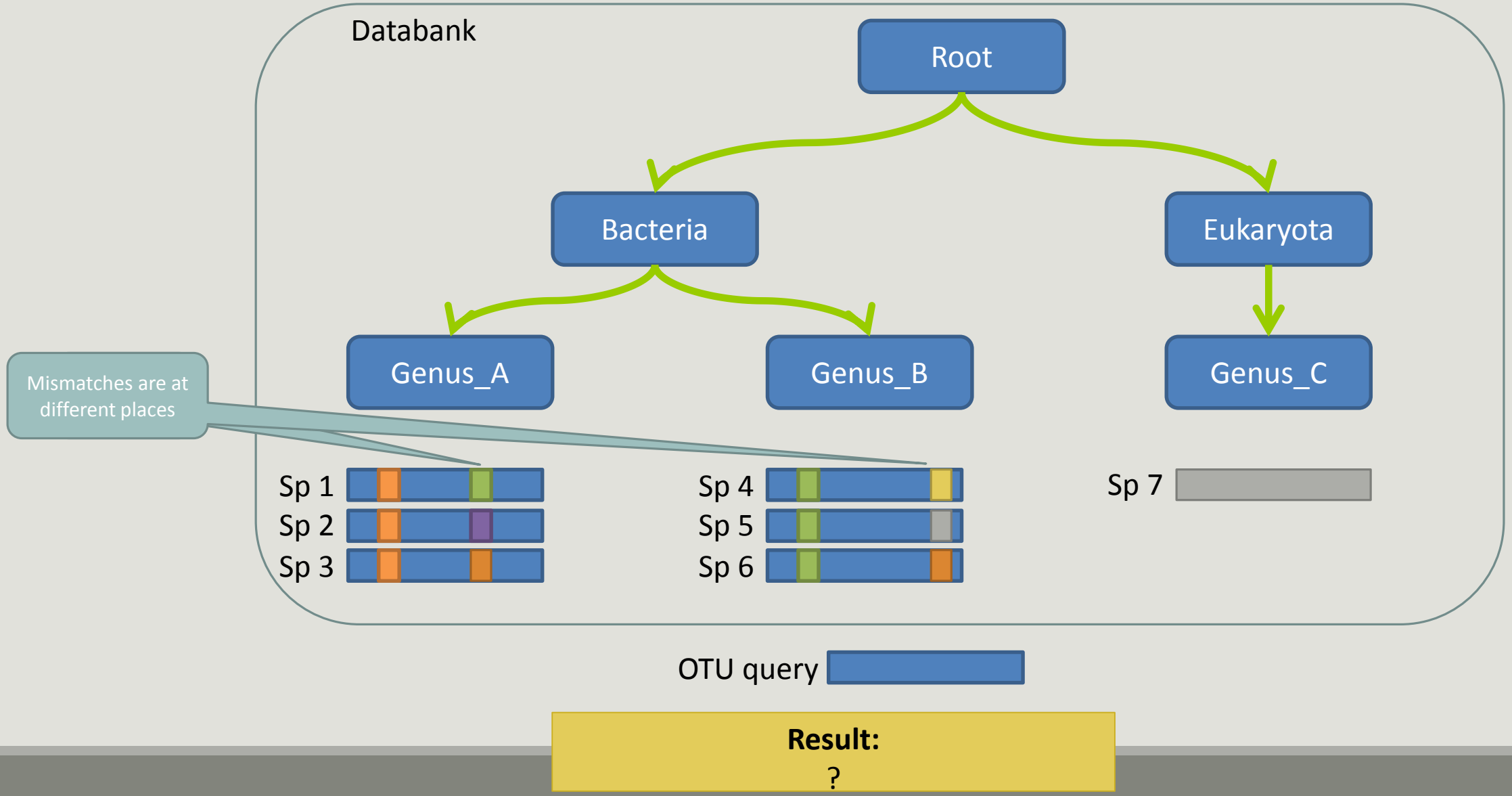
Many species in one genus and little in the other: So, RDP can give very different results

Influenced by heterogeneity in last ranks

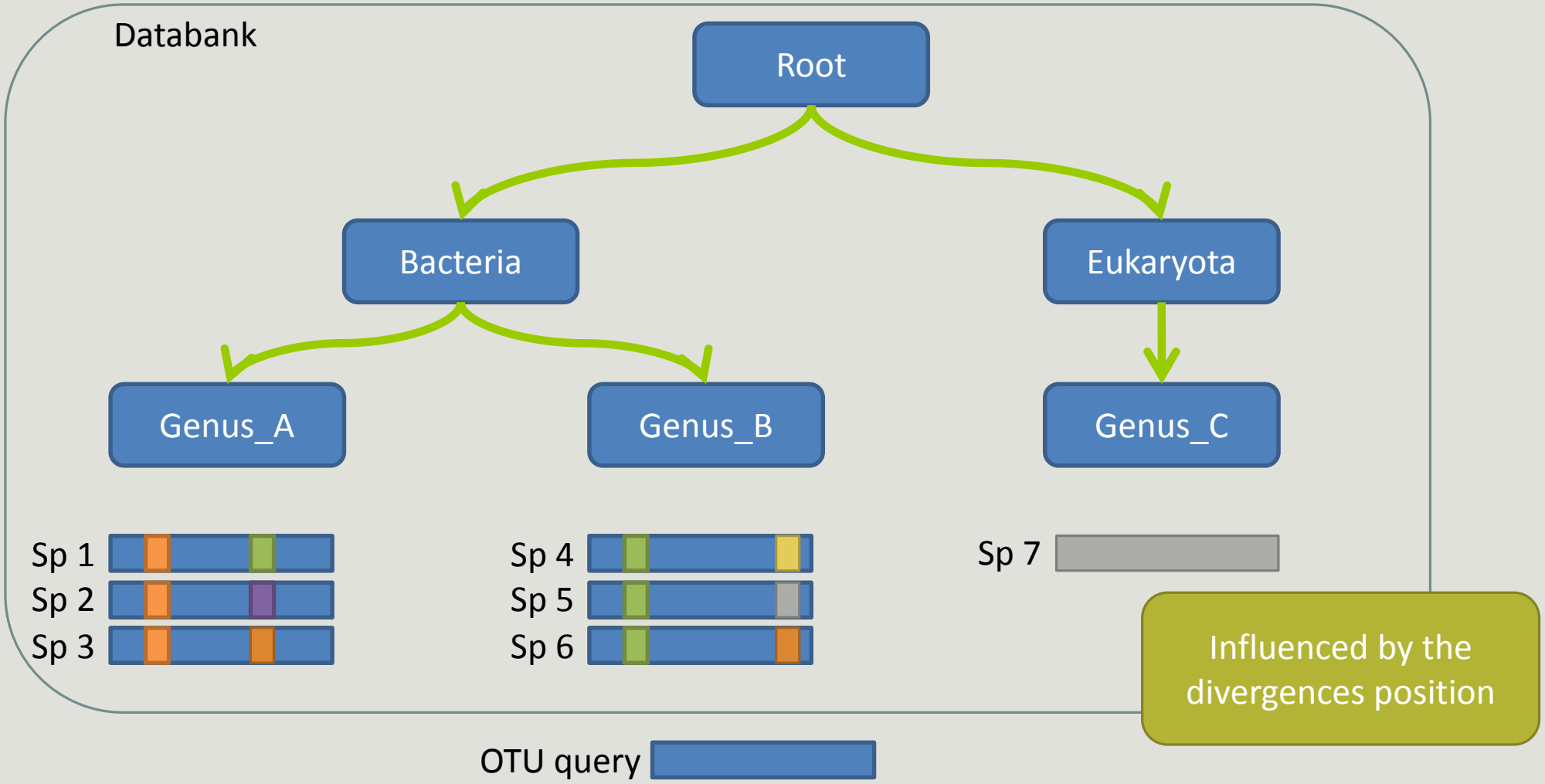
Result:

Bacteria(100); Genus_A(90); spX(0.1) OR Bacteria(100); Genus_B(10); spX(0.1)

The dysfunctions of RDP n°3 ?



The dysfunctions of RDP n°3 ?



Si le mismatch se fait sur un mot très "significatif" dans le profil de k-mers, RDP ne tombera que rarement sur l'espèce lors du bootstrap. Avec une même distance d'édition (2 mismatchs) on peut donc avoir une grande différence de bootstrap pour peu que le mot affecté soit important dans le profil.

Divergence on the composition of microbial communities at the different taxonomic ranks

RDPClassifier

NCBI blastn+

Reliable ?

Taxonomic ranks	Average divergence of the affiliations of the 10 samples (%) 500setA	Average divergence of the affiliations of the 10 samples (%) 100setA
Kingdom	0.00	0.00
Phylum	0.46	0.41
Class	0.64	0.50
Order	0.94	0.68
Familly	1.18	0.78
Genus	1.76	1.30
Species	23.87	34.80

Identical V3-V4

solution

Report on abundance table, the multiple identical affiliations

Only one best hit

Taxonomic ranks	Average divergence of the affiliations of the 10 samples (%) 500setA	Average divergence of the affiliations of the 10 samples (%) 100setA
Kingdom	0.00	0.00
Phylum	0.46	0.41
Class	0.64	0.50
Order	0.94	0.68
Familly	1.18	0.78
Genus	1.76	1.30
Species	23.87	34.80

Multiple best hit

Taxonomic ranks	Median divergence of the affiliations of the 10 samples (%) 500setA	Median divergence of the affiliations of the 10 samples (%) 100setA
Kingdom	0.00	0.00
Phylum	0.46	0.41
Class	0.64	0.50
Order	0.93	0.68
Familly	1.17	0.78
Genus	1.60	1.00
Species	6.63	5.75

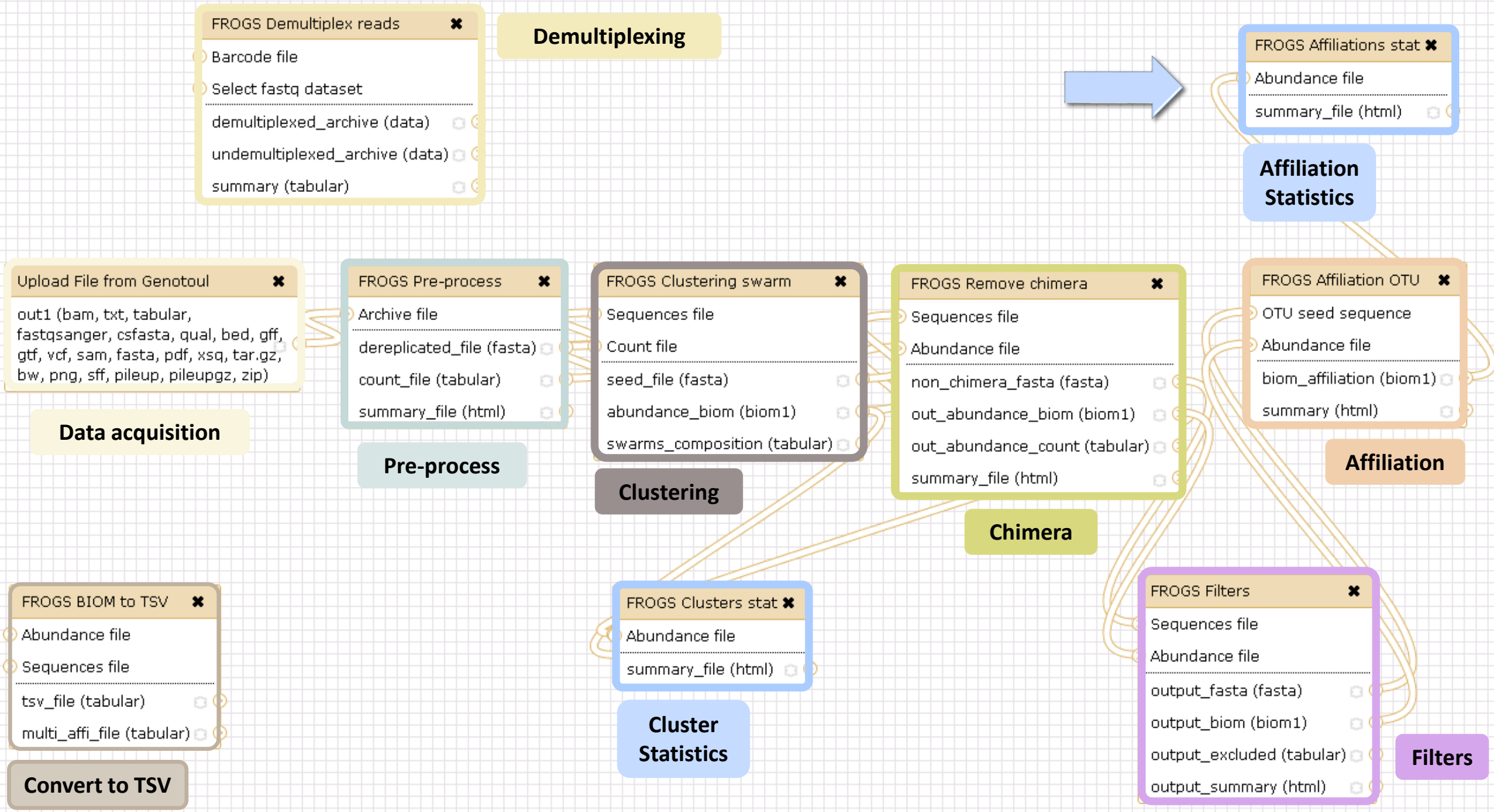
With the FROGS guideline

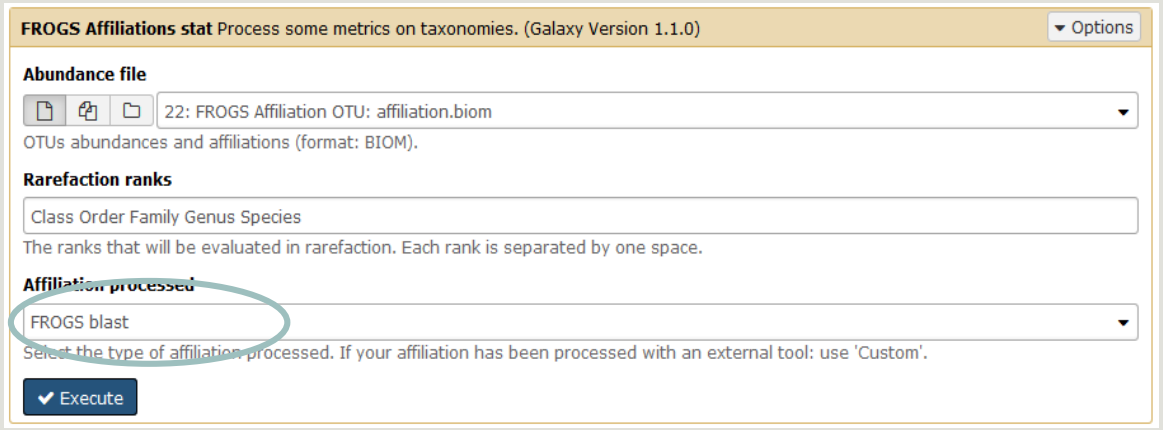
Taxonomic ranks	Median divergence of the affiliations of the 10 samples (%) 500setA filter: 0.005% - 505 OTUs	Median divergence of the affiliations of the 10 samples (%) 100setA filter: 0.005% - 100 OTUs
Kingdom	0.00	0.00
Phylum	0.38	0.38
Class	0.57	0.48
Order	0.81	0.64
Familly	1.08	0.74
Genus	1.43	0.76
Species	1.53	0.78

Careful: Multi hit blast table is non exhaustive !

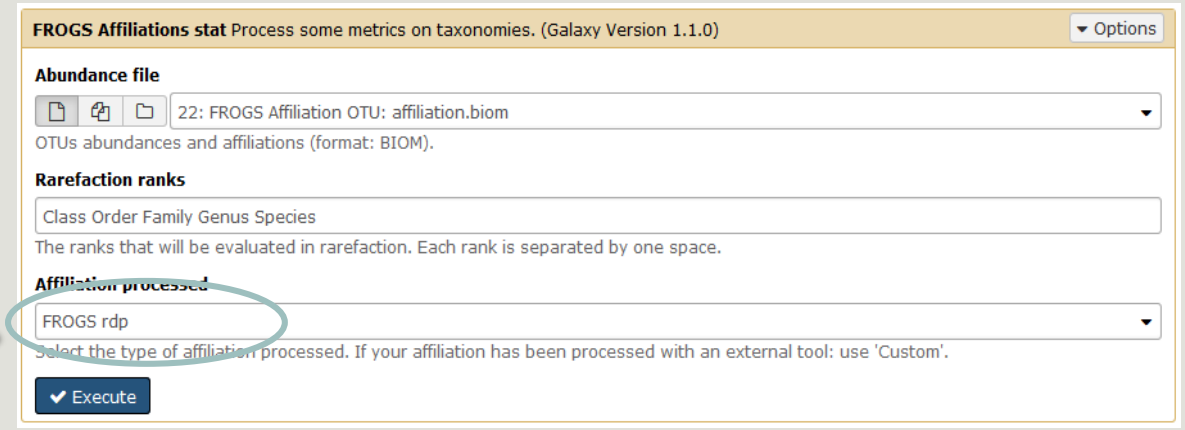
- Chimera (multiple affiliation)
- V3V4 included in others
- Missed primers on some 16S during database building

Affiliation Stat


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
FROGS Affiliations stat
Abundance file
summary_file (html)
Affiliation Statistics
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
Convert to TSV
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters

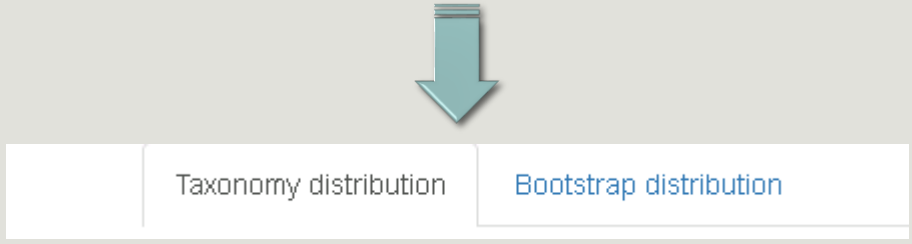

FROGS Affiliations stat Process some metrics on taxonomies. (Galaxy Version 1.1.0)
Options
Abundance file
22: FROGS Affiliation OTU: affiliation.biom
OTUs abundances and affiliations (format: BIOM).
Rarefaction ranks
Class Order Family Genus Species
The ranks that will be evaluated in rarefaction. Each rank is separated by one space.
FROGS blast
Execute

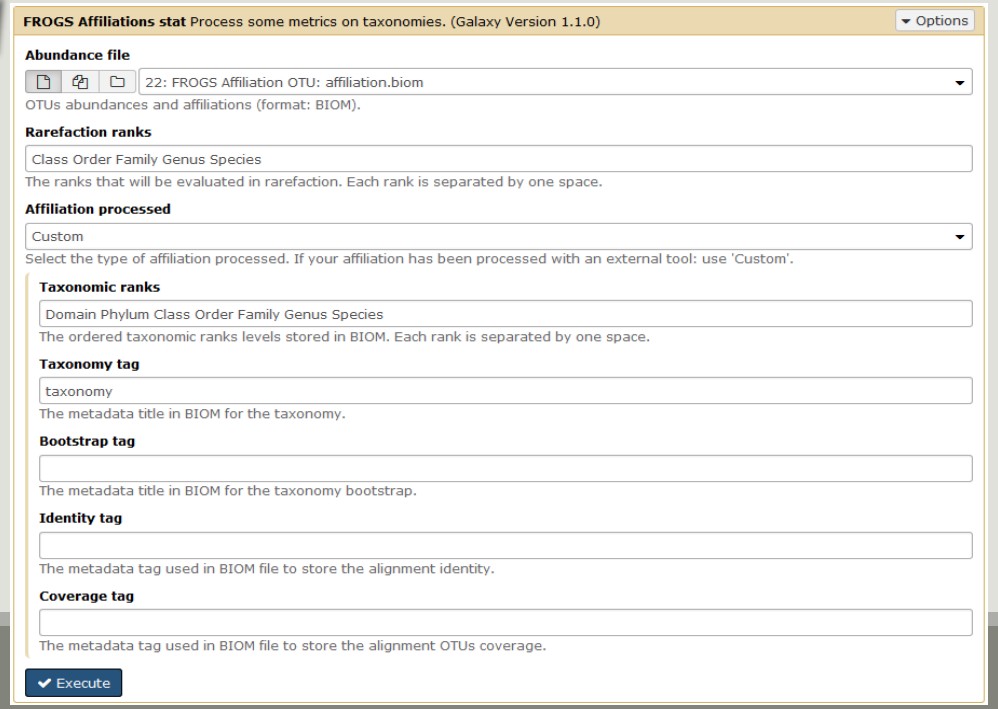
OR


FROGS Affiliations stat Process some metrics on taxonomies. (Galaxy Version 1.1.0)
Options
Abundance file
22: FROGS Affiliation OTU: affiliation.biom
OTUs abundances and affiliations (format: BIOM).
Rarefaction ranks
Class Order Family Genus Species
The ranks that will be evaluated in rarefaction. Each rank is separated by one space.
FROGS rdp
Execute

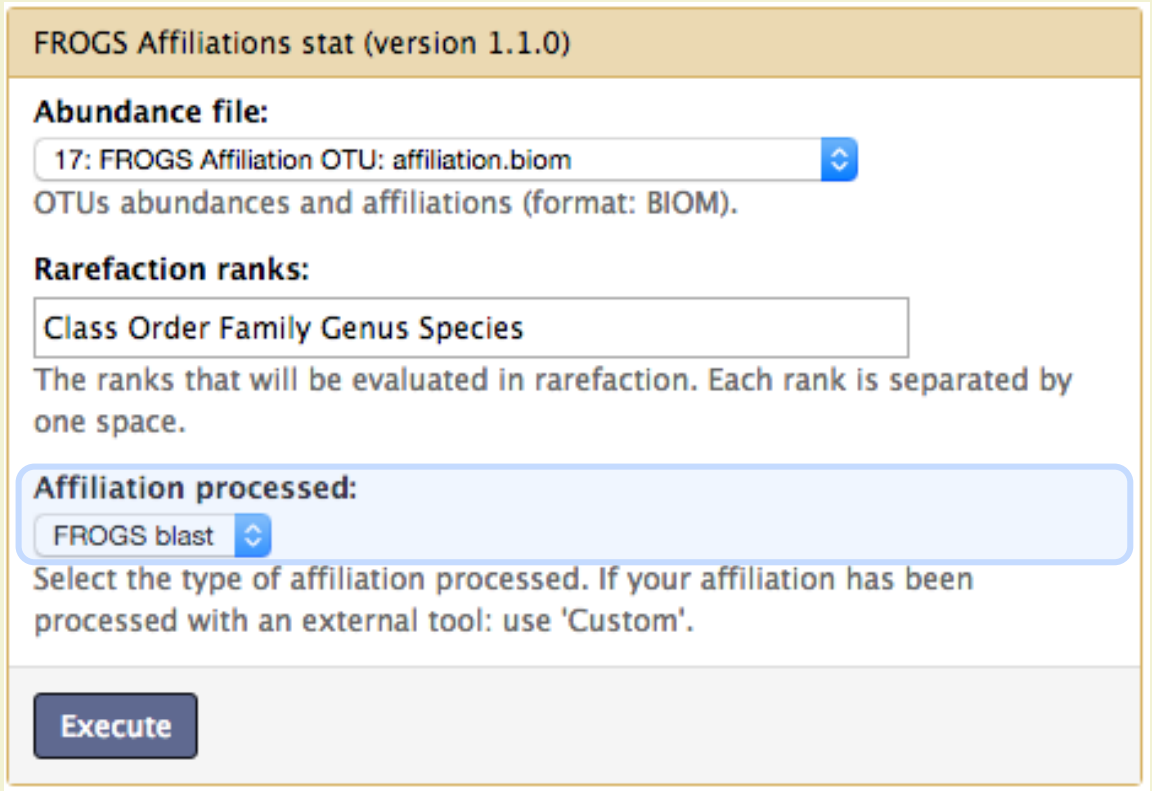

Taxonomy distribution
Alignment distribution

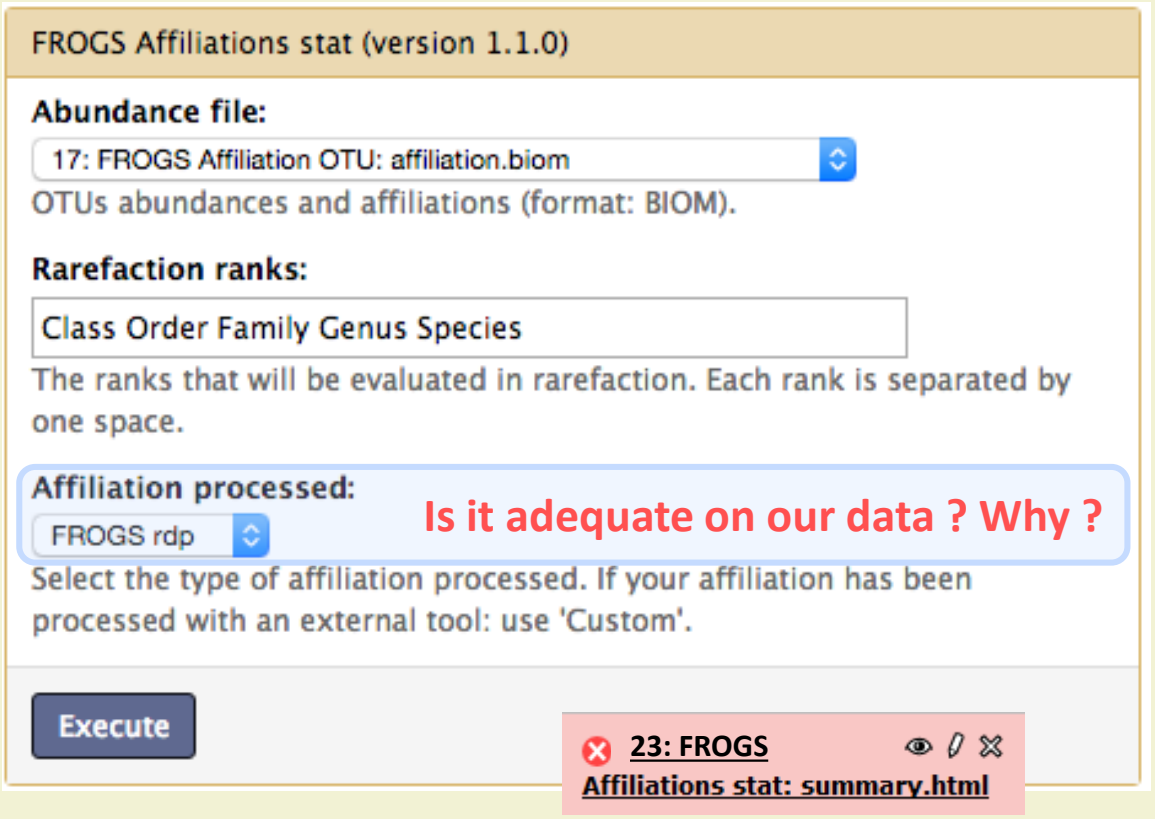
OR


Taxonomy distribution
Bootstrap distribution


FROGS Affiliations stat Process some metrics on taxonomies. (Galaxy Version 1.1.0)
Options
Abundance file
22: FROGS Affiliation OTU: affiliation.biom
OTUs abundances and affiliations (format: BIOM).
Rarefaction ranks
Class Order Family Genus Species
The ranks that will be evaluated in rarefaction. Each rank is separated by one space.
Affiliation processed
Custom
Select the type of affiliation processed. If your affiliation has been processed with an external tool: use 'Custom'.
Taxonomic ranks
Domain Phylum Class Order Family Genus Species
The ordered taxonomic ranks levels stored in BIOM. Each rank is separated by one space.
Taxonomy tag
taxonomy
The metadata title in BIOM for the taxonomy.
Bootstrap tag
The metadata title in BIOM for the taxonomy bootstrap.
Identity tag
The metadata tag used in BIOM file to store the alignment identity.
Coverage tag
The metadata tag used in BIOM file to store the alignment OTUs coverage.
Execute

Exercise 7.2


FROGS Affiliations stat (version 1.1.0)
Abundance file:
17: FROGS Affiliation OTU: affiliation.biom
OTUs abundances and affiliations (format: BIOM).
Rarefaction ranks:
Class Order Family Genus Species
The ranks that will be evaluated in rarefaction. Each rank is separated by one space.
Affiliation processed:
FROGS blast
Select the type of affiliation processed. If your affiliation has been processed with an external tool: use 'Custom'.
Execute

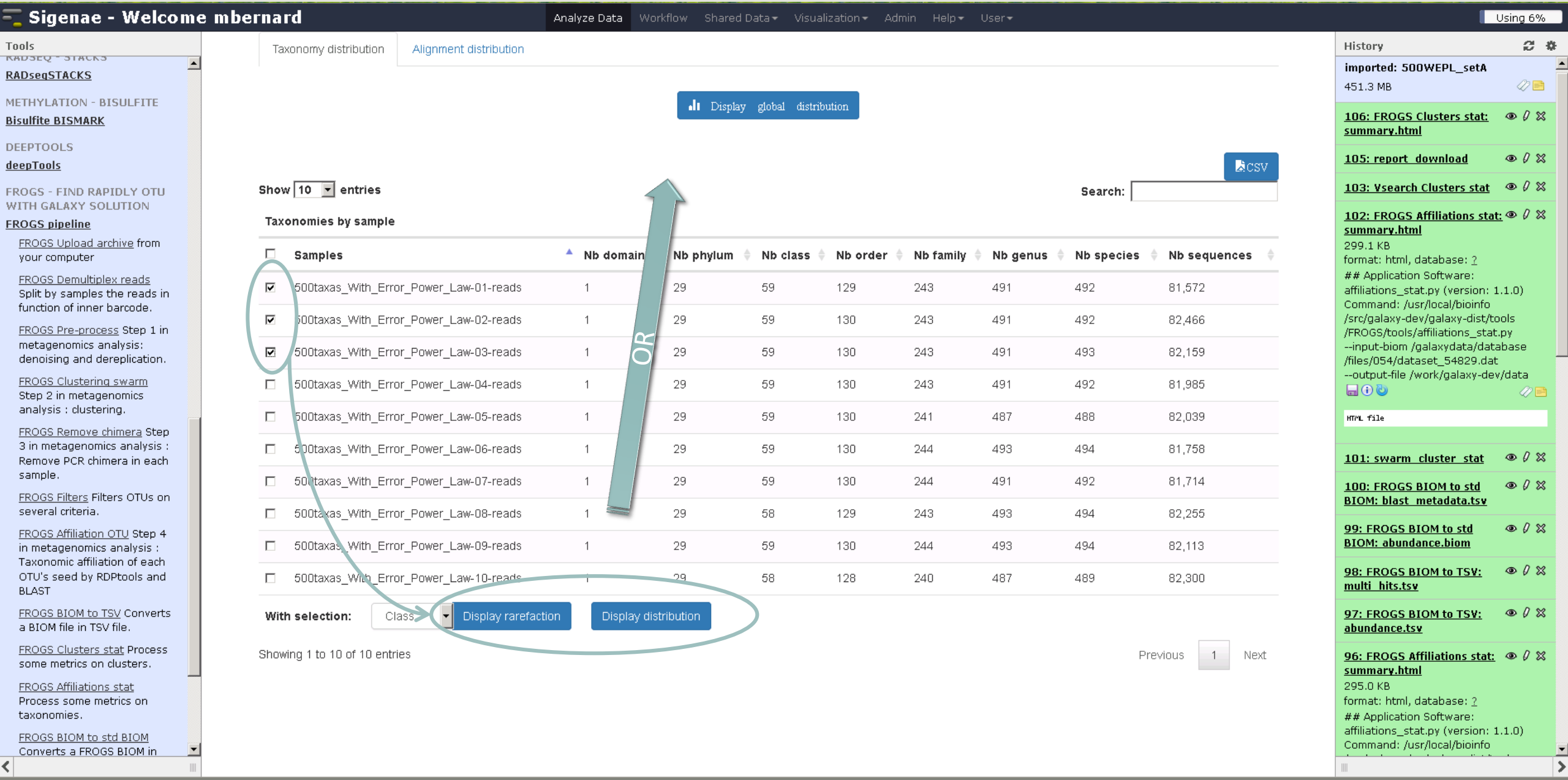

FROGS Affiliations stat (version 1.1.0)
Abundance file:
17: FROGS Affiliation OTU: affiliation.biom
OTUs abundances and affiliations (format: BIOM).
Rarefaction ranks:
Class Order Family Genus Species
The ranks that will be evaluated in rarefaction. Each rank is separated by one space.
Affiliation processed:
FROGS rdp
Is it adequate on our data ? Why ?
Select the type of affiliation processed. If your affiliation has been processed with an external tool: use 'Custom'.
Execute
23: FROGS
Affiliations stat: summary.html

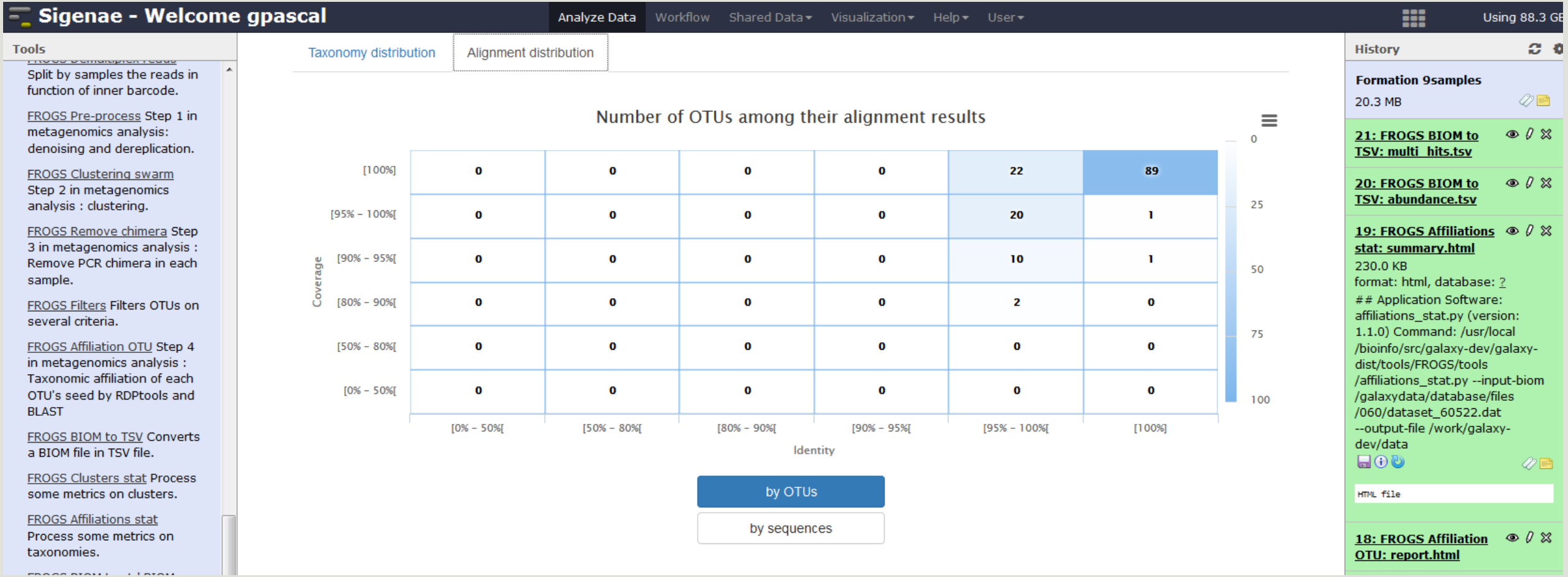
Exercise 7.2

→ objectives :

understand rarefaction curve and sunburst

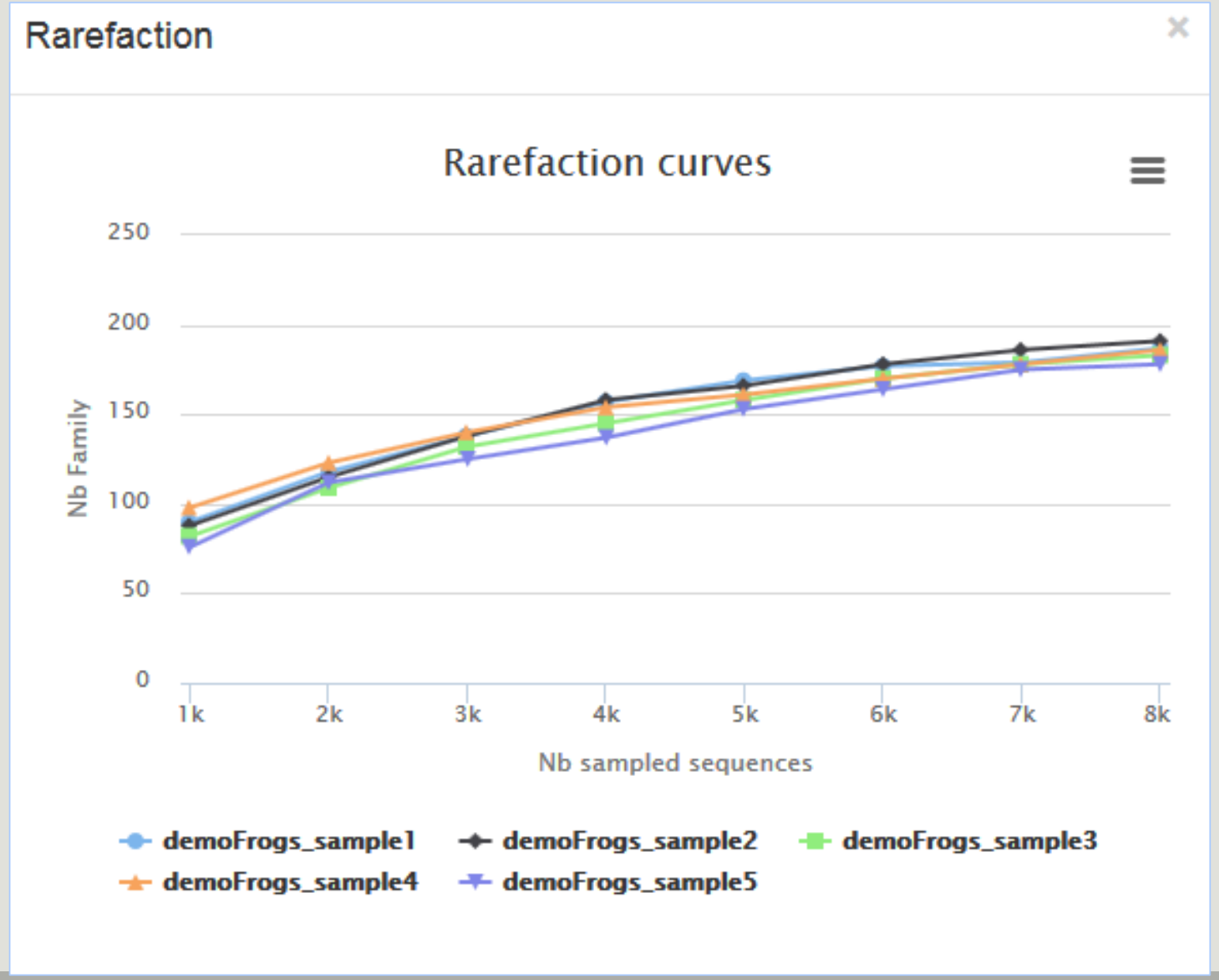
1. Explore the Affiliation stat results on FROGS blast affiliation.
2. What kind of graphs can you generate? What do they mean?


Sigenae - Welcome mbernard
Analyze Data
Workflow
Shared Data
Visualization
Admin
Help
User
Using 6%
Tools
RADseqSTACKS
METHYLATION - BISULFITE
Bisulfite BISMARK
DEEPTOOLS
deepTools
FROGS - FIND RAPIDLY OTU WITH GALAXY SOLUTION
FROGS pipeline
FROGS Upload archive from your computer
FROGS Demultiplex reads Split by samples the reads in function of inner barcode.
FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication.
FROGS Clustering swarm Step 2 in metagenomics analysis : clustering.
FROGS Remove chimera Step 3 in metagenomics analysis : Remove PCR chimera in each sample.
FROGS Filters Filters OTUs on several criteria.
FROGS Affiliation OTU Step 4 in metagenomics analysis : Taxonomic affiliation of each OTU's seed by RDPtools and BLAST
FROGS BIOM to TSV Converts a BIOM file in TSV file.
FROGS Clusters stat Process some metrics on clusters.
FROGS Affiliations stat Process some metrics on taxonomies.
FROGS BIOM to std BIOM Converts a FROGS BIOM in
Taxonomy distribution
Alignment distribution
Display global distribution
CSV
Show 10 entries
Search:
Taxonomies by sample
Samples
Nb domain
Nb phylum
Nb class
Nb order
Nb family
Nb genus
Nb species
Nb sequences
500taxas_With_Error_Power_Law-01-reads 1 29 59 129 243 491 492 81,572
500taxas_With_Error_Power_Law-02-reads 1 29 59 130 243 491 492 82,466
500taxas_With_Error_Power_Law-03-reads 1 29 59 130 243 491 493 82,159
500taxas_With_Error_Power_Law-04-reads 1 29 59 130 243 491 492 81,985
500taxas_With_Error_Power_Law-05-reads 1 29 59 130 241 487 488 82,039
500taxas_With_Error_Power_Law-06-reads 1 29 59 130 244 493 494 81,758
500taxas_With_Error_Power_Law-07-reads 1 29 59 130 244 491 492 81,714
500taxas_With_Error_Power_Law-08-reads 1 29 58 129 243 493 494 82,255
500taxas_With_Error_Power_Law-09-reads 1 29 59 130 244 493 494 82,113
500taxas_With_Error_Power_Law-10-reads 1 29 58 128 240 487 489 82,300
OR
With selection:
Class
Display rarefaction
Display distribution
Showing 1 to 10 of 10 entries
Previous
1
Next
History
imported: 500WEPL_setA
451.3 MB
106: FROGS Clusters stat: summary.html
105: report_download
103: Vsearch Clusters stat
102: FROGS Affiliations stat: summary.html
299.1 KB
format: html, database: ?
Application Software: affiliations_stat.py (version: 1.1.0)
Command: /usr/local/bioinfo /src/galaxy-dev/galaxy-dist/tools /FROGS/tools/affiliations_stat.py --input-biom /galaxydata/database /files/054/dataset_54829.dat --output-file /work/galaxy-dev/data
HTML file
101: swarm_cluster_stat
100: FROGS BIOM to std BIOM: blast_metadata.tsv
99: FROGS BIOM to std BIOM: abundance.biom
98: FROGS BIOM to TSV: multi_hits.tsv
97: FROGS BIOM to TSV: abundance.tsv
96: FROGS Affiliations stat: summary.html
295.0 KB
format: html, database: ?
Application Software: affiliations_stat.py (version: 1.1.0)
Command: /usr/local/bioinfo


Sigenae - Welcome gpascal
Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 88.3 GB
Tools
Split by samples the reads in function of inner barcode.
FROGS Pre-process Step 1 in metagenomics analysis: denoising and dereplication.
FROGS Clustering swarm Step 2 in metagenomics analysis : clustering.
FROGS Remove chimera Step 3 in metagenomics analysis : Remove PCR chimera in each sample.
FROGS Filters Filters OTUs on several criteria.
FROGS Affiliation OTU Step 4 in metagenomics analysis : Taxonomic affiliation of each OTU's seed by RDPtools and BLAST
FROGS BIOM to TSV Converts a BIOM file in TSV file.
FROGS Clusters stat Process some metrics on clusters.
FROGS Affiliations stat Process some metrics on taxonomies.
Taxonomy distribution
Alignment distribution
Number of OTUs among their alignment results
Coverage
[100%] 0 0 0 0 22 89
[95% – 100%[0 0 0 0 20 1
[90% – 95%[0 0 0 0 10 1
[80% – 90%[0 0 0 0 2 0
[50% – 80%[0 0 0 0 0 0
[0% – 50%[0 0 0 0 0 0
[0% – 50%[[50% – 80%[[80% – 90%[[90% – 95%[[95% – 100%[[100%]
Identity
0 25 50 75 100
by OTUs
by sequences
History
Formation 9samples
20.3 MB
21: FROGS BIOM to TSV: multi_hits.tsv
20: FROGS BIOM to TSV: abundance.tsv
19: FROGS Affiliations stat: summary.html
230.0 KB
format: html, database: ?
Application Software: affiliations_stat.py (version: 1.1.0) Command: /usr/local /bioinfo/src/galaxy-dev/galaxy-dist/tools/FROGS/tools /affiliations_stat.py --input-biom /galaxydata/database/files /060/dataset_60522.dat --output-file /work/galaxy-dev/data
HTML file
18: FROGS Affiliation OTU: report.html

Available only after AFFILIATION TOOL

Samples size ~8500 sequences



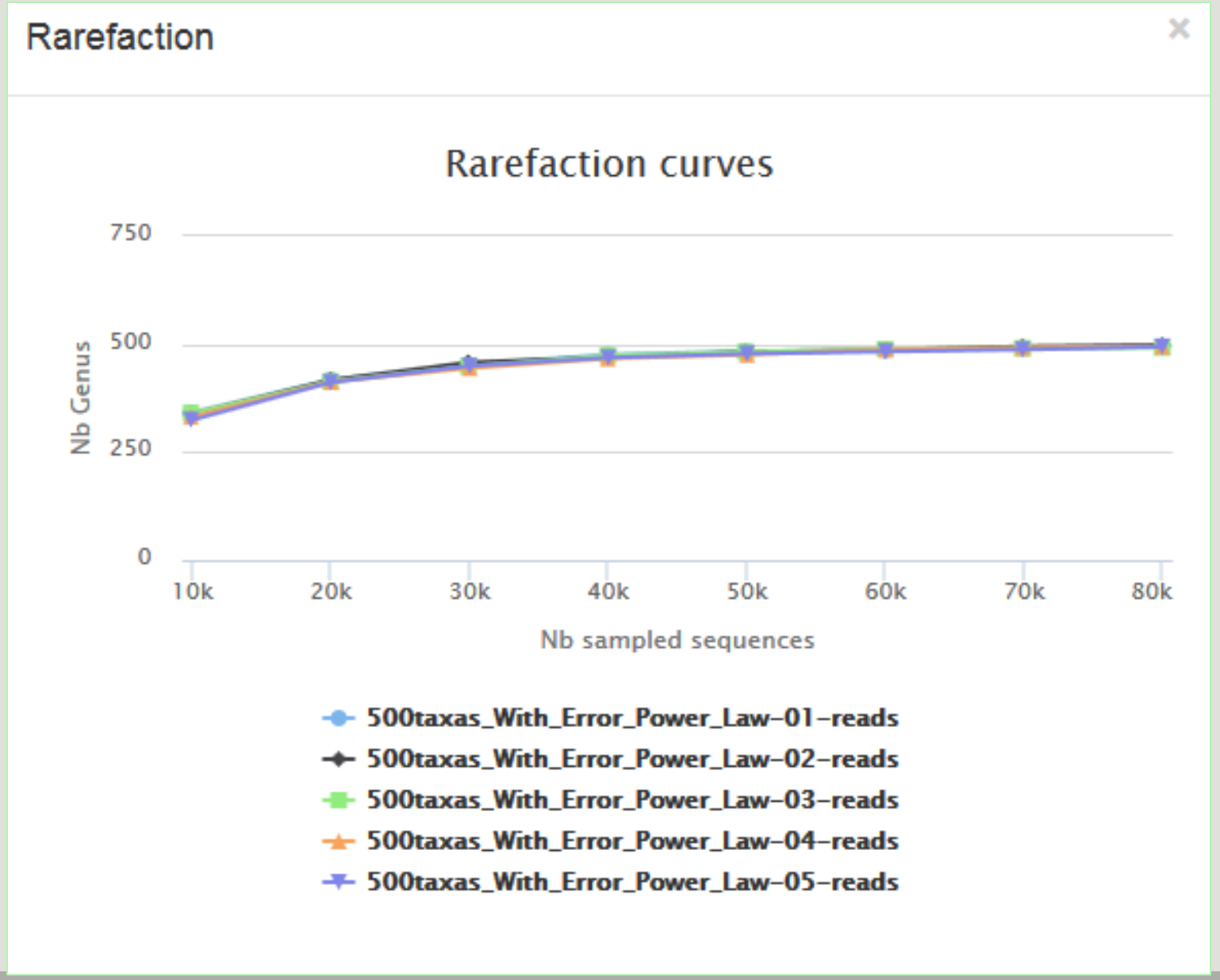
The curve continues to rise

The number of sequences per sample is not large enough to cover all of the bacterial families

Rarefaction tab

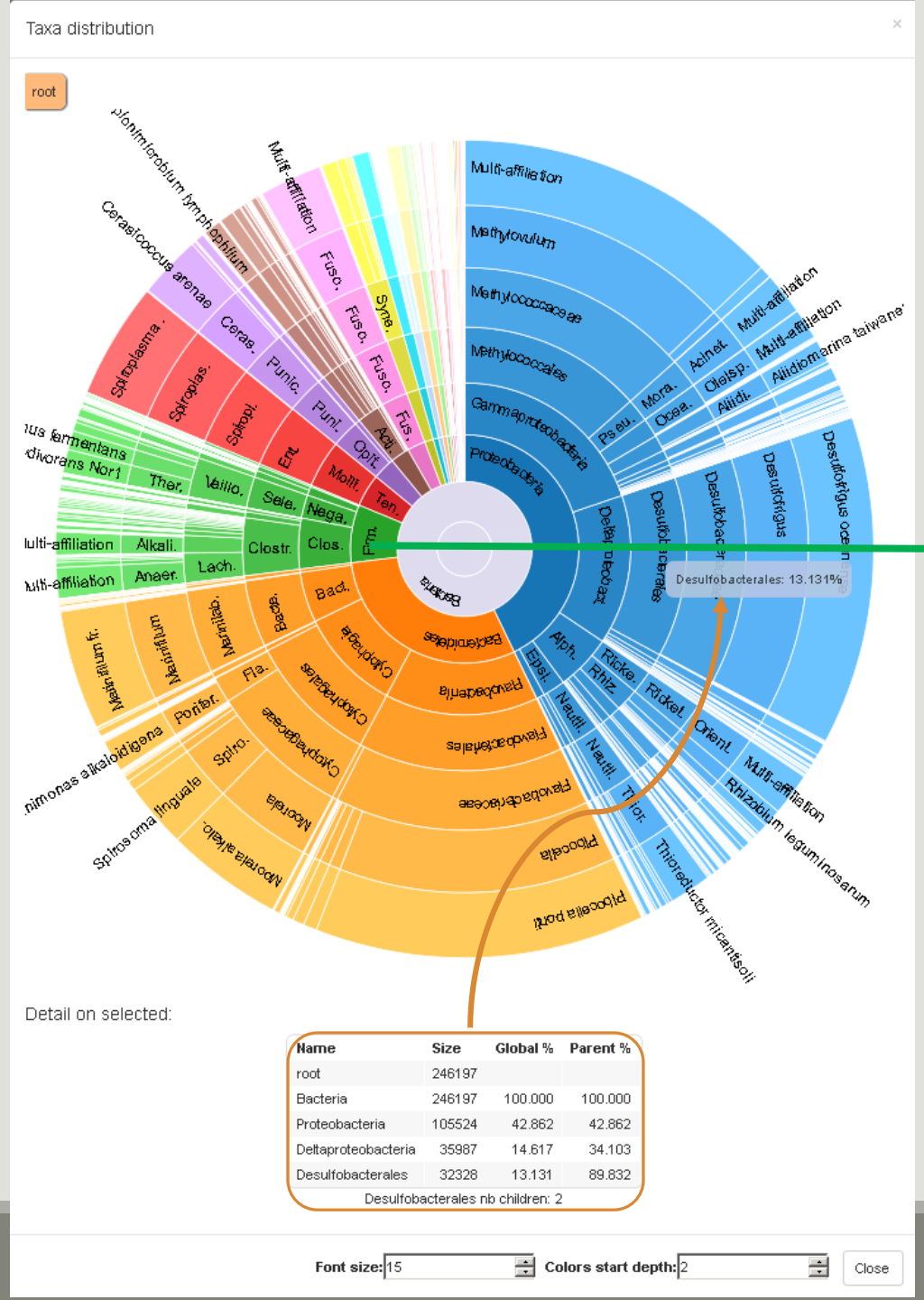
Available only after AFFILIATION TOOL

Samples size ~85 000 sequences

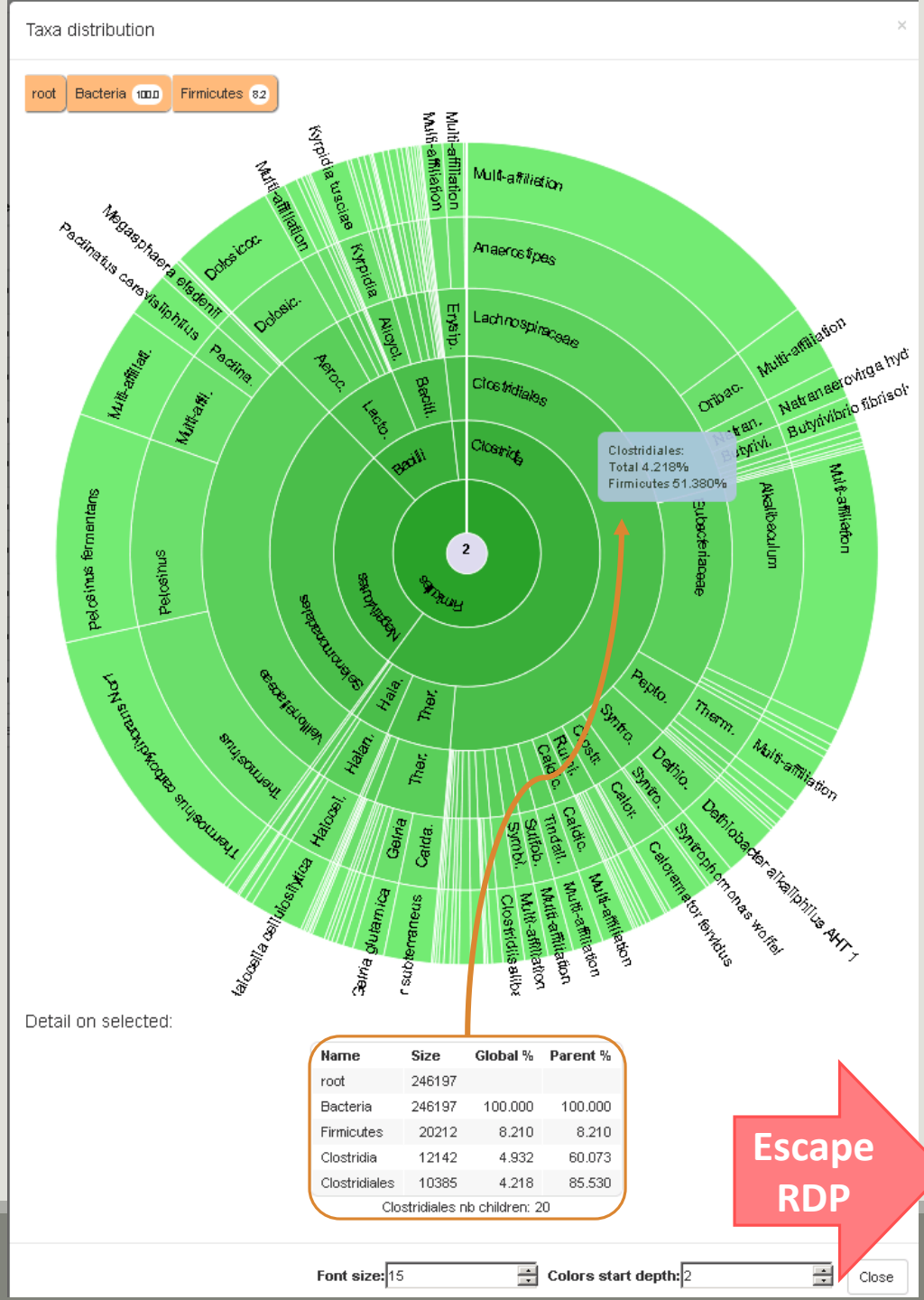


The curve slows to rise with ~50 000 sequences

With 60 000 sequences, we catch almost all genus of bacteria

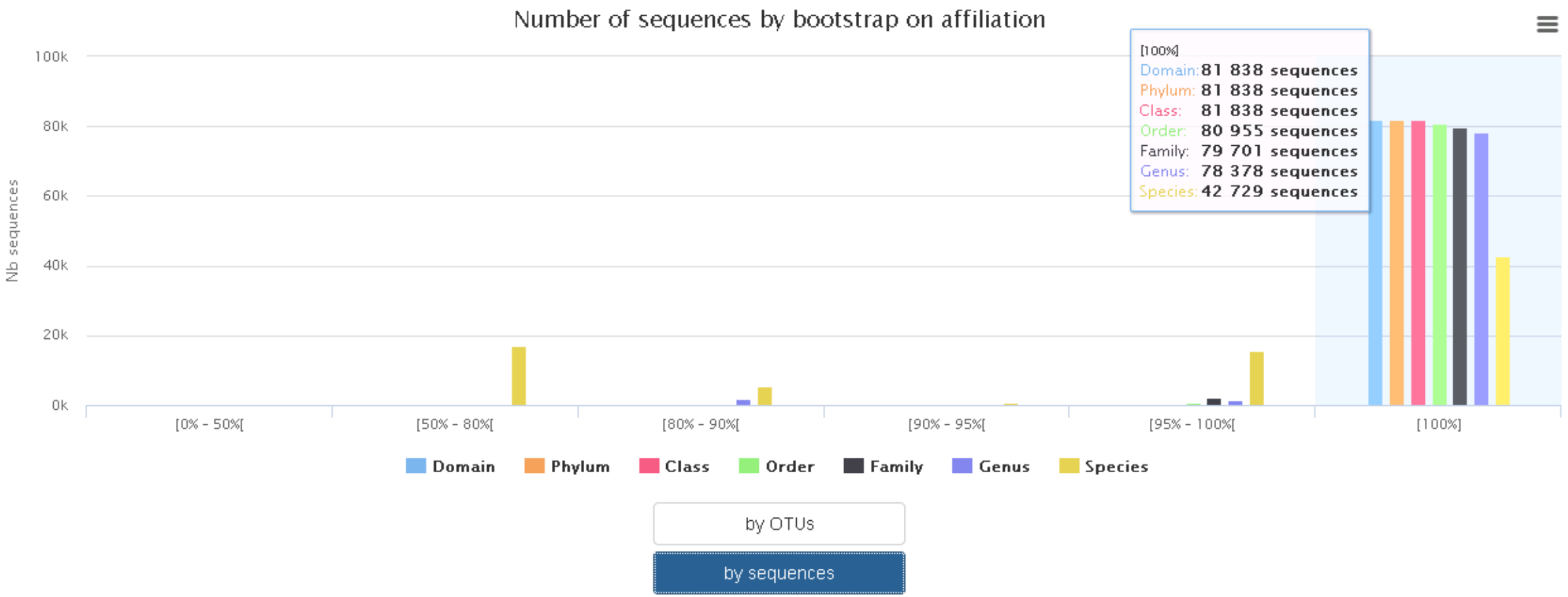


Zoom in on firmicutes



Escape RDP

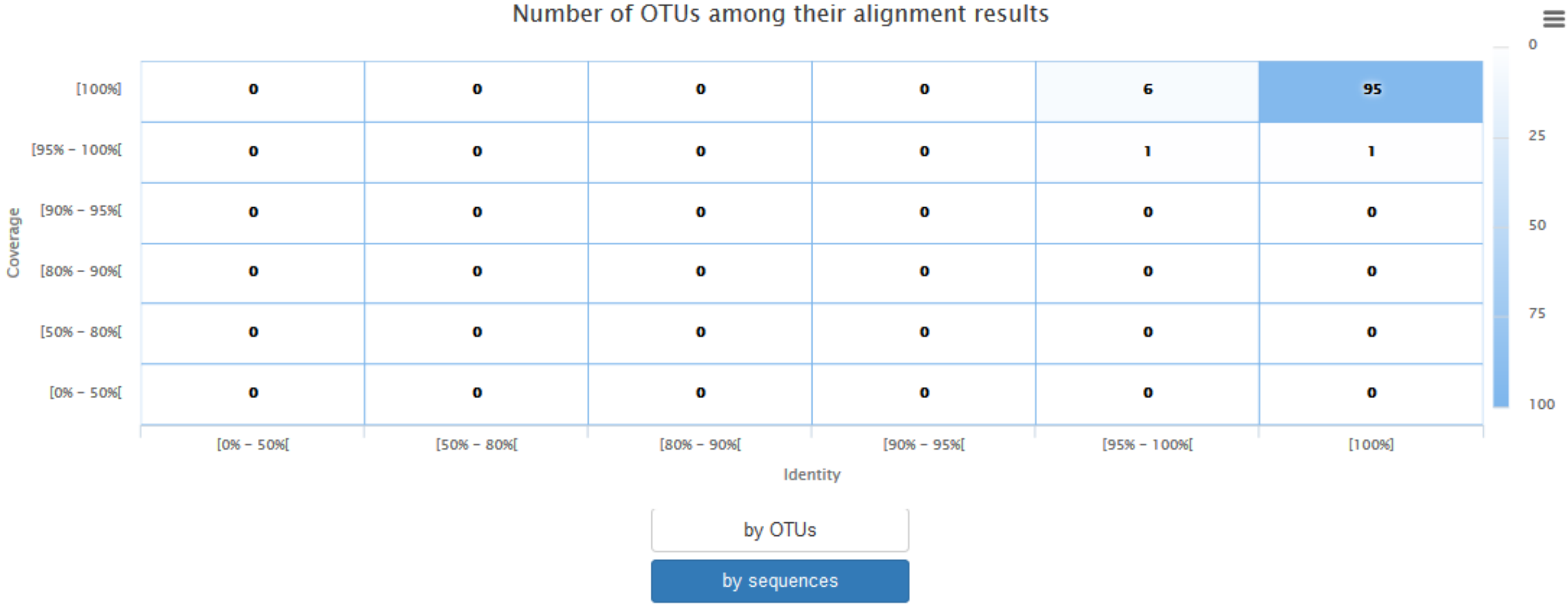
Taxonomy distribution | Bootstrap distribution



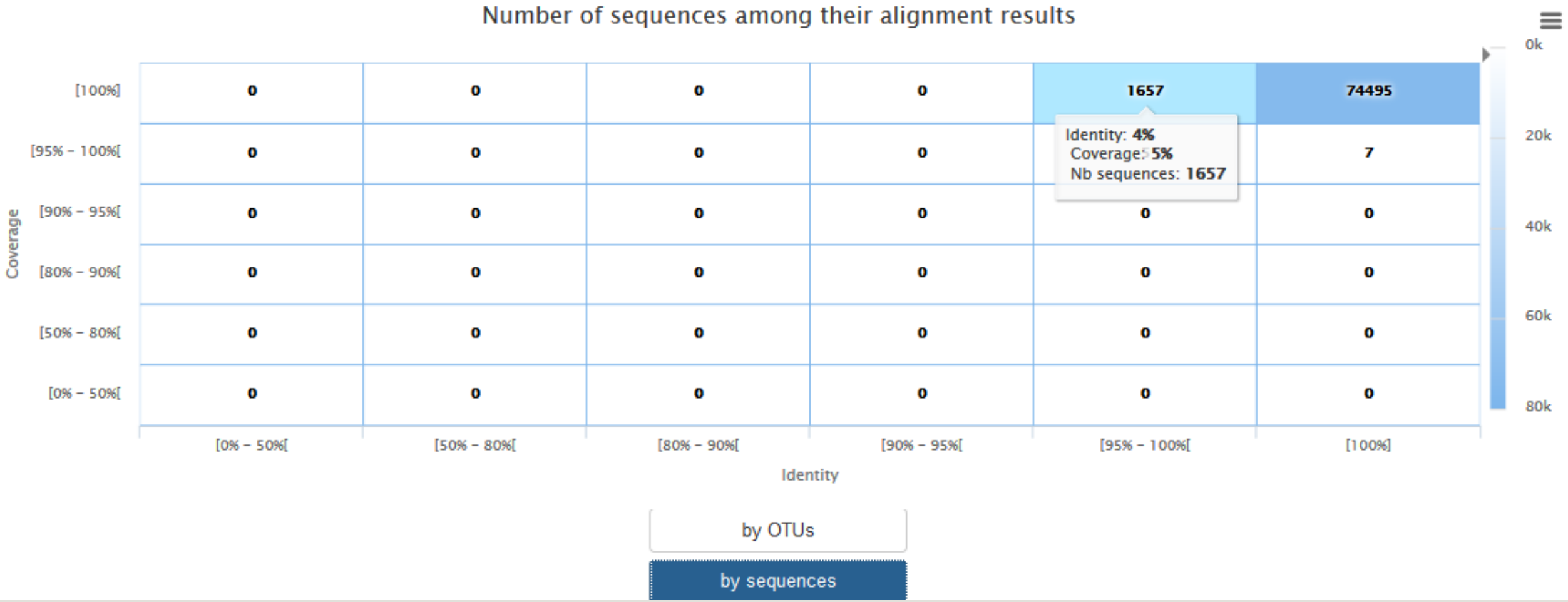
by OTUs

by sequences

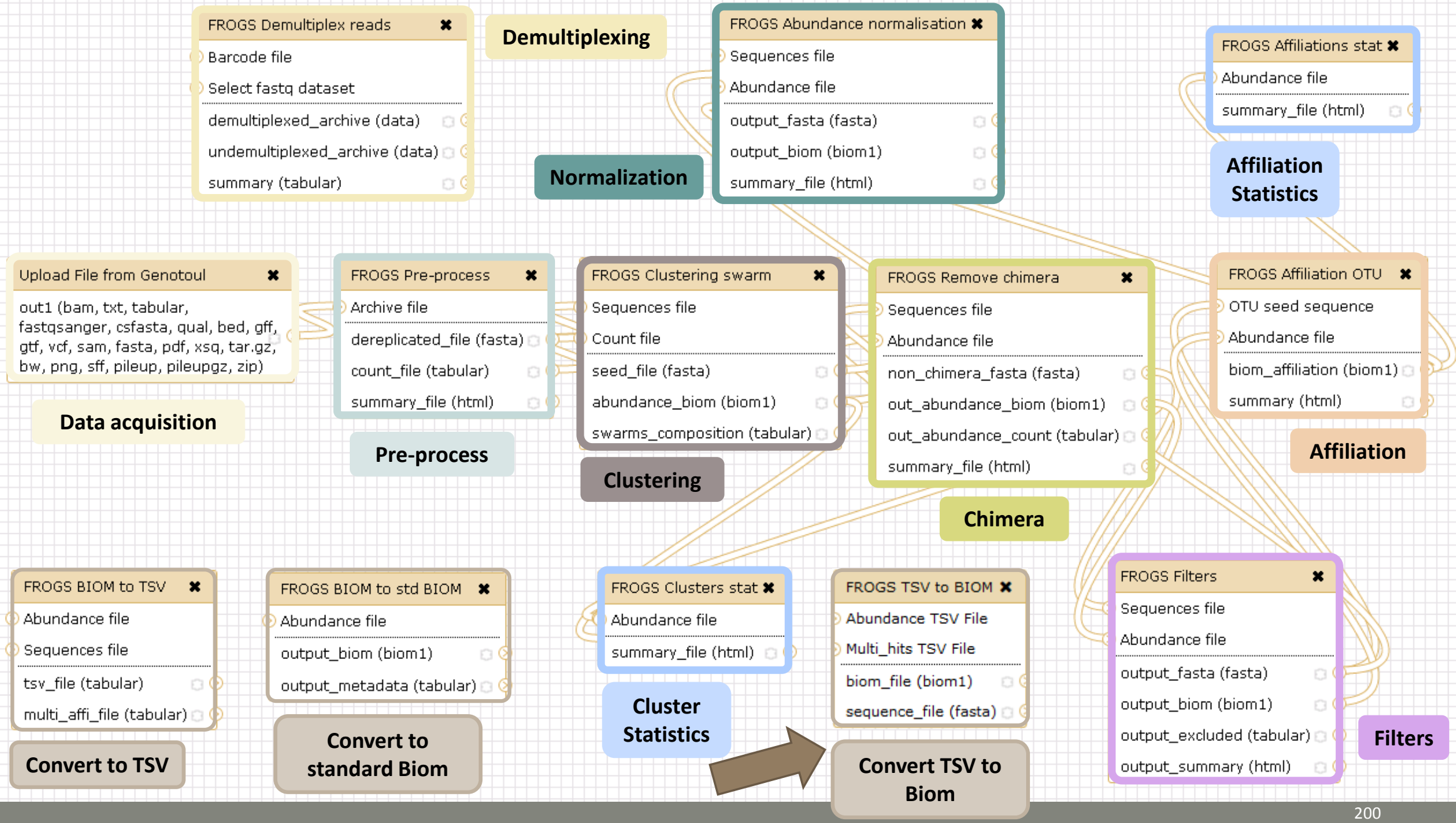
Taxonomy distribution | Alignment distribution



Taxonomy distribution | Alignment distribution



TSV to BIOM


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
FROGS Abundance normalisation
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
summary_file (html)
Normalization
FROGS Affiliations stat
Abundance file
summary_file (html)
Affiliation Statistics
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
Convert to TSV
FROGS BIOM to std BIOM
Abundance file
output_biom (biom1)
output_metadata (tabular)
Convert to standard Biom
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS TSV to BIOM
Abundance TSV File
Multi_hits TSV File
biom_file (biom1)
sequence_file (fasta)
Convert TSV to Biom
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters

TSV to BIOM

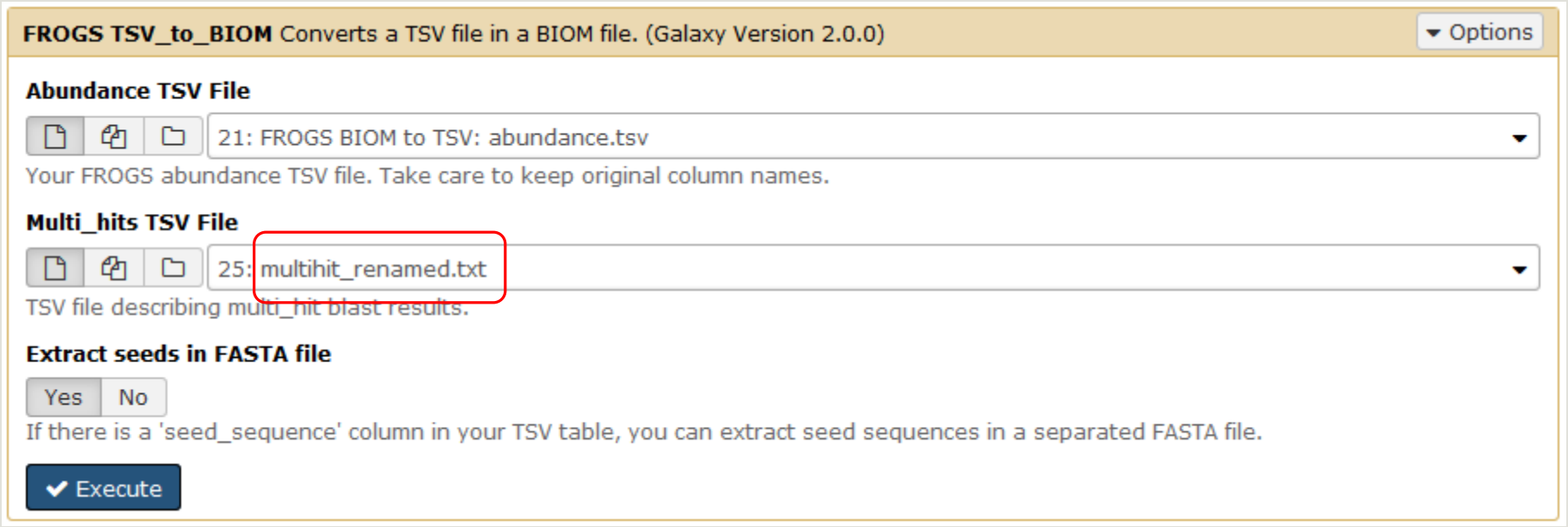
After modifying your abundance TSV file you can again:

- generate rarefaction curve
- sunburst 

Careful :

- do not modify column name
- do not remove column
- take care to choose a taxonomy available in your multi_hit TSV file
- if deleting line from multi_hit, take care to not remove a complete cluster without removing all "multi tags" in you abundance TSV file.
- if you want to rename a taxon level (ex : genus "Ruminiclostridium 5;" to genus "Ruminiclostridium;"), do not forget to modify also your multi_hit TSV file.

TSV to BIOM


FROGS TSV_to_BIOM Converts a TSV file in a BIOM file. (Galaxy Version 2.0.0)
Options
Abundance TSV File
21: FROGS BIOM to TSV: abundance.tsv
Your FROGS abundance TSV file. Take care to keep original column names.
Multi_hits TSV File
25: multihit_renamed.txt
TSV file describing multi_hit blast results.
Extract seeds in FASTA file
Yes
No
If there is a 'seed_sequence' column in your TSV table, you can extract seed sequences in a separated FASTA file.
Execute

Your Turn! – 8

PLAY WITH TSV_TO_BIOM

Exercise 8

→ objectives : Play with multi-affiliation and TSV_to_BIOM

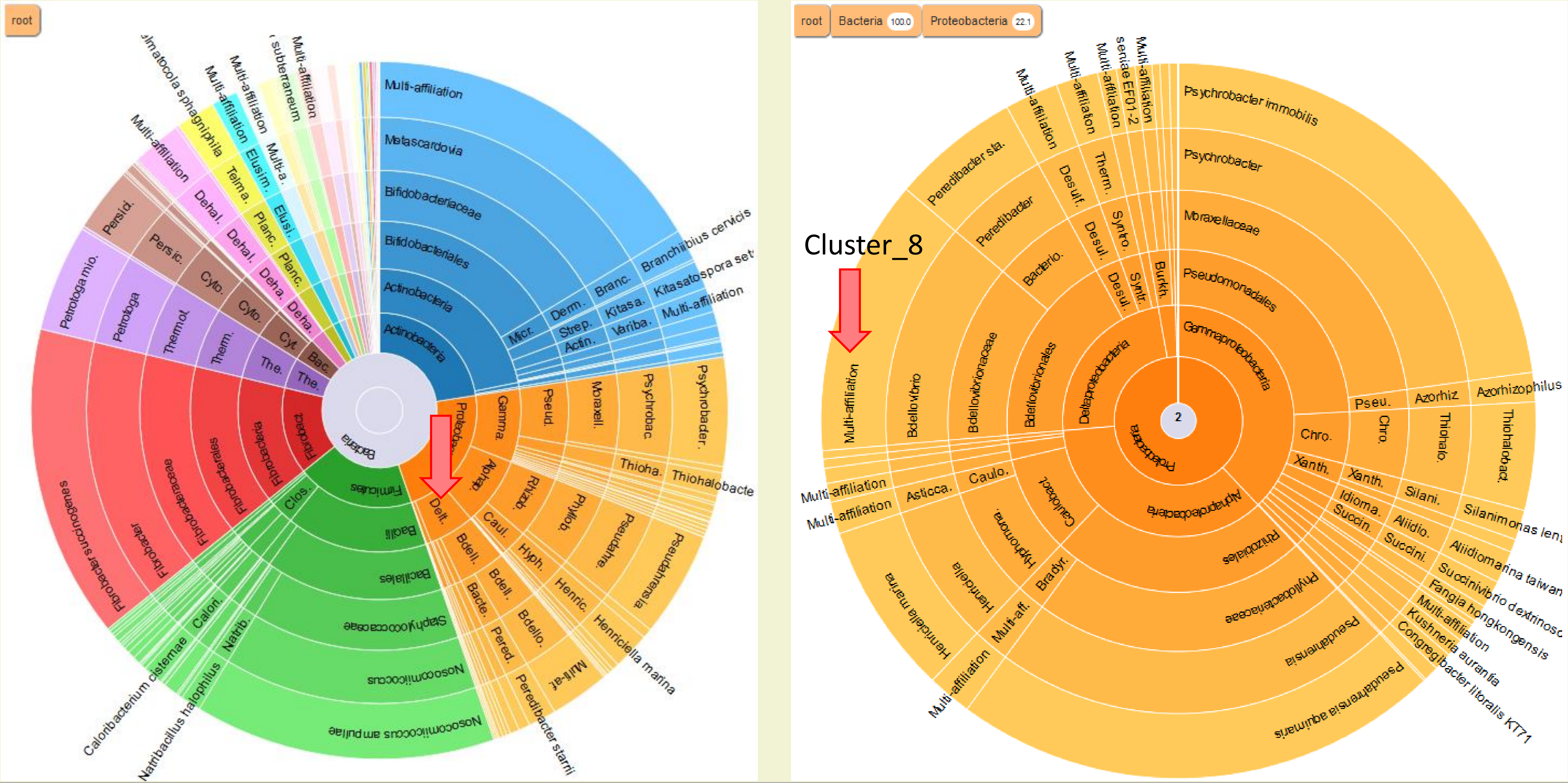
1. Observe in Multi_hit.tsv and abundance.tsv cluster_8 annotation

#blast_taxonomy	blast_subject	observation_name	observation_sum
Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Metascardovia;Multi-affiliation	multi-subject	Cluster_1	13337
Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;Fibrobacter;Fibrobacter succinogenes	AJ496032.1.1410	Cluster_2	11830
Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Nosocomiicoccus;Nosocomiicoccus ampullae	EU240886.1.1502	Cluster_3	11405
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Psychrobacter;Psychrobacter immobilis	U39399.1.1477	Cluster_4	4125
Bacteria;Thermotogae;Thermotogae;Thermotogales;Thermotogaceae;Petrotoga;Petrotoga miotherma	FR733705.1.1499	Cluster_5	4034
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Pseudahrensia;Pseudahrensia aquimaris	GU575117.1.1441	Cluster_6	3966
Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Persicitalea;Persicitalea jodogahamensis	multi-subject	Cluster_7	2433
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio;Multi-affiliation	multi-subject	Cluster_8	2268

Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus	CP007656.1036900.1038415
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus str. Tiberius	CP002930.1837665.1839157
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus str. Tiberius	CP002930.842397.843889
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus	AJ292760.1.1334
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus	
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus	
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus	AF084850.1.1436
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus HD100	BX842648.123565.125058
Cluster_8	Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	Bdellovibrio bacteriovorus HD100	BX842650.295616.297109

Bdellovibrio bacteriovorus

2. Observe le diversity diagramm



Exercise 8

3. How to change affiliation of cluster 8 ????

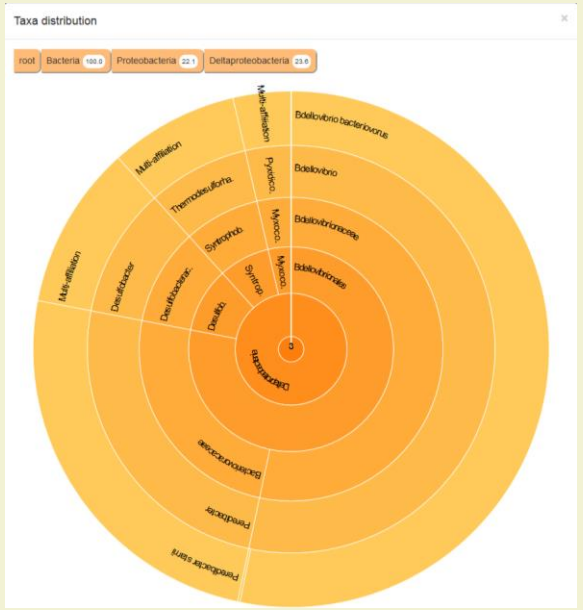
Exercise 8

4. Modify multi_hit.tsv and keep only :

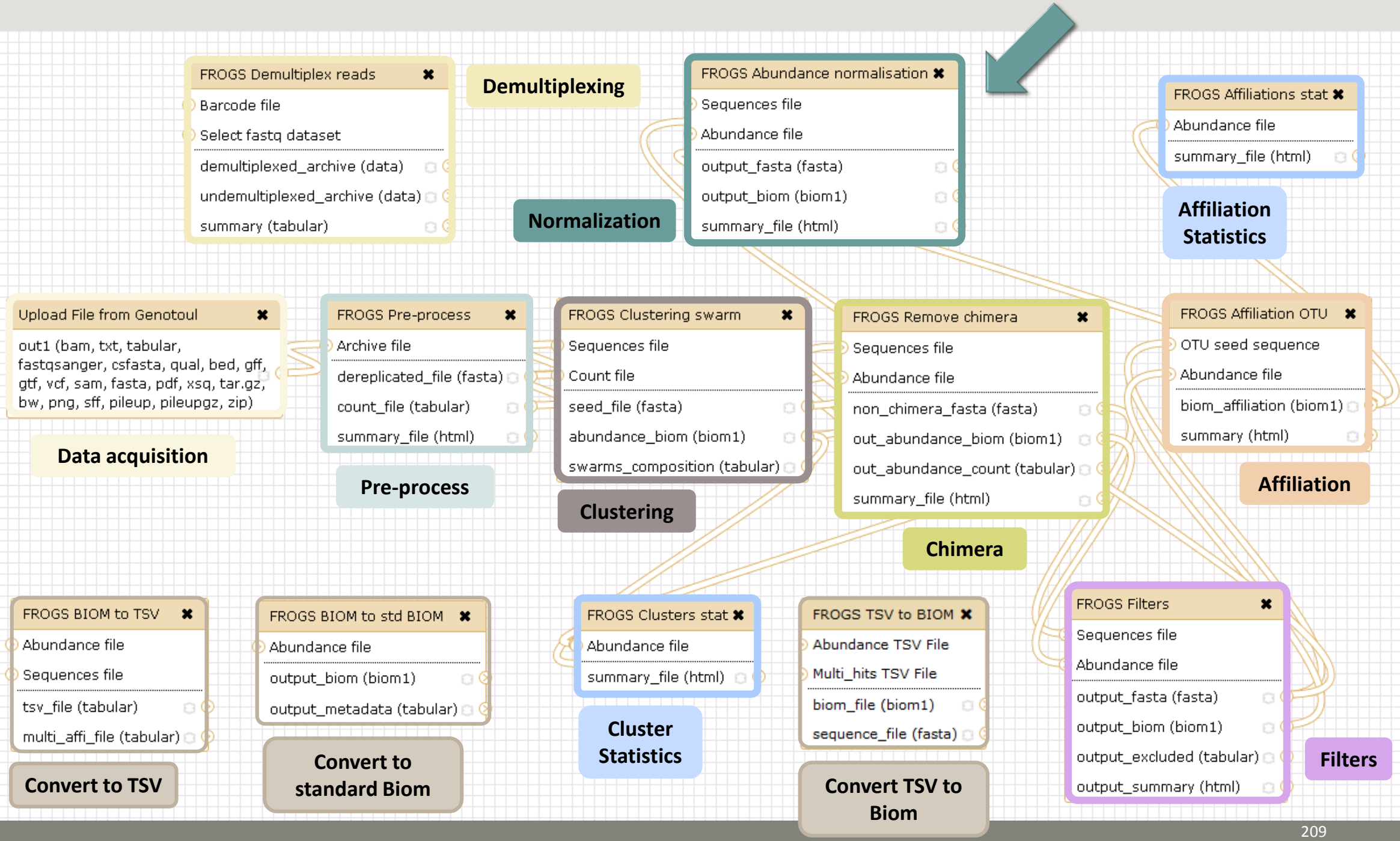
Cluster_8 Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio;Bdellovibrio bacteriovorus CP007656.1036900.1038415

Careful, no quotes around text !!!

5. Upload the new multihit file.
6. Create a new biom with a TSV_to_BIOM tool
7. Launch again the affilation_stat tool on this new biom
8. Observe the diversity diagram



Normalization


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
FROGS Abundance normalisation
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
summary_file (html)
Normalization
FROGS Affiliations stat
Abundance file
summary_file (html)
Affiliation Statistics
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
Convert to TSV
FROGS BIOM to std BIOM
Abundance file
output_biom (biom1)
output_metadata (tabular)
Convert to standard Biom
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS TSV to BIOM
Abundance TSV File
Multi_hits TSV File
biom_file (biom1)
sequence_file (fasta)
Convert TSV to Biom
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters

Normalization

Conserve a predefined number of sequence per sample:

- update Biom abundance file
- update seed fasta file

May be used when :

- Low sequencing sample
- Required for some statistical methods to compare the samples in pairs

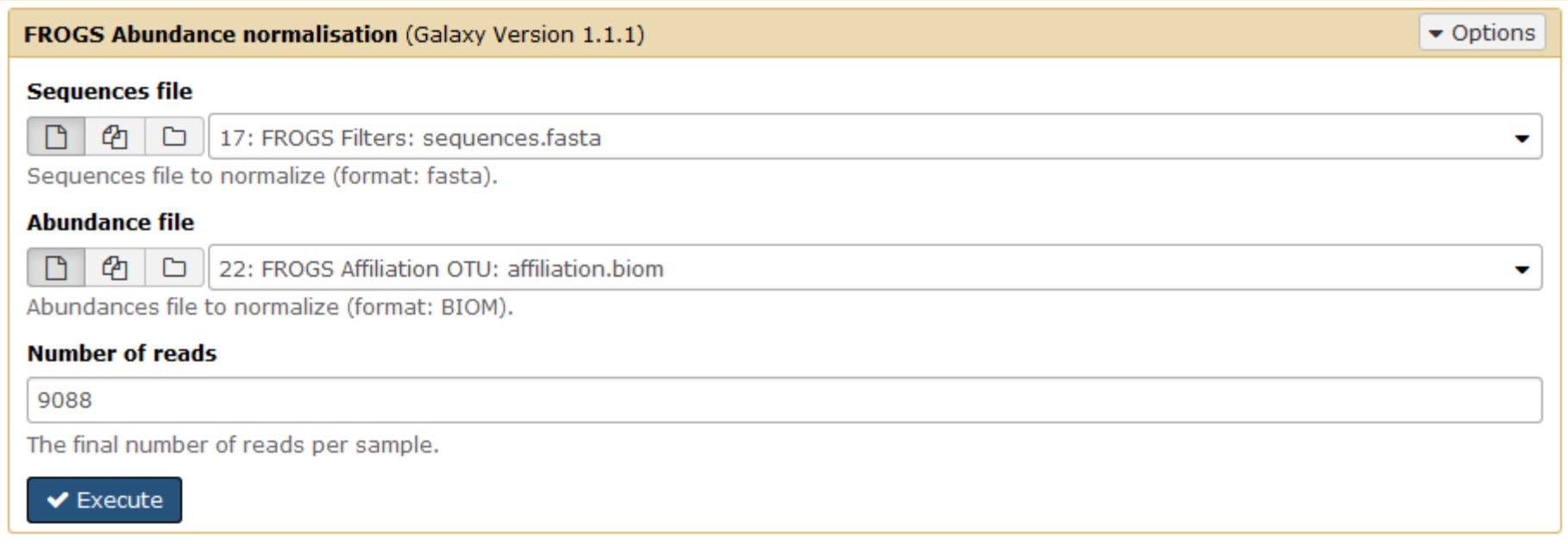
Your Turn! – 9

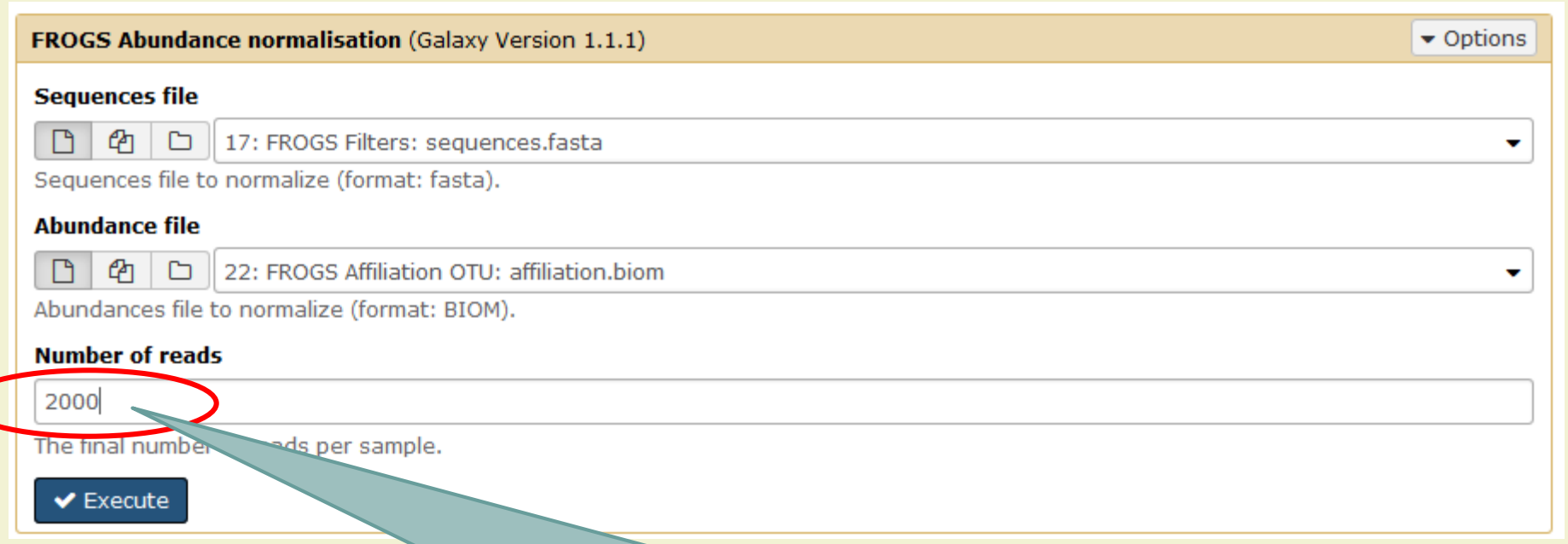
LAUNCH NORMALIZATION TOOL

Exercise 9

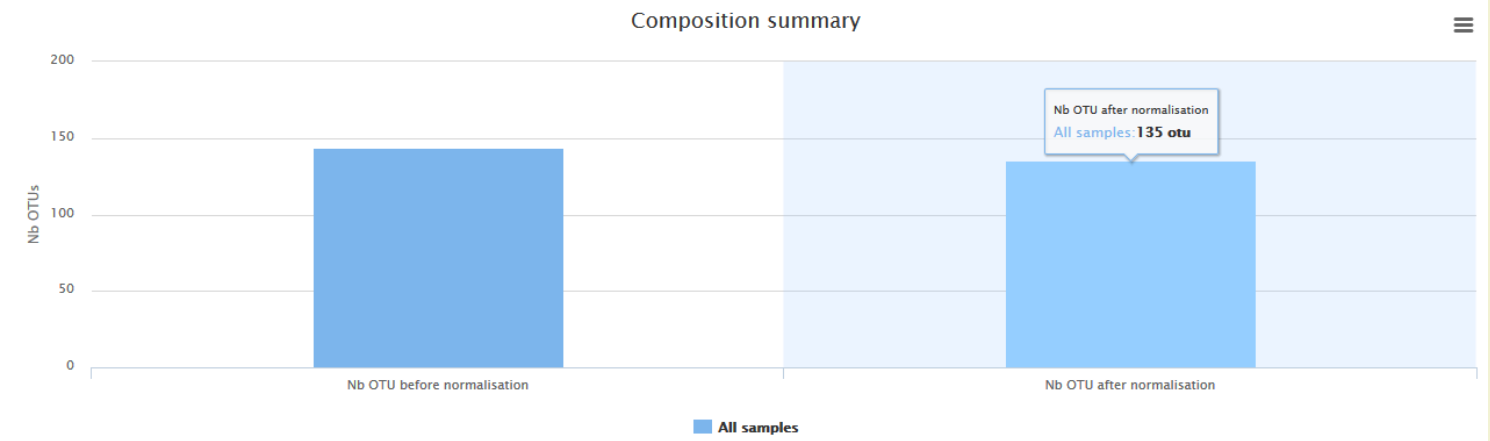
Launch Normalization Tool

1. What is the smallest sequenced samples ?
2. Normalize your data from Affiliation based on this number of sequence
3. Explore the report HTML result.
4. Try other threshold and explore the report HTML result
   What do you remark ?


FROGS Abundance normalisation (Galaxy Version 1.1.1)
Options
Sequences file
17: FROGS Filters: sequences.fasta
Sequences file to normalize (format: fasta).
Abundance file
22: FROGS Affiliation OTU: affiliation.biom
Abundances file to normalize (format: BIOM).
Number of reads
9088
The final number of reads per sample.
Execute



Or, this number can be chosen according to the rarefaction curve. For example, we can choose the smallest number of sequences that still retain all the genus.



CSV

Show 10 entries

Search:

Composition by sample

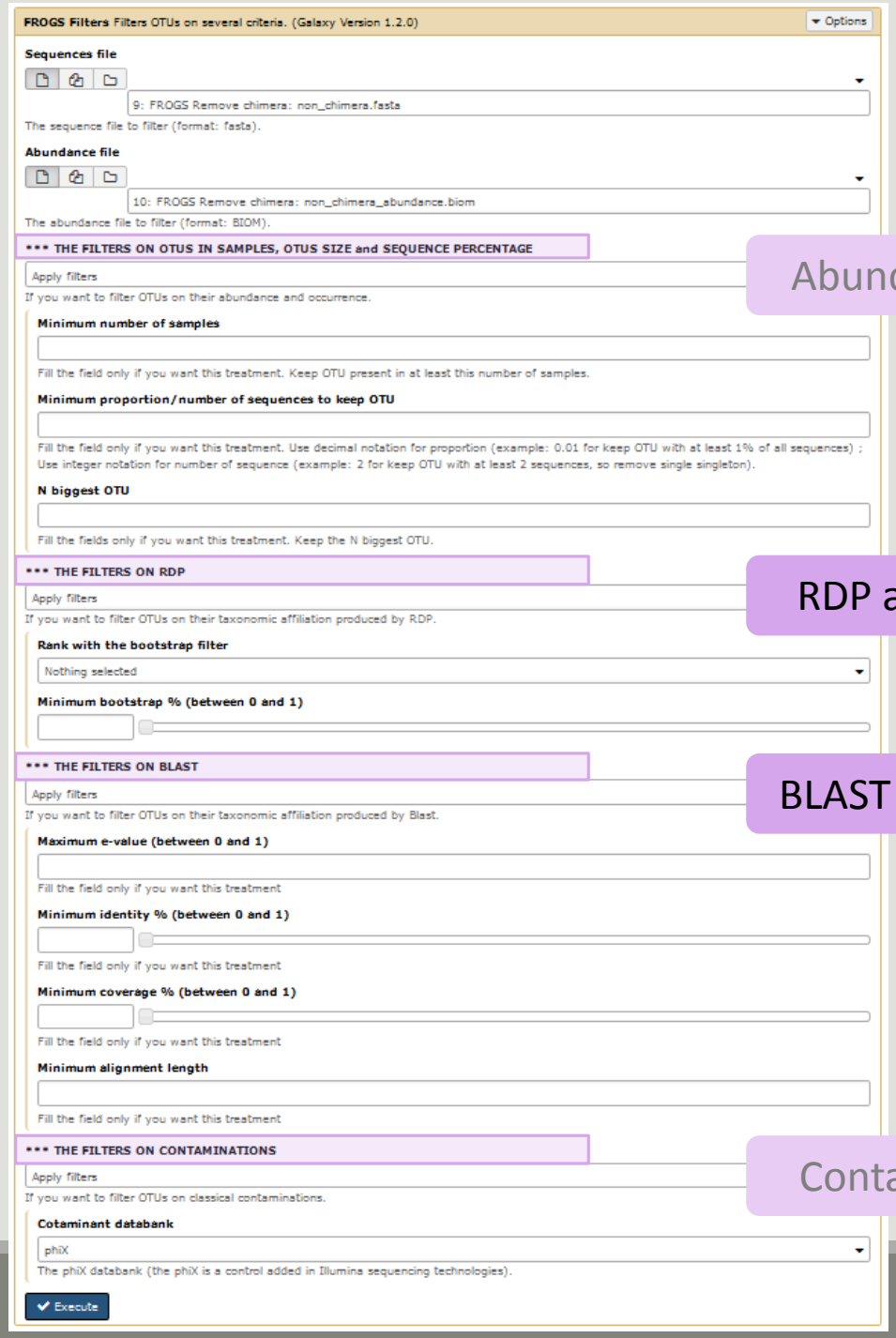
Sample	Nb OTU before normalisation	Nb OTU after normalisation
100_10000seq_sampleA1_cutadapt	144	135
100_10000seq_sampleA2_cutadapt	144	135
100_10000seq_sampleA3_cutadapt	144	135
100_10000seq_sampleB1_cutadapt	144	135
100_10000seq_sampleB2_cutadapt	144	135
100_10000seq_sampleB3_cutadapt	144	135
100_10000seq_sampleC1_cutadapt	144	135
100_10000seq_sampleC2_cutadapt	144	135
100_10000seq_sampleC3_cutadapt	144	135

Showing 1 to 9 of 9 entries

Previous 1 Next

Filters on affiliations

Do not forget, with filter tool we can filter the data based on their affiliation



Abundance filters

RDP affiliation filters

BLAST affiliation filters

Contamination filter

Exercise 10

1. Apply filters to keep only data with perfect alignment.
2. How many clusters have you keep ?

FROGS Filters Filters OTUs on several criteria. (Galaxy Version 1.2.0) ▾ Options

Sequences file

17: FROGS Filters: sequences.fasta

The sequence file to filter (format: fasta).

Abundance file

22: FROGS Affiliation OTU: affiliation.biom

The abundance file to filter (format: BIOM).

***** THE FILTERS ON OTUS IN SAMPLES, OTUS SIZE and SEQUENCE PERCENTAGE**

No filters

If you want to filter OTUs on their abundance and occurrence.

***** THE FILTERS ON RDP**

No filters

If you want to filter OTUs on their taxonomic affiliation produced by RDP.

***** THE FILTERS ON BLAST**

Apply filters

If you want to filter OTUs on their taxonomic affiliation produced by Blast.

Maximum e-value (between 0 and 1)

Fill the field only if you want this treatment

Minimum identity % (between 0 and 1)

1

Fill the field only if you want this treatment

Minimum coverage % (between 0 and 1)

1

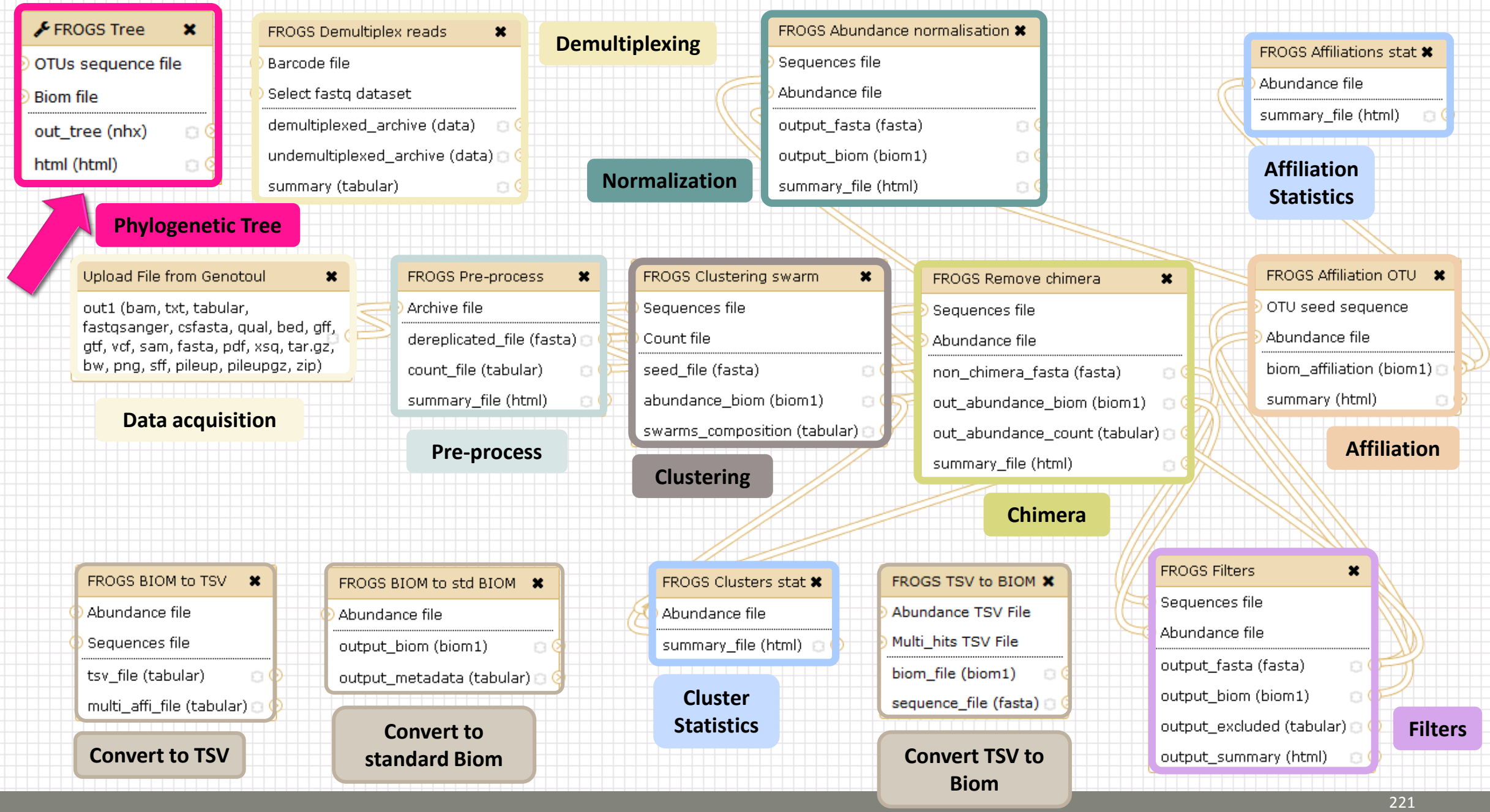
Fill the field only if you want this treatment

Minimum alignment length

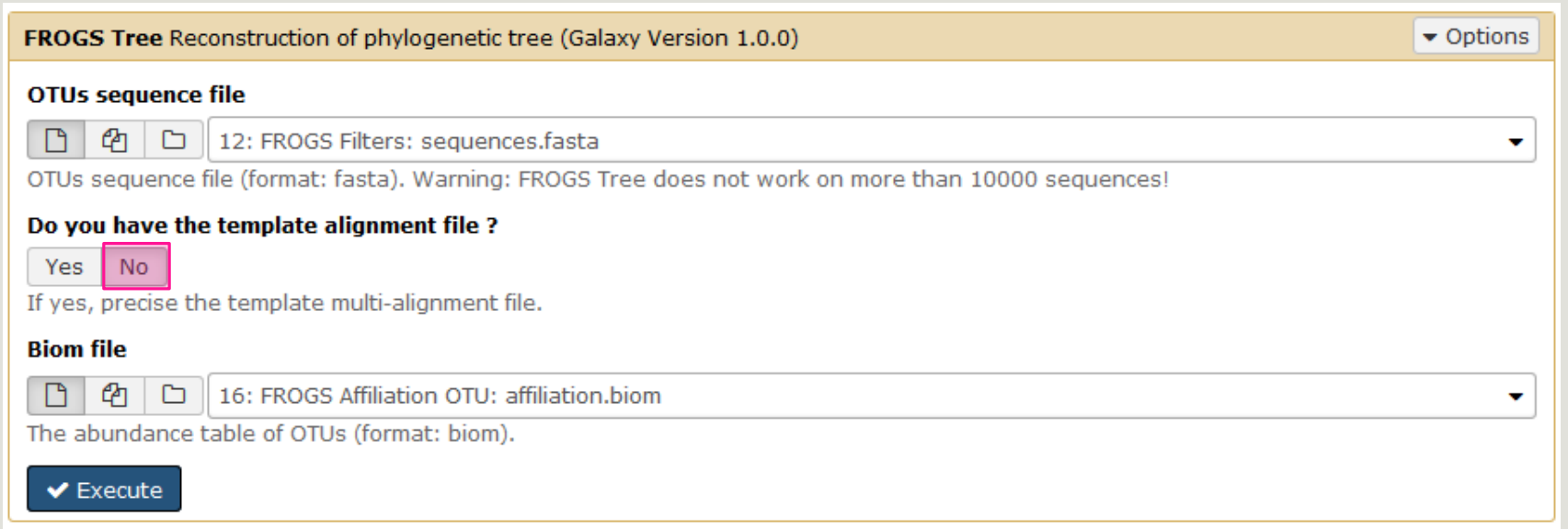
Fill the field only if you want this treatment

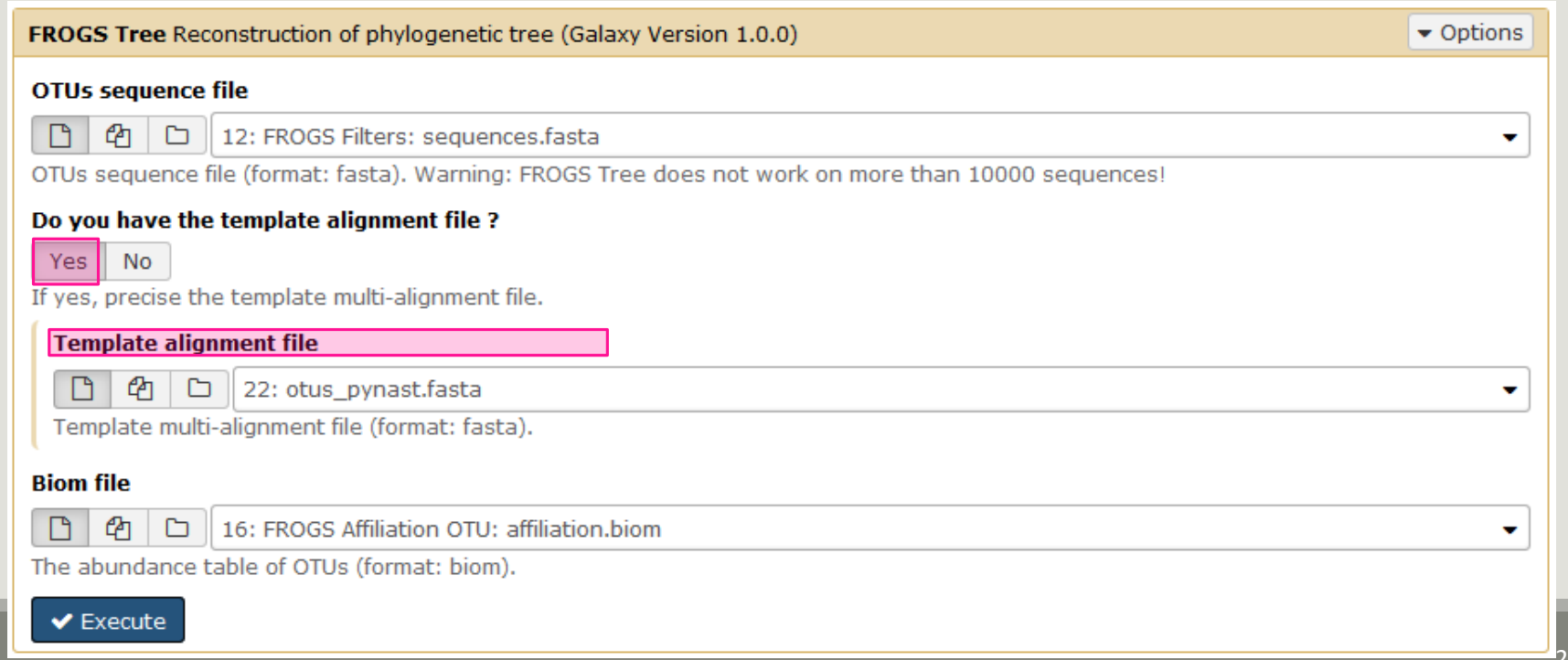
FROGS Tree

CREATE A PHYLOGENETICS TREE OF OTUS


FROGS Tree
OTUs sequence file
Biom file
out_tree (nhx)
html (html)
Phylogenetic Tree
FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Demultiplexing
FROGS Abundance normalisation
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
summary_file (html)
Normalization
FROGS Affiliations stat
Abundance file
summary_file (html)
Affiliation Statistics
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
Data acquisition
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
Pre-process
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
Clustering
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
Chimera
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
Affiliation
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
Convert to TSV
FROGS BIOM to std BIOM
Abundance file
output_biom (biom1)
output_metadata (tabular)
Convert to standard Biom
FROGS Clusters stat
Abundance file
summary_file (html)
Cluster Statistics
FROGS TSV to BIOM
Abundance TSV File
Multi_hits TSV File
biom_file (biom1)
sequence_file (fasta)
Convert TSV to Biom
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
Filters

2 choices to do your phylogenetics tree

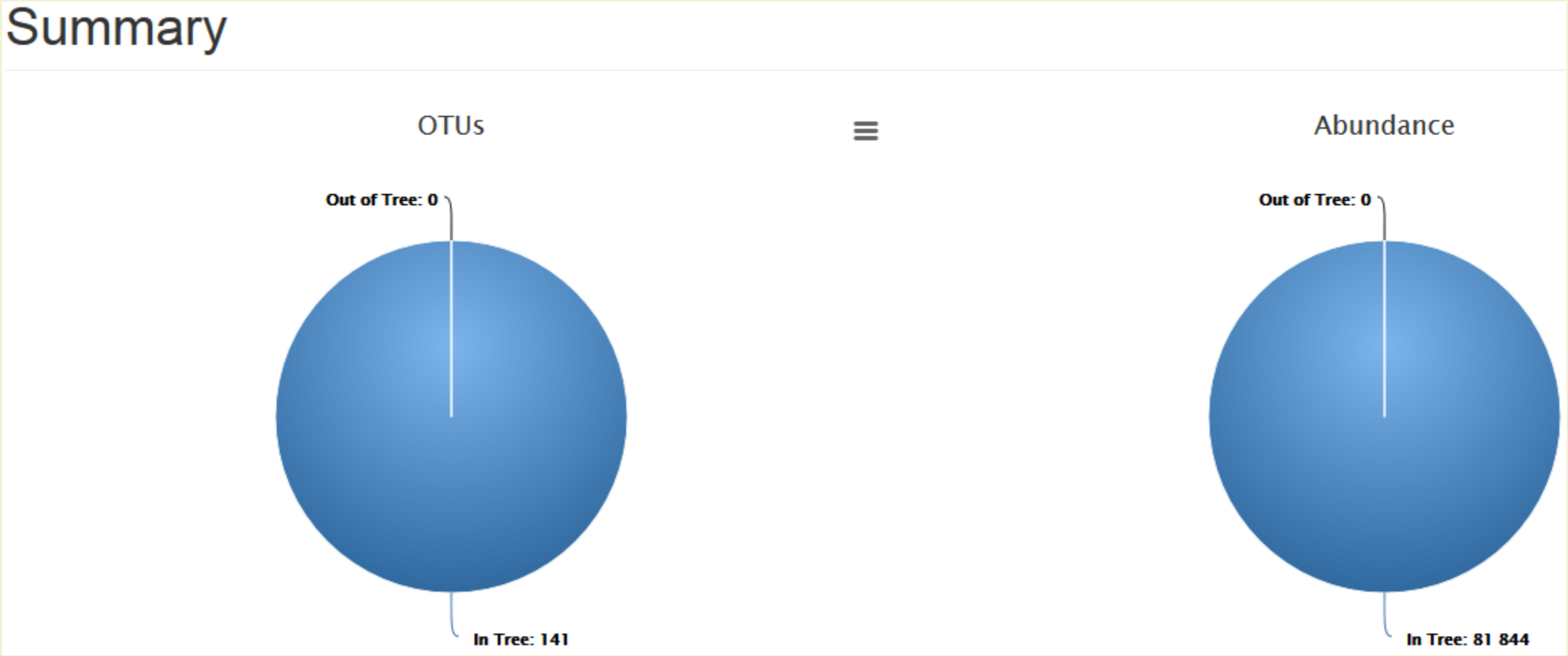


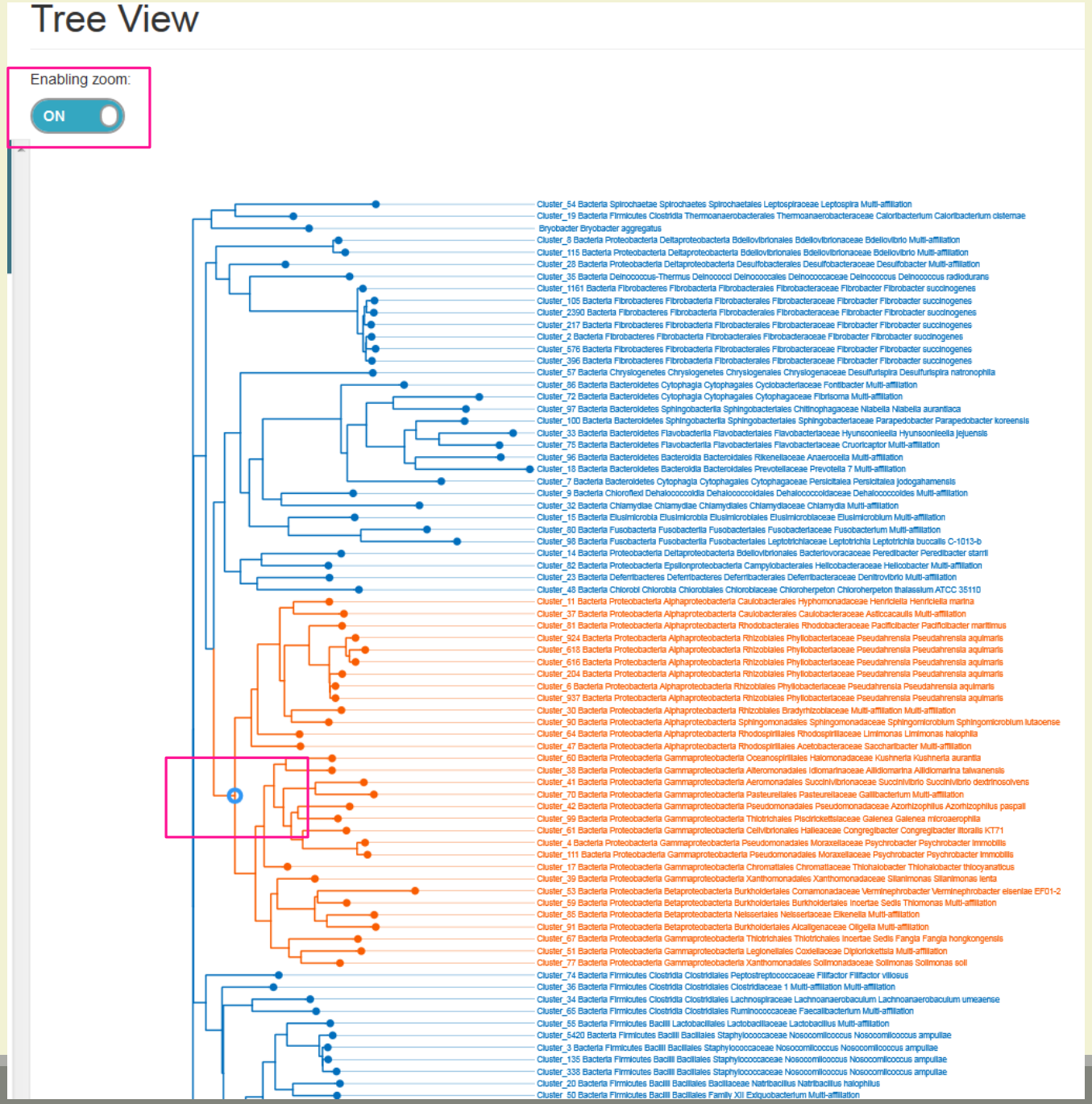


Exercise 10

1. Create a tree with the filtered OTUs without template
2. Explore the HTML file
3. Look tree.nwk

Summary


OTUs
Out of Tree: 0
In Tree: 141
Abundance
Out of Tree: 0
In Tree: 81 844



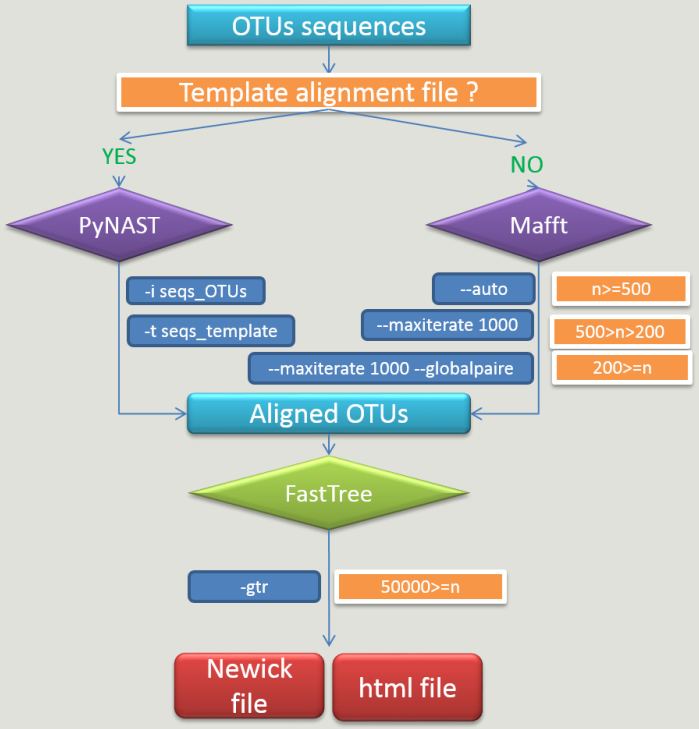
Tree.nwk:

(((Cluster_54:0.19489,Cluster_19:0.07629)0.892:0.03423,Cluster_58:0.13306)0.853:0.02661,((((Cluster_8:0.00054,Cluster_115:0.01025)1.000:0.16828,(Cluster_28:0.07332, ...)))

How works FROGS TREE ?

Pynast needs alignment template to go fast

But if your species is not similar at 75% with a sequence in the template, your species will be not in the tree !



To find templates:

Based on 16S GreenGenes databank
https://github.com/biocore/qiime-default-reference/blob/master/qiime_default_reference/gg_13_8_otus/rep_set_aligned/85_otus.pynast.fasta.gz

Based on 16S SILVA databank
https://www.arb-silva.de/fileadmin/silva_databases/qiime/Silva_128_release.tgz

Tool descriptions

What it does

FROGS Pre-process filters and dereplicates amplicons for use in diversity analysis.

Inputs/Outputs

Inputs

By sample your sequences and their qualities.

Illumina inputs

> **Usage:** The amplicons have been sequenced in paired-end. The amplicon expected length is inferior than the R1 and R2 length. R1 and R2 can be merge by the common region.
> **Files:** One R1 and R2 by sample (format FASTQ)
> **Example:** splA_R1.fastq.gz, splA_R2.fastq.gz, splB_R1.fastq.gz, splB_R2.fastq.gz

OR

> **Usage:** The single end sequencing cover all the amplicons or the R1 and R2 have already been overlaped.
> **Files:** One sequence file by sample (format FASTQ).
> **Example:** splA.fastq.gz, splB.fastq.gz

454 inputs

> **Files:** One sequence file by sample (format FASTQ)
> **Example:** splA.fastq.gz, splB.fastq.gz

These files must be added sample by sample or provide in an archive file (tar.gz).

Remark: In an archive if you use R1 and R2 files they names must end with *_R1* and *_R2*.

Outputs

Sequence file (dereplicated.fasta):

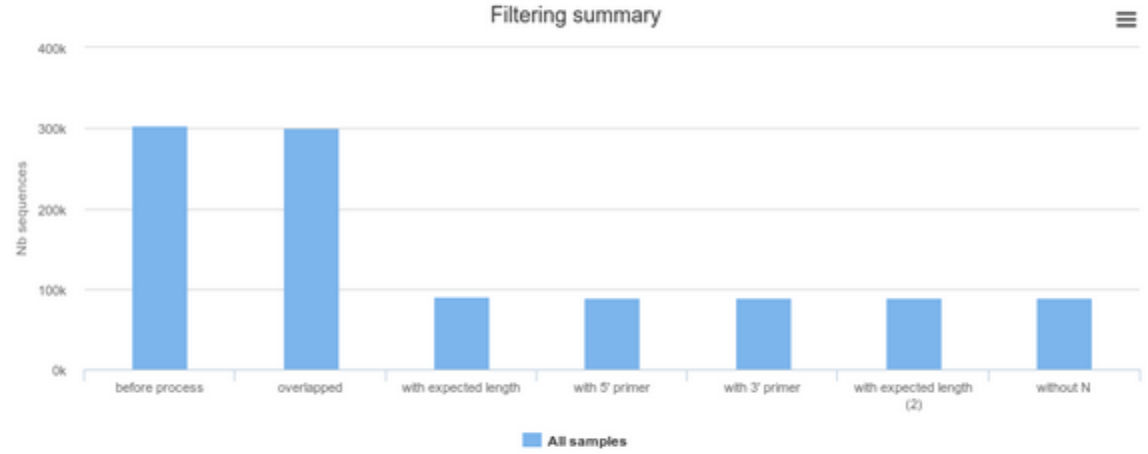
> Only one file with all samples sequences (format FASTA). These sequences are dereplicated: strictly identical sequence are represented only one and the initial count is kept in count file.

Count file (count.tsv):

> This file contains the count of all uniq sequences in each sample (format TSV).

Summary file (excluded_data.html):

> This file presents the ordered filters and the number of sequences passing these (format HTML).



Show 10 entries Search:

Filtering by sample

Sample	before process	overlapped	with expected length	with 5' primer	with 3' primer	with expected length (2)	without N
sampleA	90,126	90,126	90,126	89,697	89,697	89,697	89,697
sampleB	213,043	209,801	0	0	0	0	0

Showing 1 to 2 of 2 entries Previous 1 Next

How it works

Steps	Illumina	454
1	For uncontiged data: contig read1 and read2 with a maximum of 10% mismatch in the overlaped region (FLASh)	/
2	Filter contig sequence on its length which must be between Minimum amplicon size" and "Maximum amplicon size"	/
3	Remove sequences where the two primers are not persent and remove primers sequence (cutadapt). The primer search accept 10% of differences	Remove sequence where the two primers are not persent, remove primers sequence and reverse complement the sequences with strand - (cutadapt). The primer search accept 10% of differences
4	Filter sequences on its length and with ambiguous nucleotids	filter sequences on its length, with ambiguous nucleotids, with at least one homopolymer with size >7nt and with distance between two poor qualities ()< 10) of <= 10 nt
5	Dereplicate sequences	Dereplicate sequences

Advices/details on parameters

Primers parameters

The primers must provided in 5' to 3' orientation.

Example:

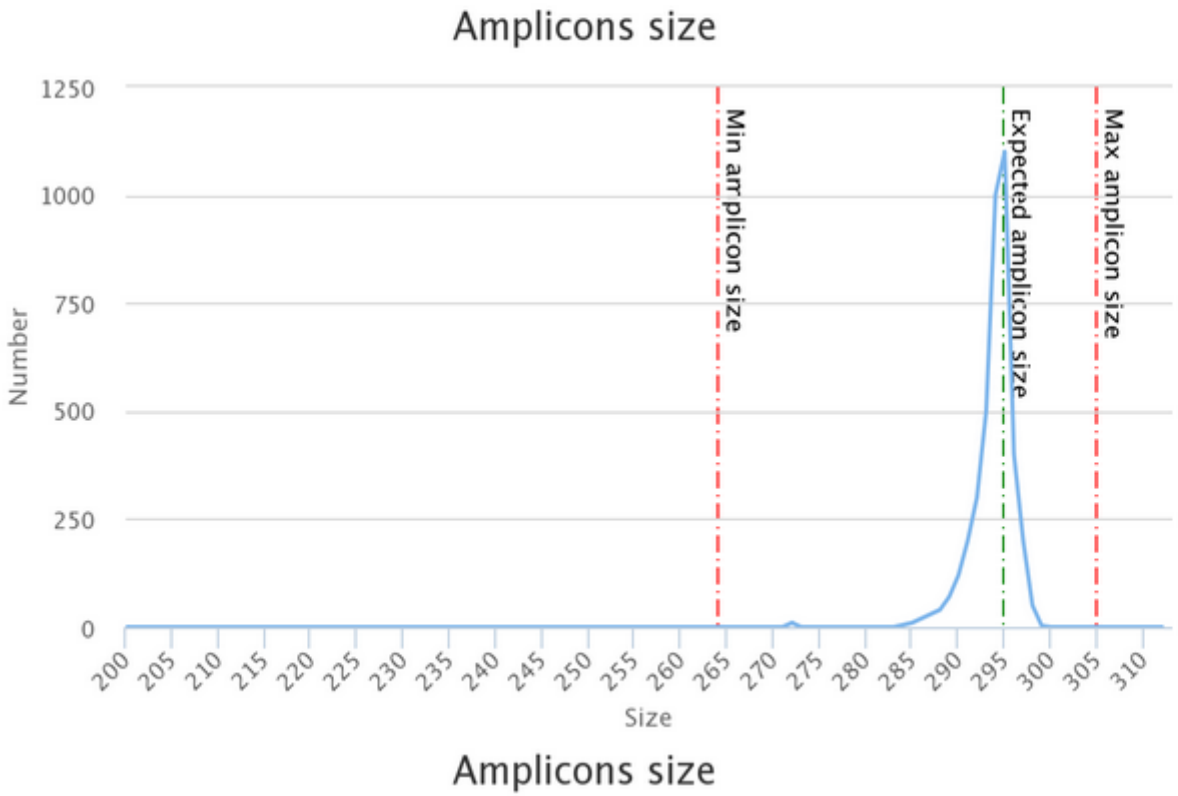
5' ATGCCC GTCGTCGTAAAATGC ATTTCAG 3'

Value for parameter 5' primer: ATGCC

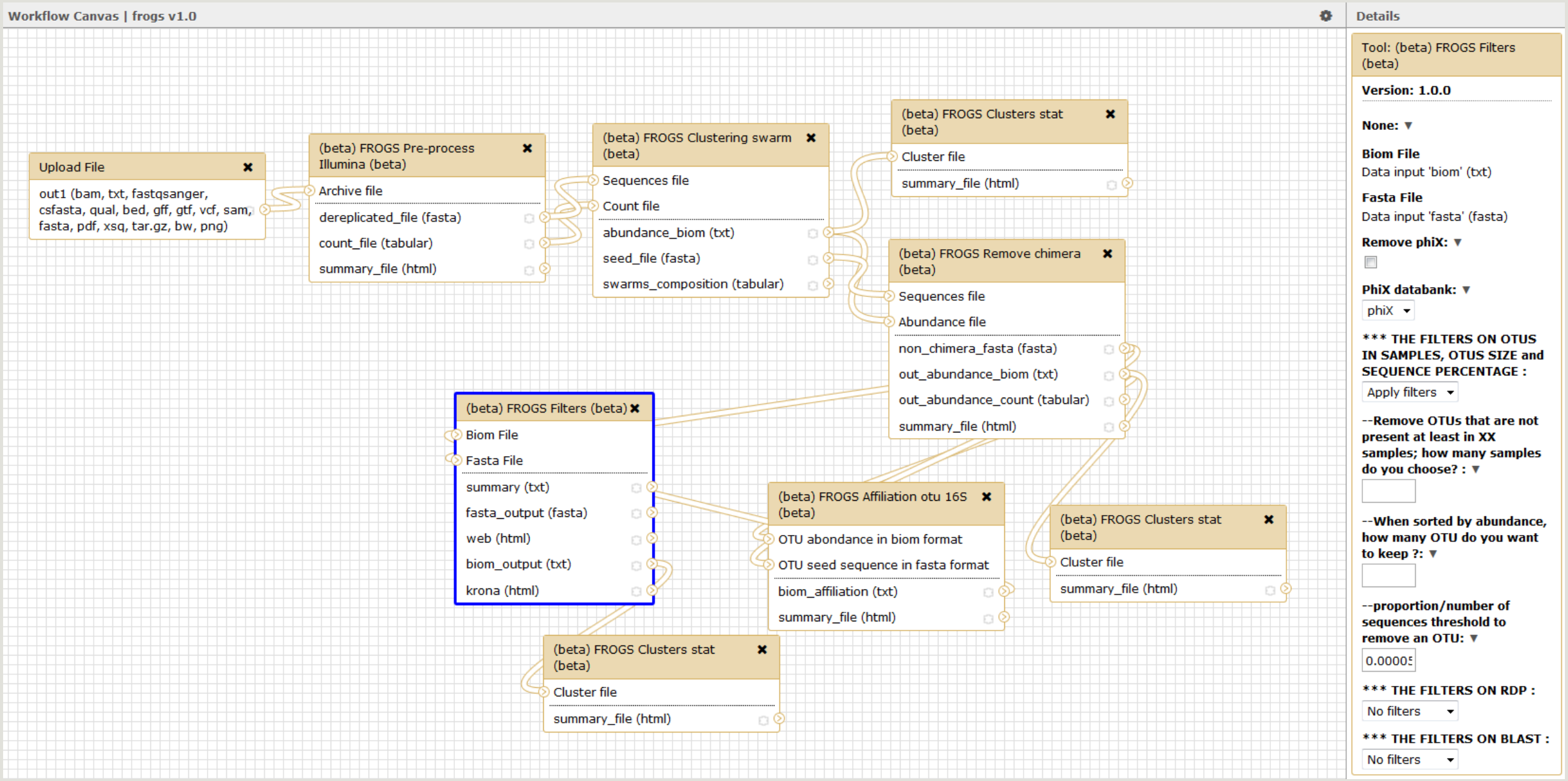
Value for parameter 3' primer: ATTTCAG

Amplicons sizes parameters

The two following images shown two examples of perfect values fors sizes parameters.



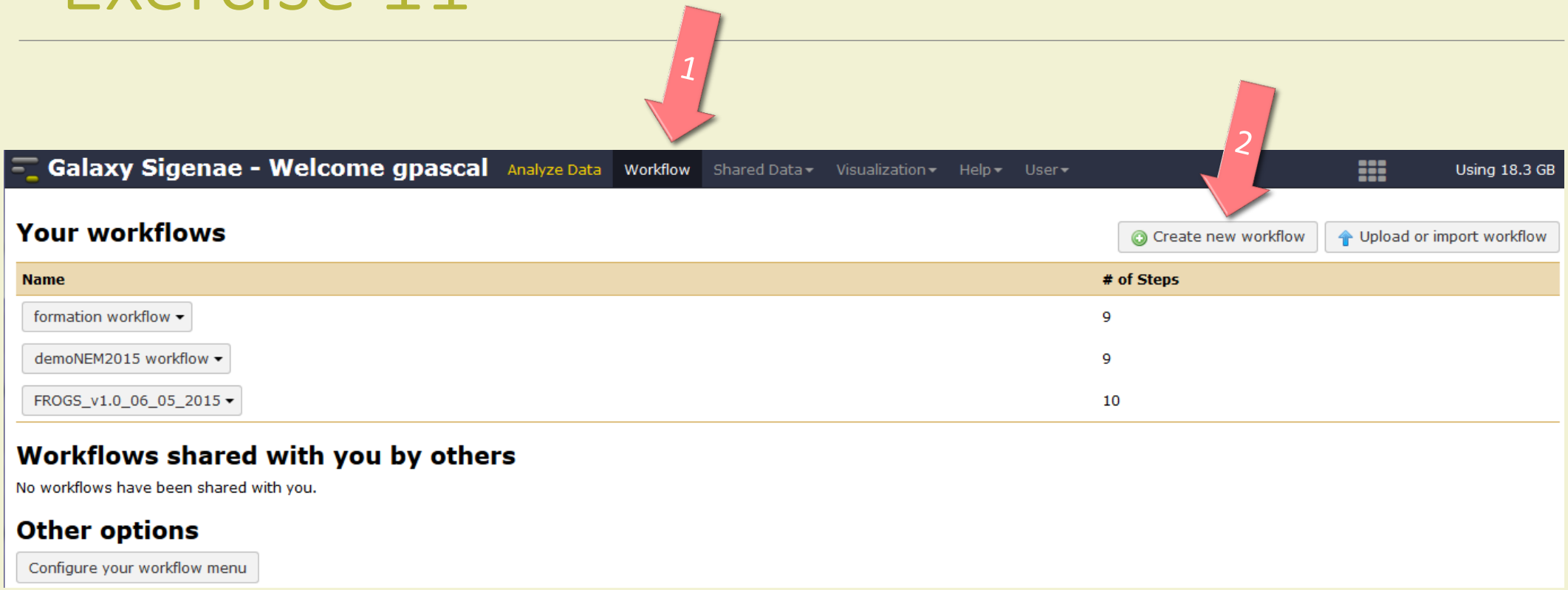
Workflow creation


Workflow Canvas | frogs v1.0
Details
Upload File
out1 (bam, txt, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png)
(beta) FROGS Pre-process Illumina (beta)
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
(beta) FROGS Clustering swarm (beta)
Sequences file
Count file
abundance_biom (txt)
seed_file (fasta)
swarms_composition (tabular)
(beta) FROGS Clusters stat (beta)
Cluster file
summary_file (html)
(beta) FROGS Remove chimera (beta)
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (txt)
out_abundance_count (tabular)
summary_file (html)
(beta) FROGS Filters (beta)
Biom File
Fasta File
summary (txt)
fasta_output (fasta)
web (html)
biom_output (txt)
krona (html)
(beta) FROGS Affiliation otu 16S (beta)
OTU abondance in biom format
OTU seed sequence in fasta format
biom_affiliation (txt)
summary_file (html)
(beta) FROGS Clusters stat (beta)
Cluster file
summary_file (html)
(beta) FROGS Clusters stat (beta)
Cluster file
summary_file (html)
Tool: (beta) FROGS Filters (beta)
Version: 1.0.0
None:
Biom File
Data input 'biom' (txt)
Fasta File
Data input 'fasta' (fasta)
Remove phiX:
PhiX databank:
phiX
*** THE FILTERS ON OTUS IN SAMPLES, OTUS SIZE and SEQUENCE PERCENTAGE :
Apply filters
--Remove OTUs that are not present at least in XX samples; how many samples do you choose? :
--When sorted by abundance, how many OTU do you want to keep ?:
--proportion/number of sequences threshold to remove an OTU:
0.00005
*** THE FILTERS ON RDP :
No filters
*** THE FILTERS ON BLAST :
No filters

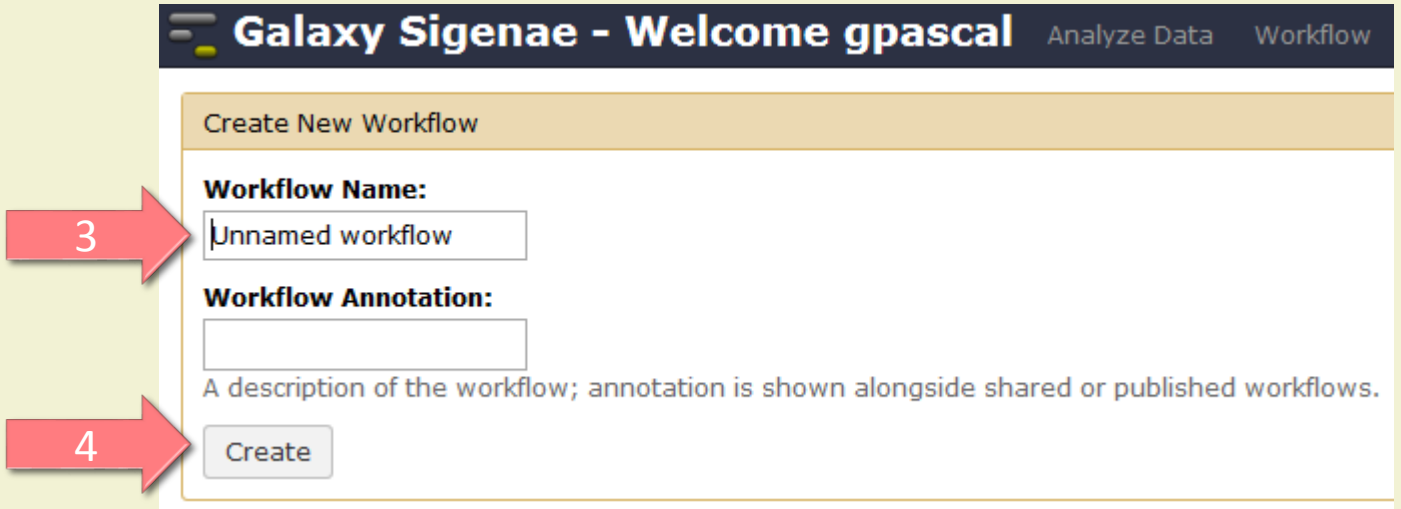
Your Turn! – 11

CREATE YOUR OWN WORKFLOW !

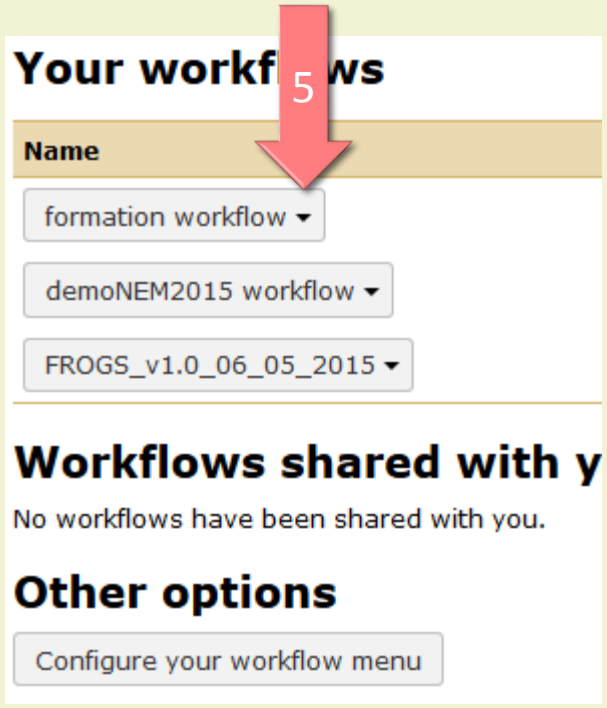
Exercise 11

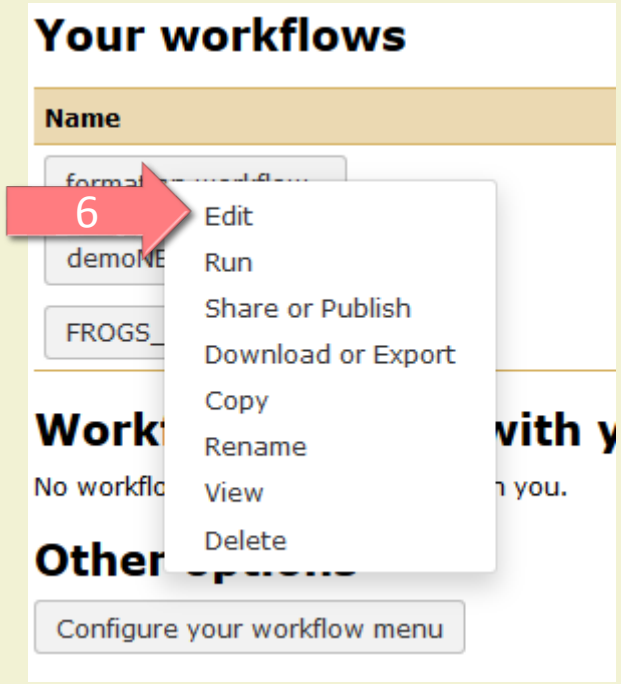

1
2
Galaxy Sigenae - Welcome gpascal
Analyze Data
Workflow
Shared Data
Visualization
Help
User
Using 18.3 GB
Your workflows
Create new workflow
Upload or import workflow
Name
# of Steps
formation workflow
9
demoNEM2015 workflow
9
FROGS_v1.0_06_05_2015
10
Workflows shared with you by others
No workflows have been shared with you.
Other options
Configure your workflow menu

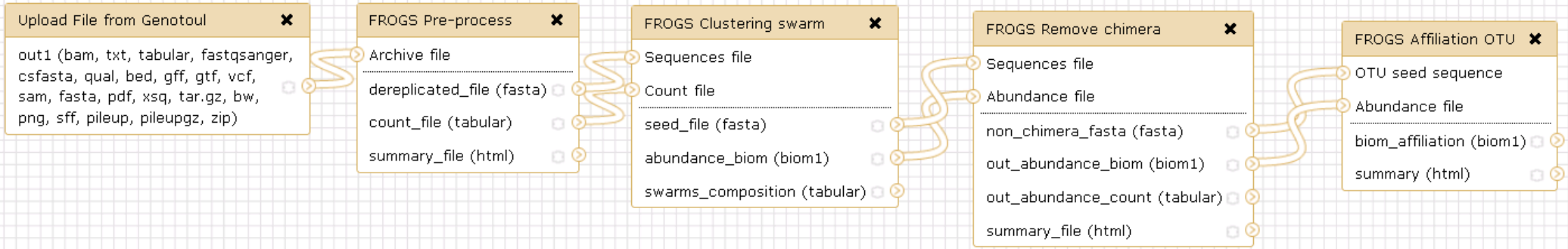
Exercise 11

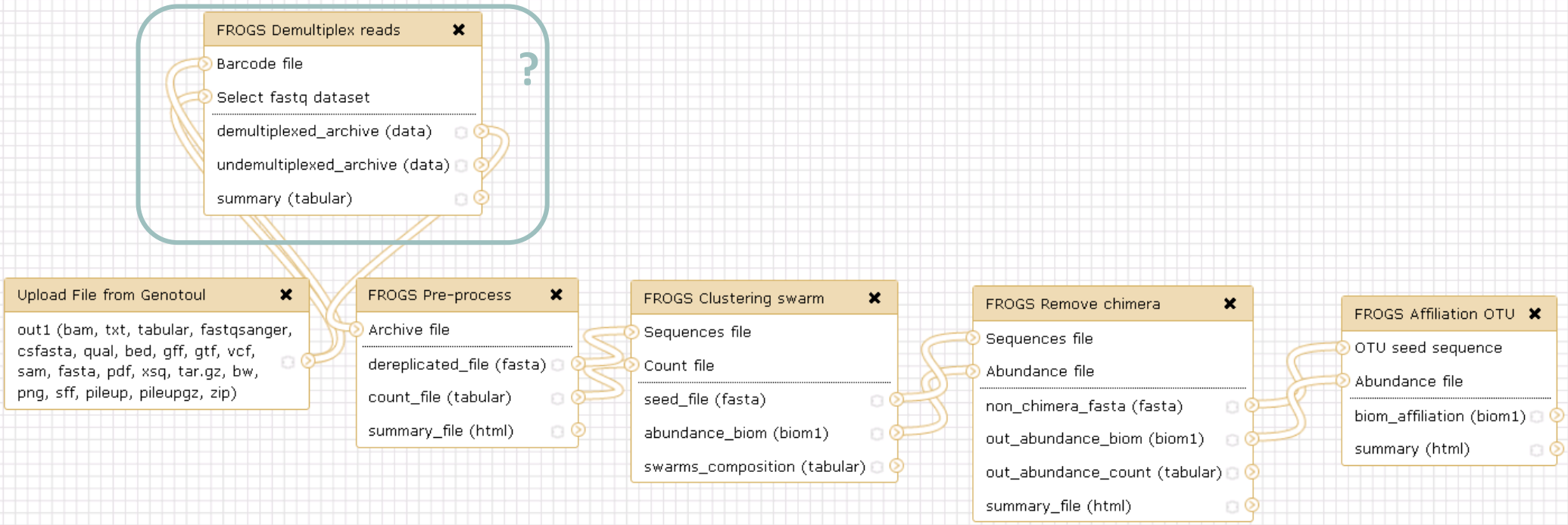

Galaxy Sigenae - Welcome gpascal
Analyze Data
Workflow
Create New Workflow
Workflow Name:
Unnamed workflow
Workflow Annotation:
A description of the workflow; annotation is shown alongside shared or published workflows.
Create
3
4

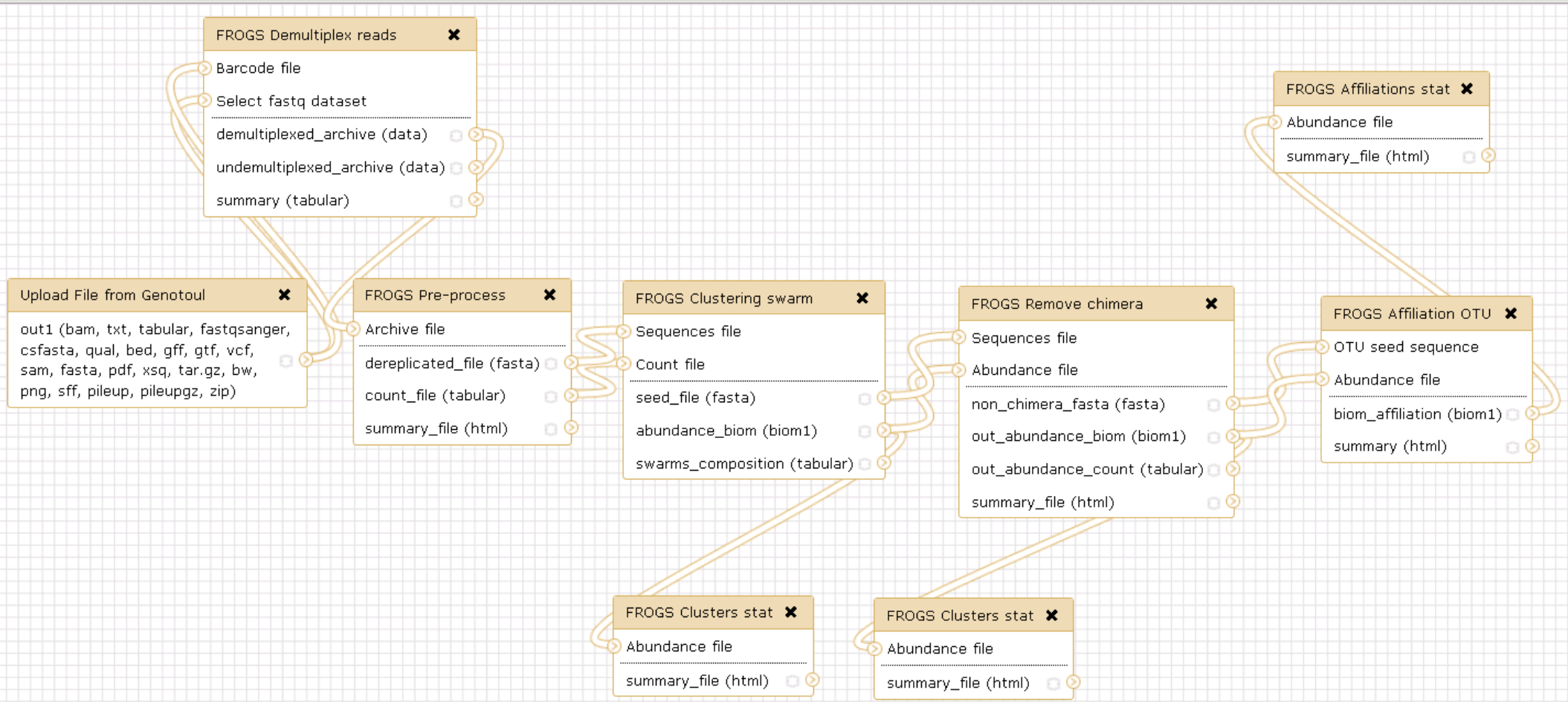
Exercise 11

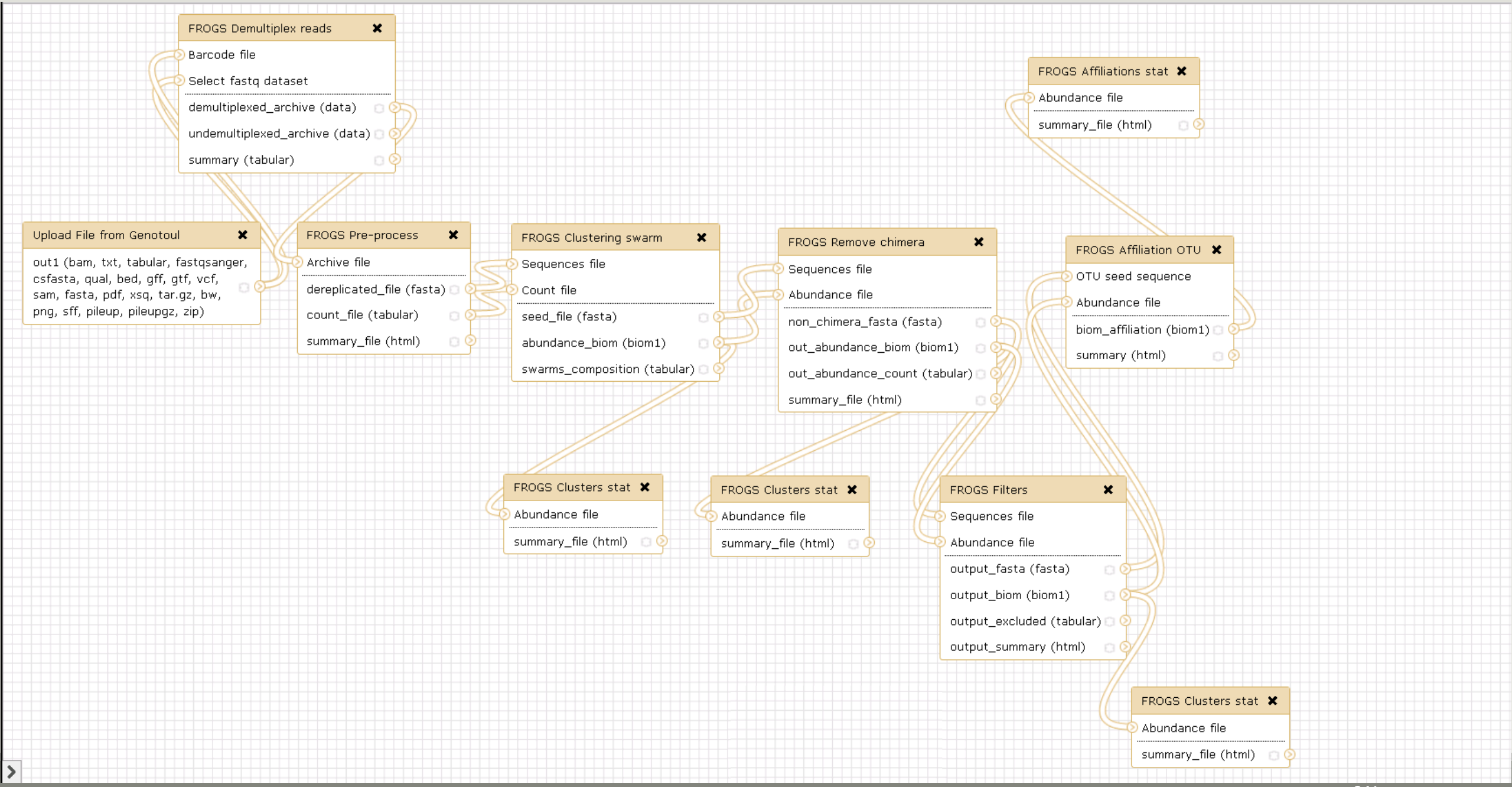

5
Your workf ws
Name
formation workflow
demoNEM2015 workflow
FROGS_v1.0_06_05_2015
Workflows shared with y
No workflows have been shared with you.
Other options
Configure your workflow menu

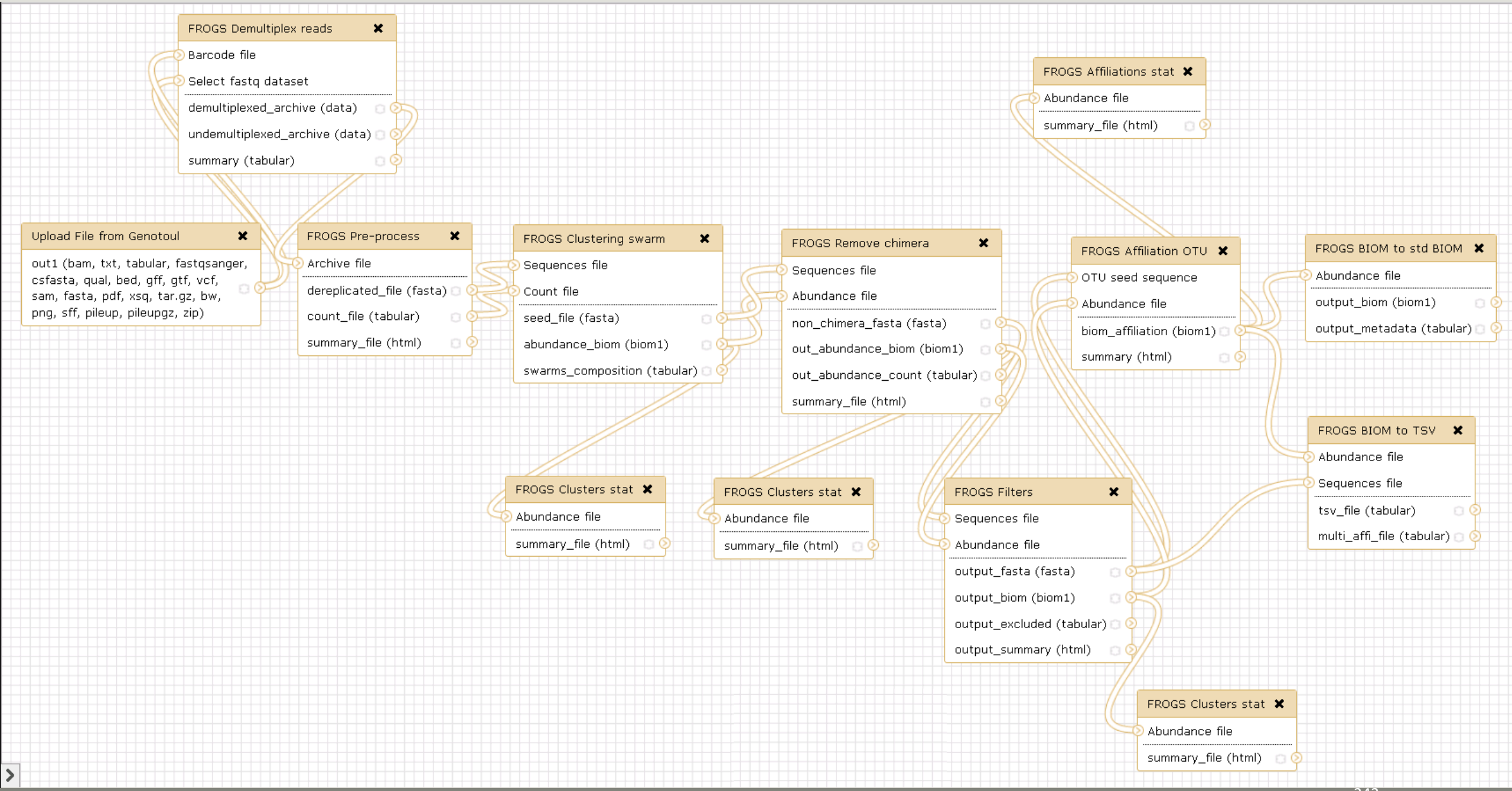

Your workflows
Name
6
Edit
Run
Share or Publish
Download or Export
Copy
Rename
View
Delete
Configure your workflow menu

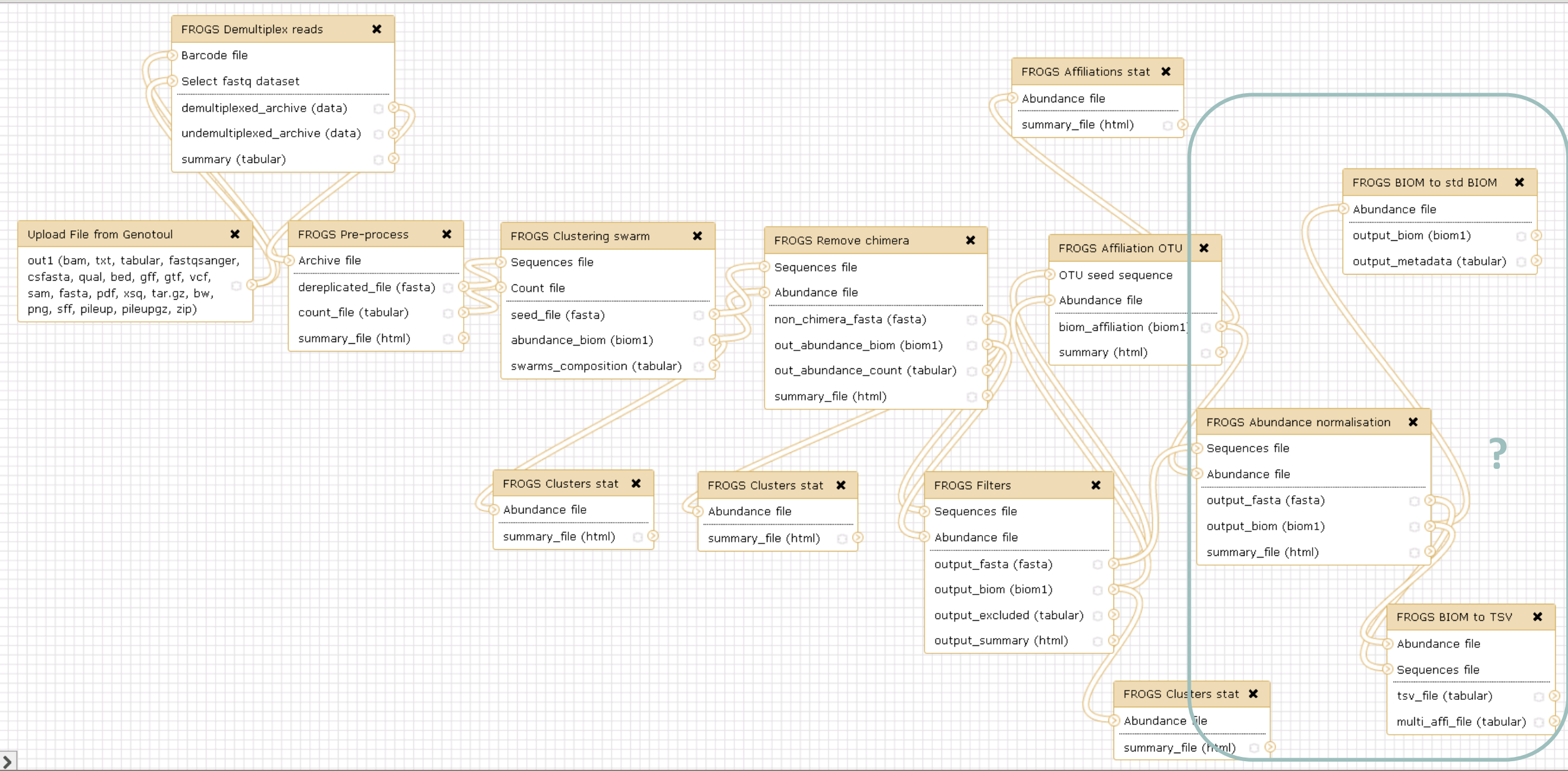

Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)

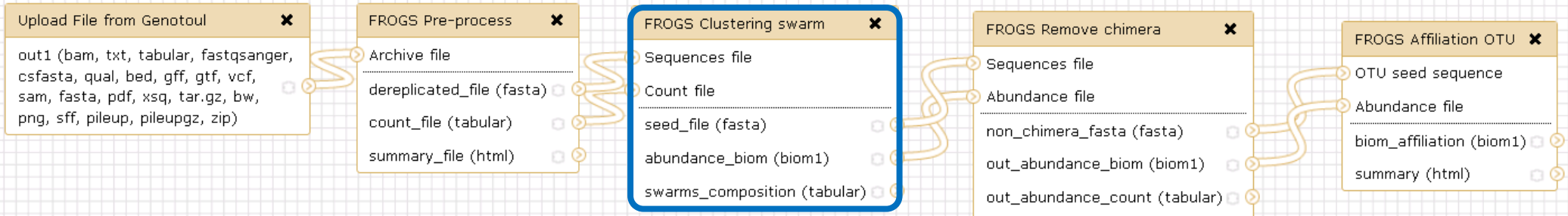

FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
?
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
FROGS Affiliations stat
Abundance file
summary_file (html)
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
FROGS Clusters stat
Abundance file
summary_file (html)
FROGS Clusters stat
Abundance file
summary_file (html)


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
FROGS Affiliations stat
Abundance file
summary_file (html)
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
FROGS Clusters stat
Abundance file
summary_file (html)
FROGS Clusters stat
Abundance file
summary_file (html)
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
FROGS Clusters stat
Abundance file
summary_file (html)


FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
FROGS Affiliations stat
Abundance file
summary_file (html)
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
FROGS BIOM to std BIOM
Abundance file
output_biom (biom1)
output_metadata (tabular)
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
FROGS Clusters stat
Abundance file
summary_file (html)
FROGS Clusters stat
Abundance file
summary_file (html)
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
FROGS Clusters stat
Abundance file
summary_file (html)

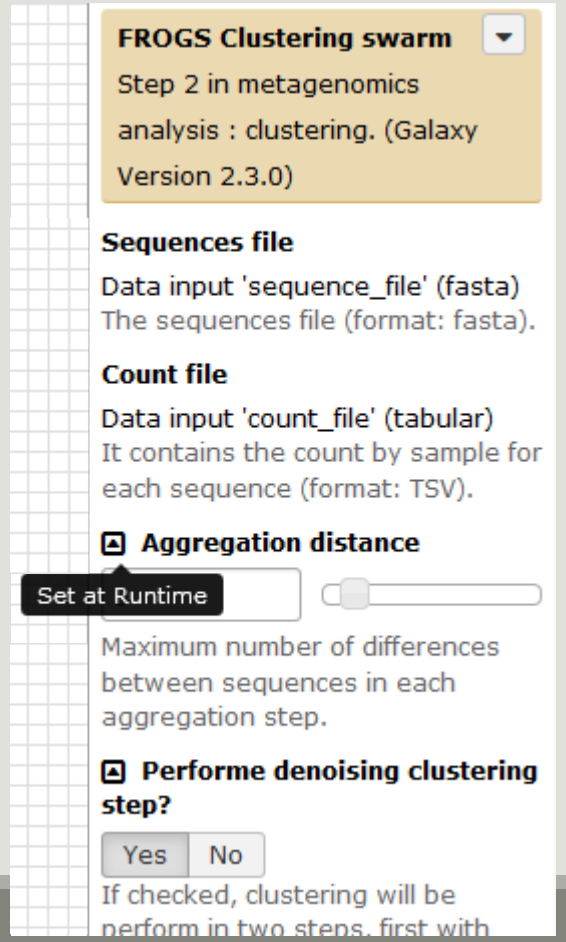

FROGS Demultiplex reads
Barcode file
Select fastq dataset
demultiplexed_archive (data)
undemultiplexed_archive (data)
summary (tabular)
Upload File from Genotoul
out1 (bam, txt, tabular, fastqsanger, csfasta, qual, bed, gff, gtf, vcf, sam, fasta, pdf, xsq, tar.gz, bw, png, sff, pileup, pileupgz, zip)
FROGS Pre-process
Archive file
dereplicated_file (fasta)
count_file (tabular)
summary_file (html)
FROGS Clustering swarm
Sequences file
Count file
seed_file (fasta)
abundance_biom (biom1)
swarms_composition (tabular)
FROGS Remove chimera
Sequences file
Abundance file
non_chimera_fasta (fasta)
out_abundance_biom (biom1)
out_abundance_count (tabular)
summary_file (html)
FROGS Affiliations stat
Abundance file
summary_file (html)
FROGS Affiliation OTU
OTU seed sequence
Abundance file
biom_affiliation (biom1)
summary (html)
FROGS BIOM to std BIOM
Abundance file
output_biom (biom1)
output_metadata (tabular)
FROGS Clusters stat
Abundance file
summary_file (html)
FROGS Clusters stat
Abundance file
summary_file (html)
FROGS Filters
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
output_excluded (tabular)
output_summary (html)
FROGS Abundance normalisation
Sequences file
Abundance file
output_fasta (fasta)
output_biom (biom1)
summary_file (html)
?
FROGS BIOM to TSV
Abundance file
Sequences file
tsv_file (tabular)
multi_affi_file (tabular)
FROGS Clusters stat
Abundance file
summary_file (html)

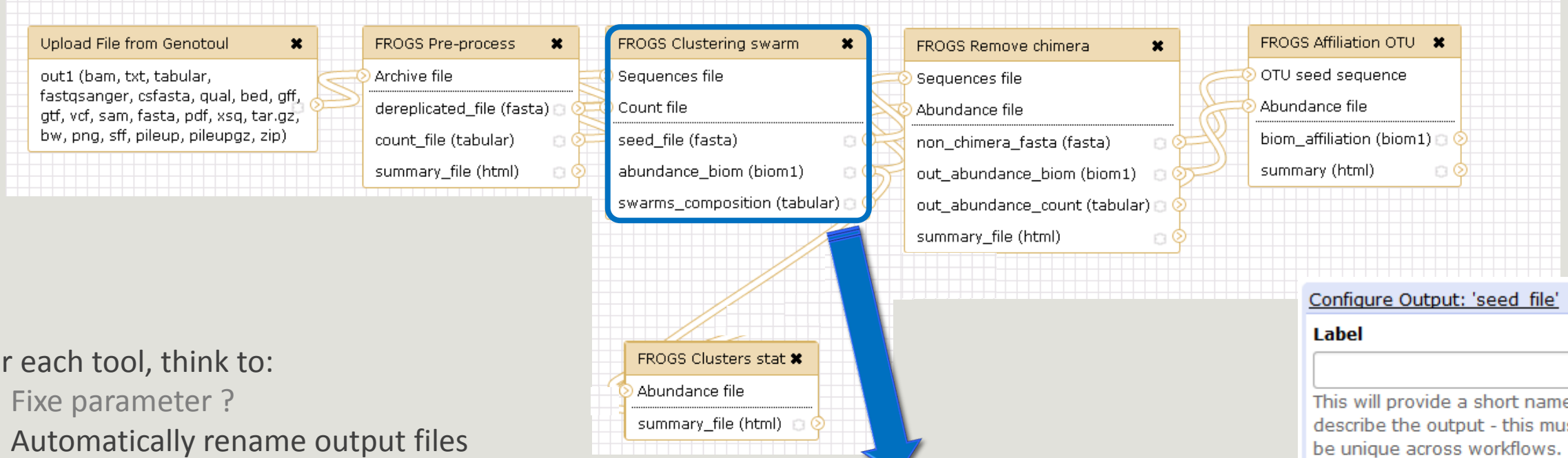


For each tool, think to:

- Fixe parameter ?

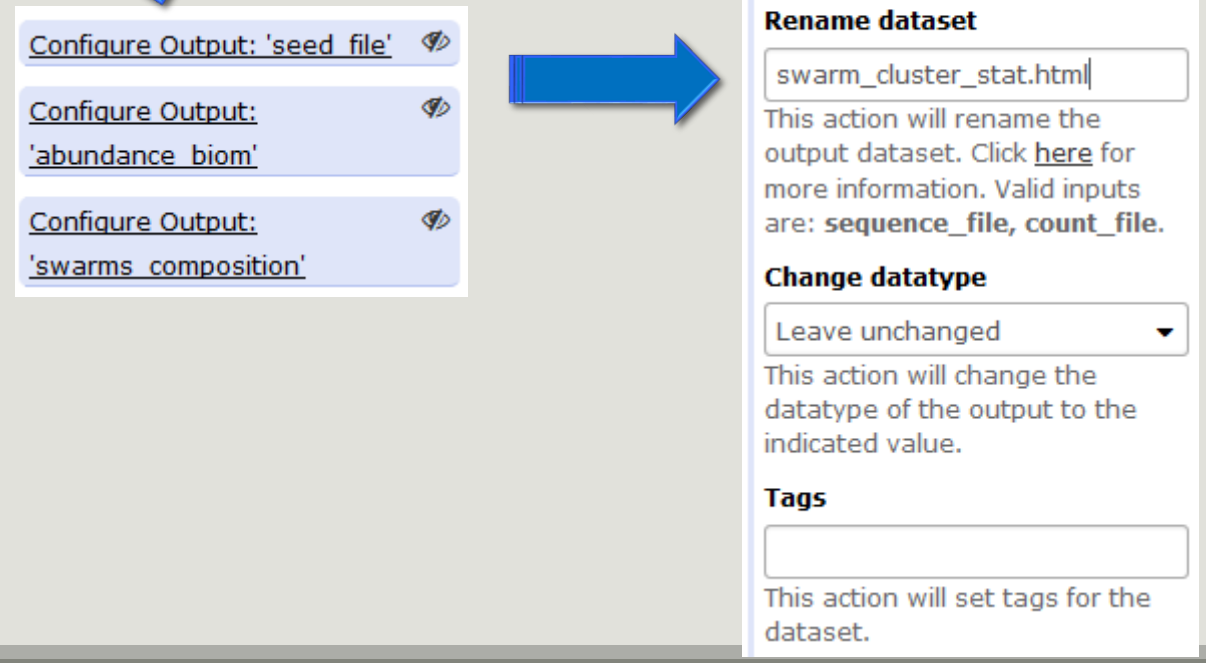
?

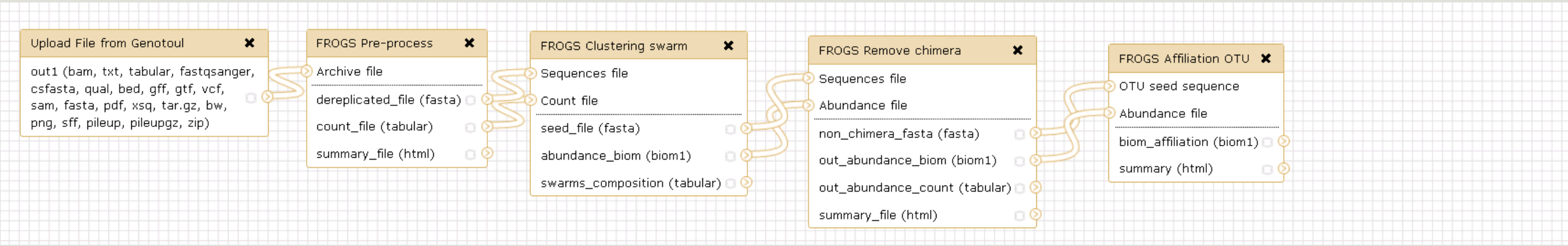




For each tool, think to:

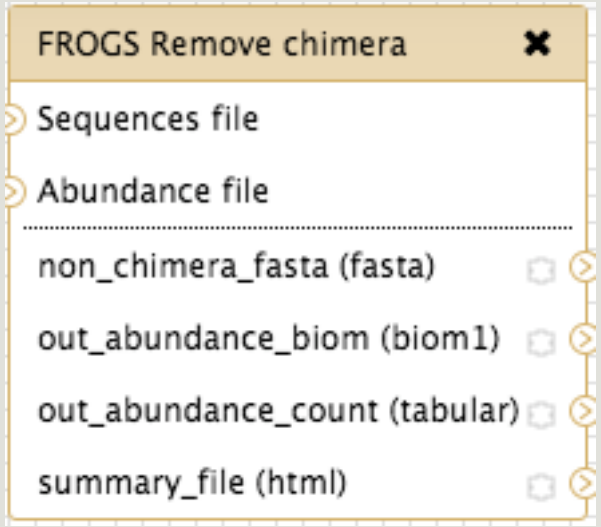
- Fixe parameter ?
- Automatically rename output files

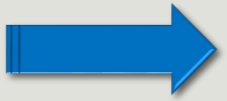


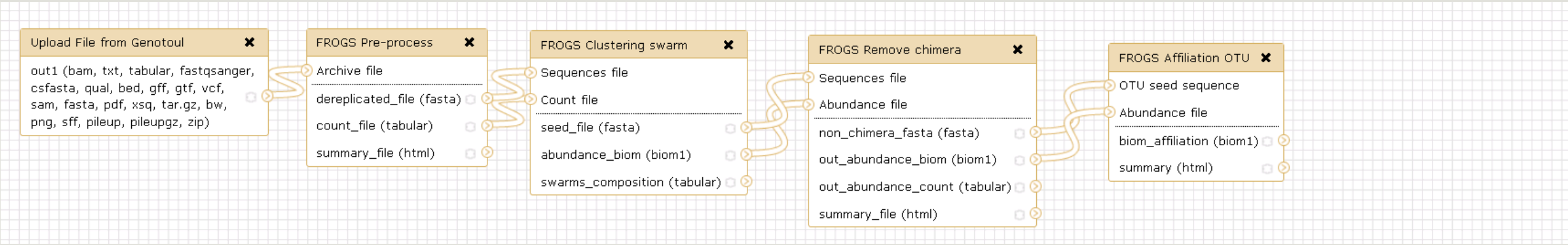


For each tool, think to:

- Fixe parameter ?
- Automatically rename output files
- Hide intermediate files ?

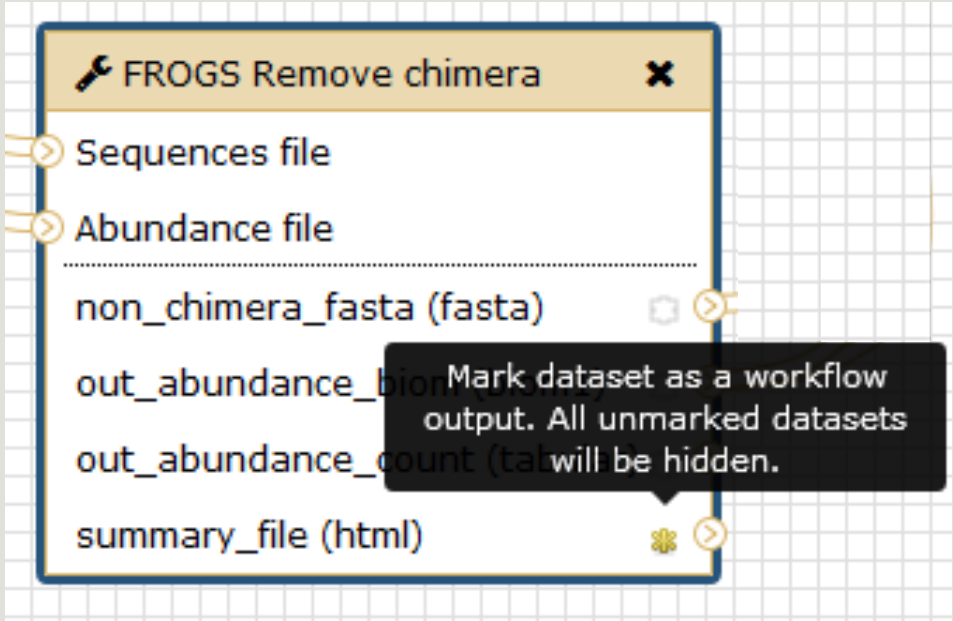


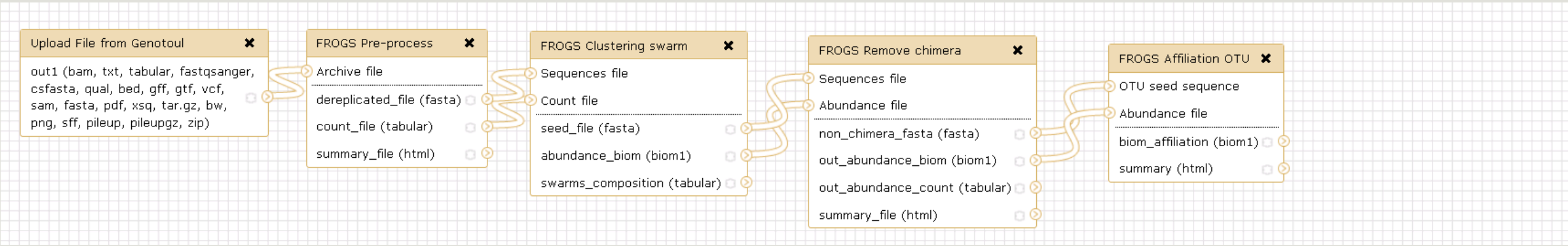




For each tool, think to:

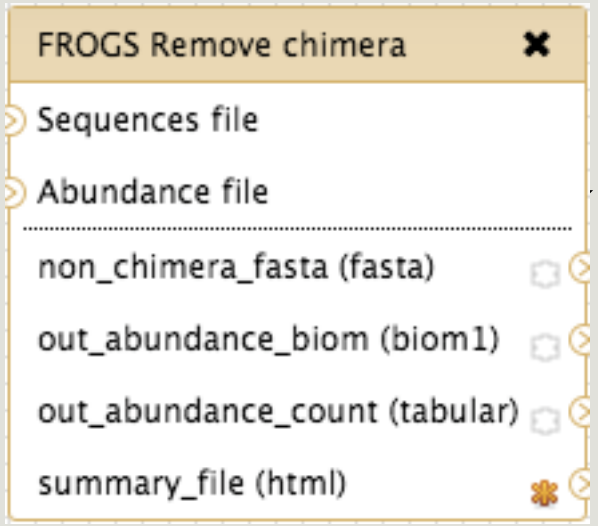
- Fixe parameter ?
- Automatically rename output files
- Hide intermediate files ?

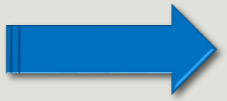


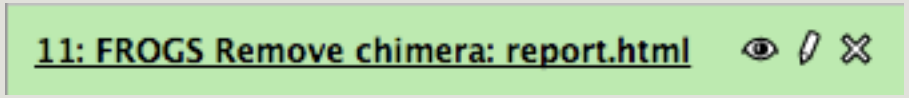


For each tool, think to:

- Fixe parameter ?
- Automatically rename output files
- Hide intermediate files ?

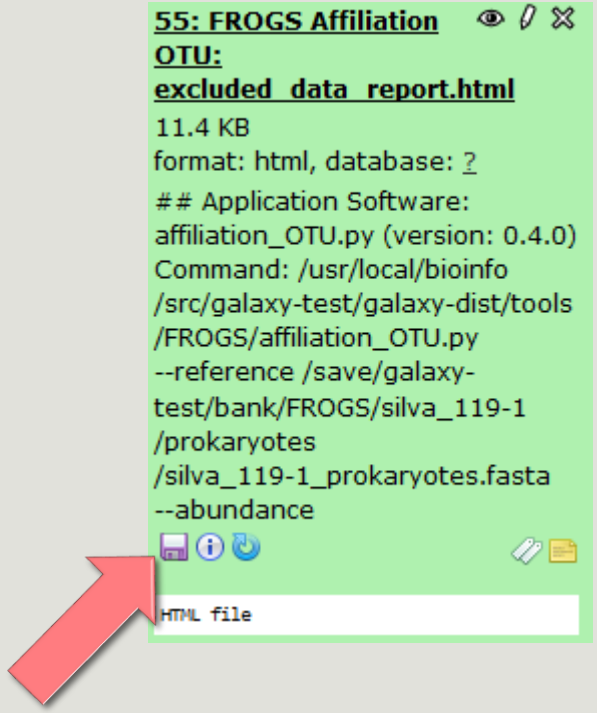






Download your data

You have to download one per one your files



FROGS BIOM to Standard BIOM

FROGS biom to standard Biom

This step is required to run R

Some figures

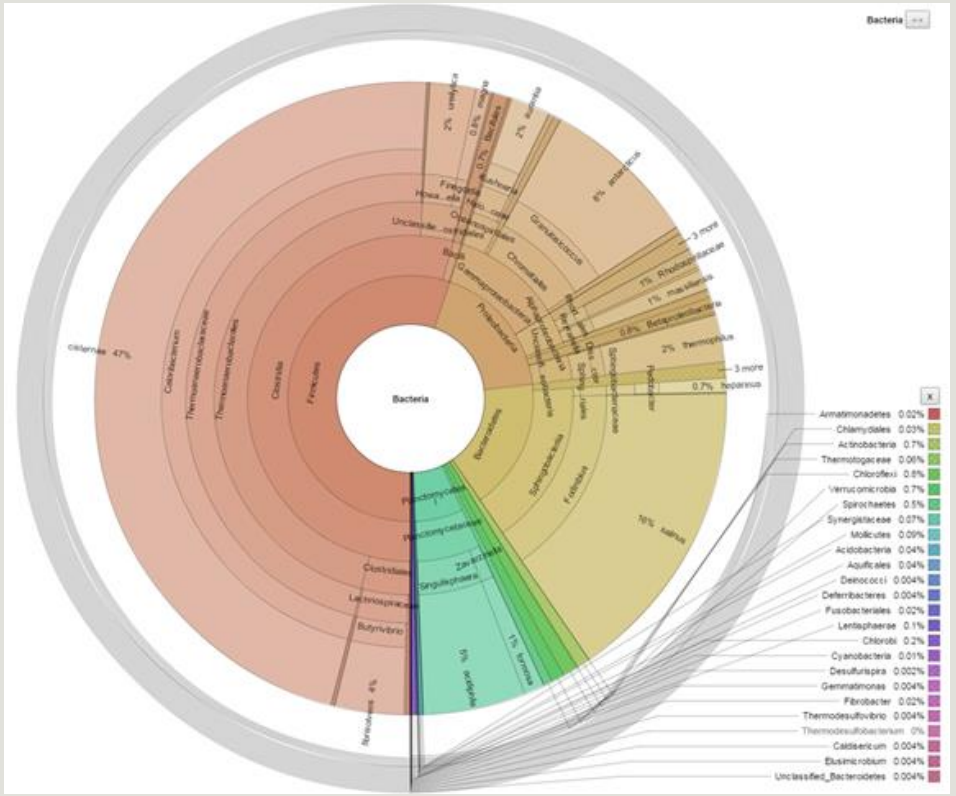
Some figures - Fast

NB SEQ	TIME with complete pipeline without Filters
50 000	40 min
400 000	4 hrs
3 500 000	2 days
10 000 000	5 days

Speed on real datasets

Simulated datasets, for testing FROGS' Accuracy

- 500 species, covering all bacterial phyla
- Power Law distribution of the species abundances
- Error rate calibrated with real sequencing runs
- 20% chimeras
- 10 samples of 100 000 sequences each (1M sequences)



Simulated dataset : 1M sequences

↓

SWARM : 109 000 clusters

↓

VSEARCH: 21 000 clusters

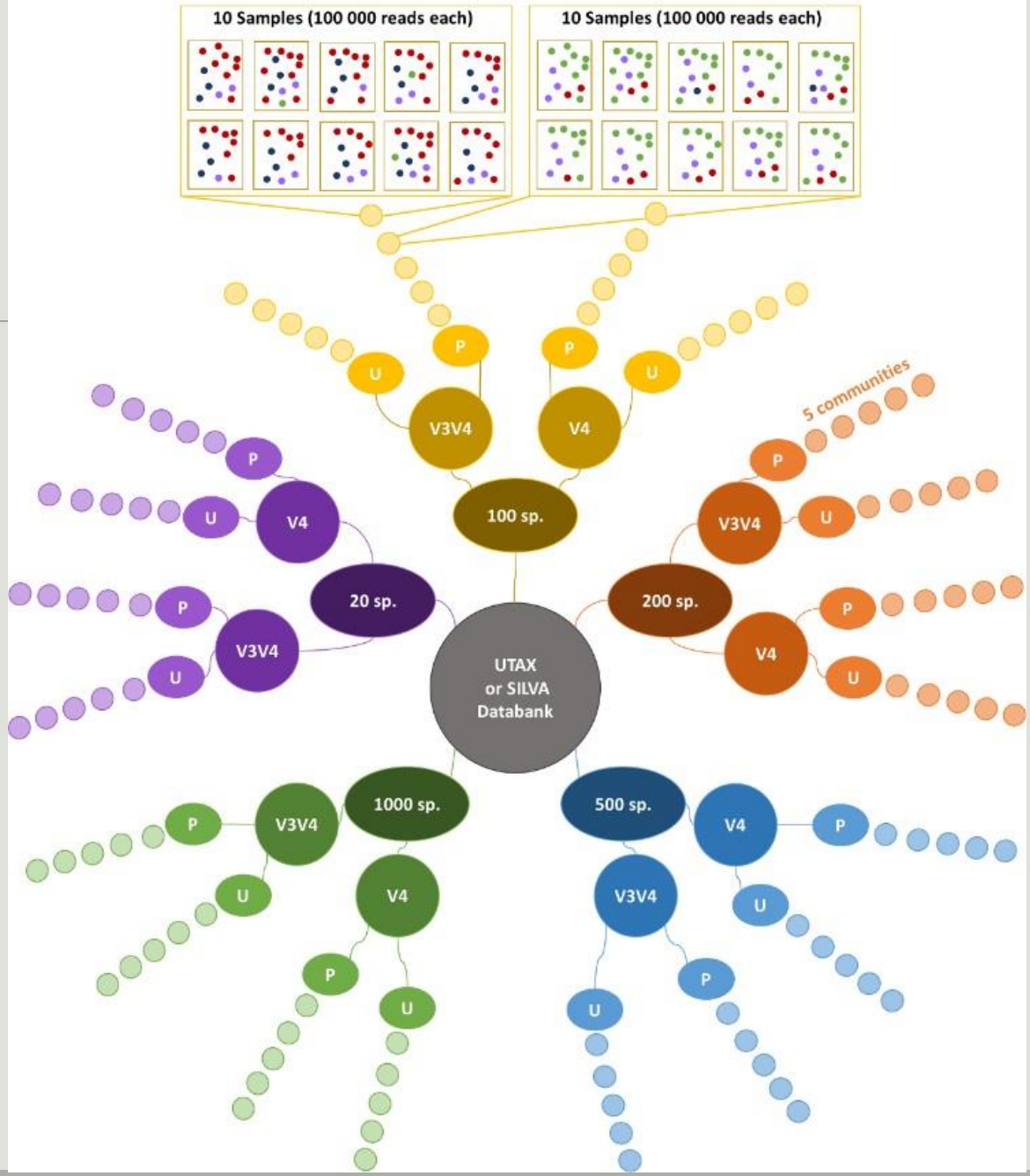
↓

filters : 0.005% **505 OTUs**

FROGS' Accuracy

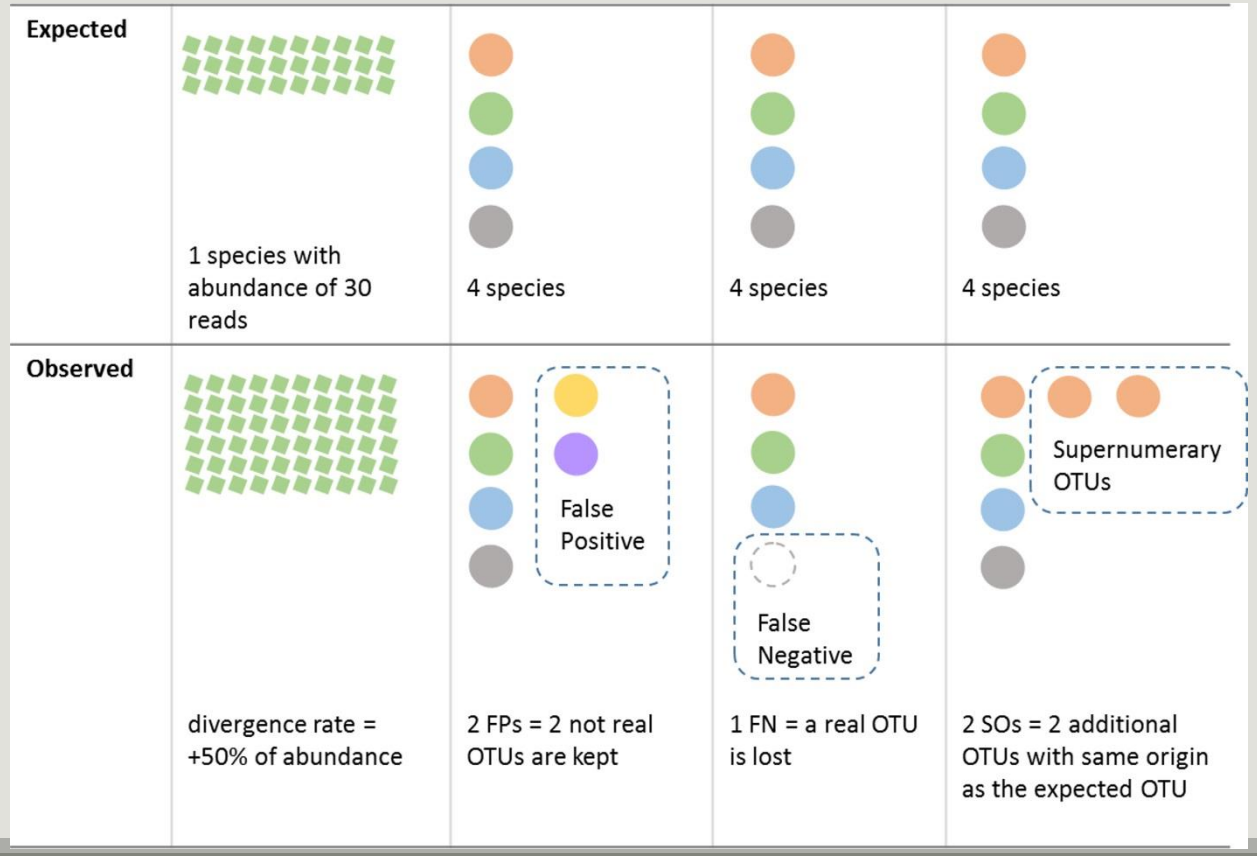
- 1.10^{+8} synthetic sequences were treated with FROGS, UPARSE and MOTHUR, QIIME, with their guidelines, to compare their performances
- 20, 100, 200, 500 or 1000 different species
- power law or a uniform distribution
- 5 to 20% of chimera

→ Divergence on the composition of microbial communities at the different taxonomic ranks



FROGS' Accuracy

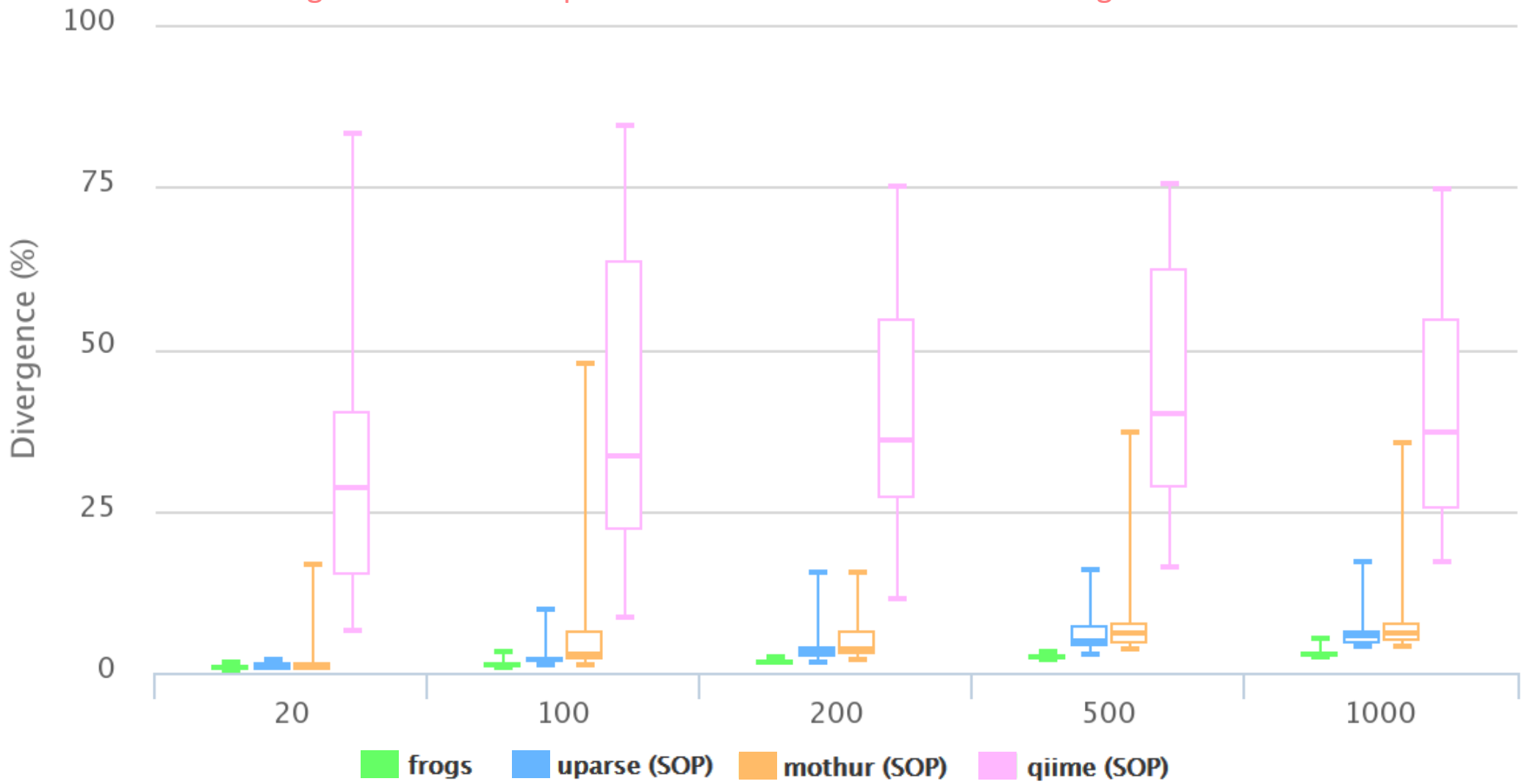
The four metrics used to compare results of FROGS, UPARSE, QIIME and MOTHUR are :

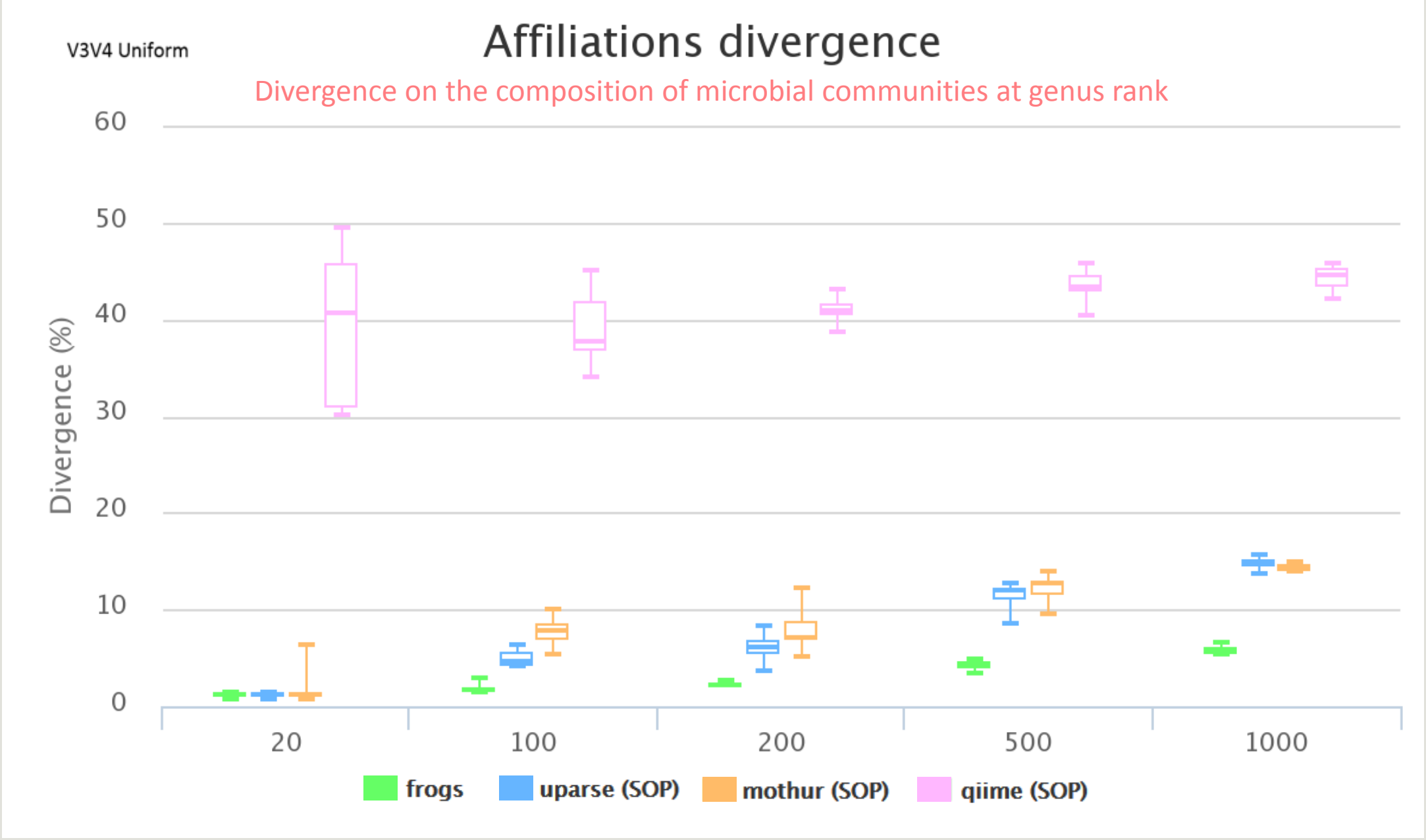


V3V4 Power Law

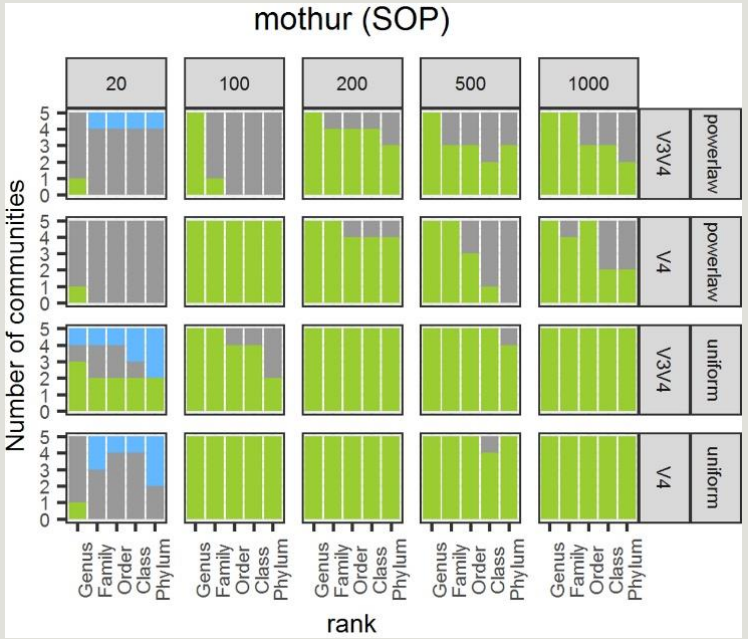
Affiliations divergence

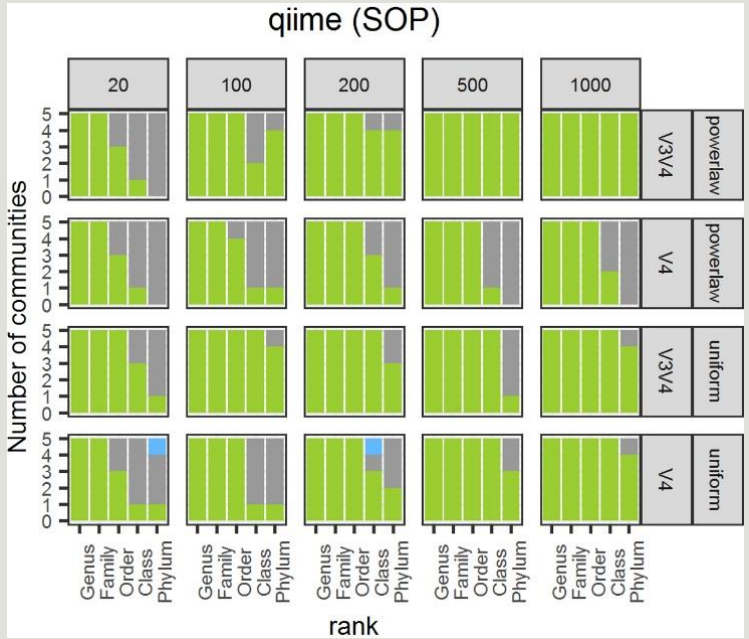
Divergence on the composition of microbial communities at genus rank




V3V4 Uniform
Affiliations divergence
Divergence on the composition of microbial communities at genus rank
Divergence (%)
60
50
40
30
20
10
0
20
100
200
500
1000
frogs
uparse (SOP)
mothur (SOP)
qiime (SOP)

The results of non-parametric paired tests (signed rank test) of Affiliation divergence on simulated data from UTAX



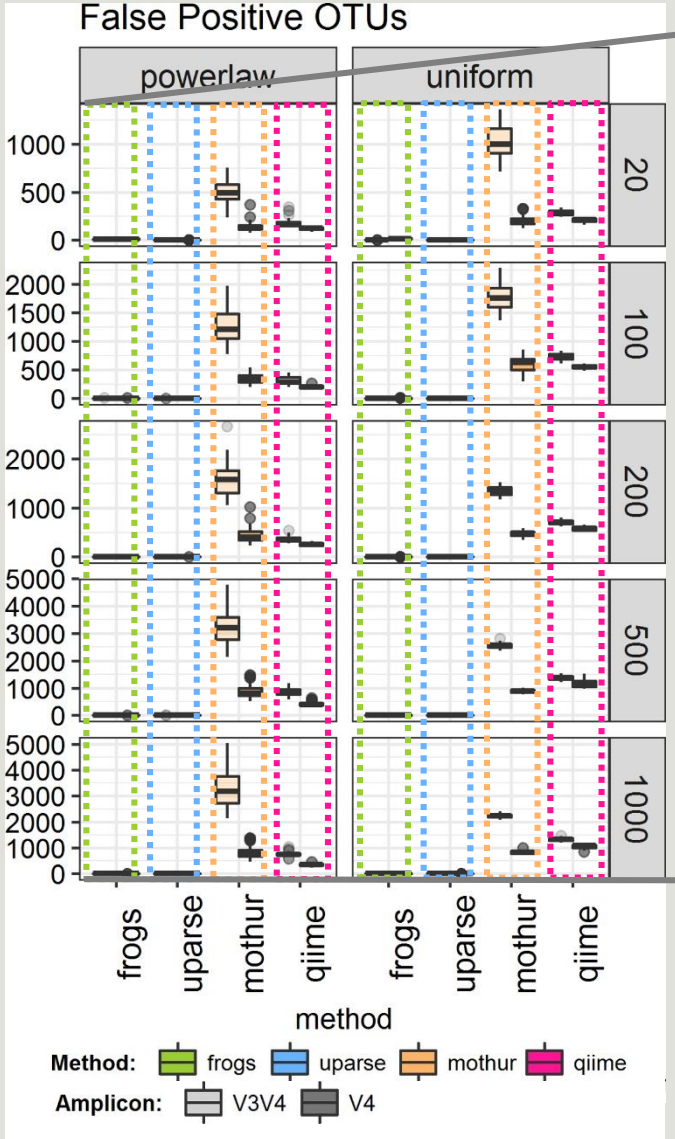


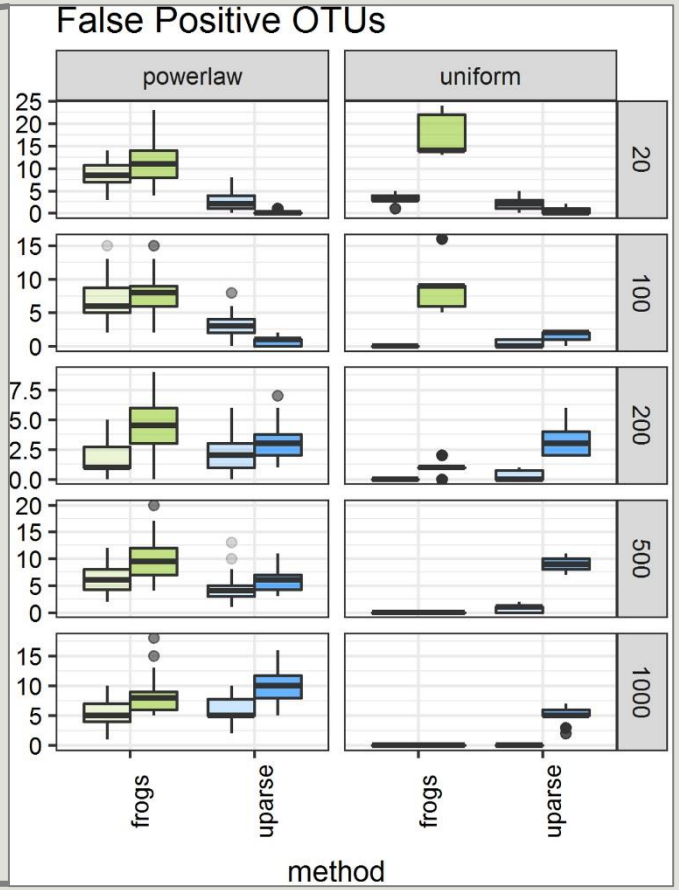
FROGS performed as well as or better than UPARSE and mothur in most settings. The infrequent condition in which FROGS performed worse than UPARSE and mothur was for small community sizes (20 species), except at genus level. It performed better than QIIME in all settings.

Huge number of FP inferred by mothur (up to 20 times more than the expected community size).

a few more FPs under power law abundance distributions and a few less under uniform abundance distributions (except for size < 100 species)

FROGS performed better than QIIME in all settings

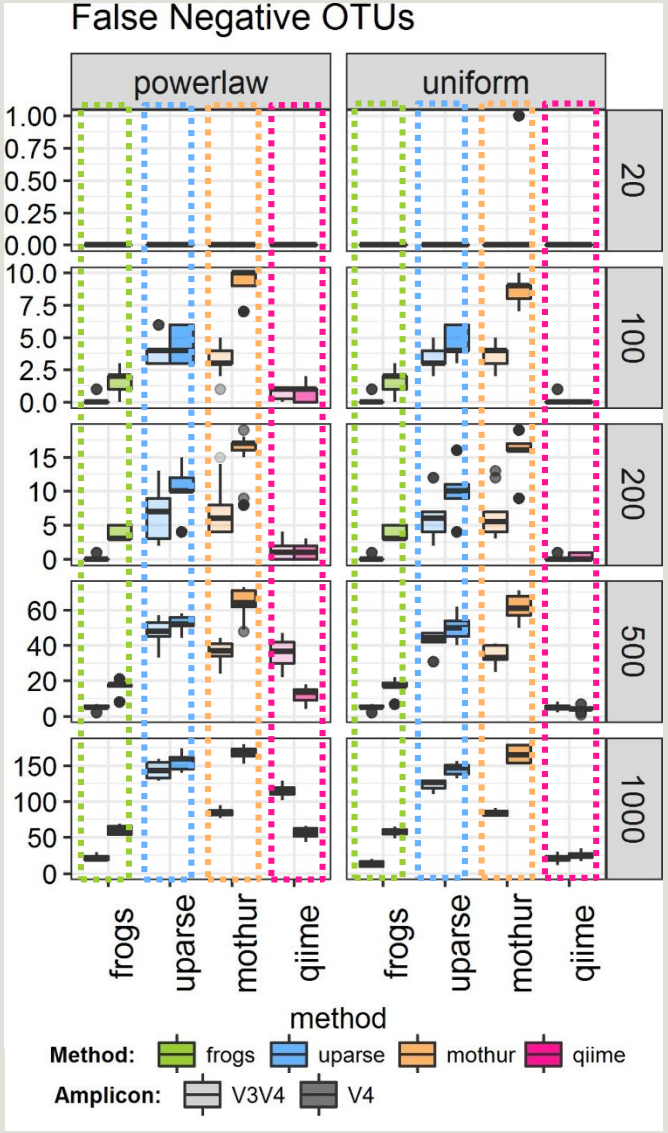




FROGS truly outperformed mothur in terms of FN taxa

FROGS always produced fewer FNs than UPARSE.

FROGS sometimes produced more FNs than QIIME, especially on the V4 region.



Conclusions on assessments

FROGS performed much better than mothur in all settings

FROGS is less conservative than UPARSE for small size communities and better (for both FPs and FNs) for large size communities

FROGS is more conservative than QIIME on the V4 region and better (for both FPs and FNs) on V3V4 regions.

FROGS maintained both the number of FP and FN OTUs low, especially in complex communities.

→ cross-validation of chimeras, only used in FROGS, which avoids confusing real OTUs with chimeras.

→ 3 step strategy (clustering by Swarm + chimera removal with cross-validation + filtering) = a low FP rate and the high probability of detecting a species that is really present in the dataset *i.e.* a high recall rate.

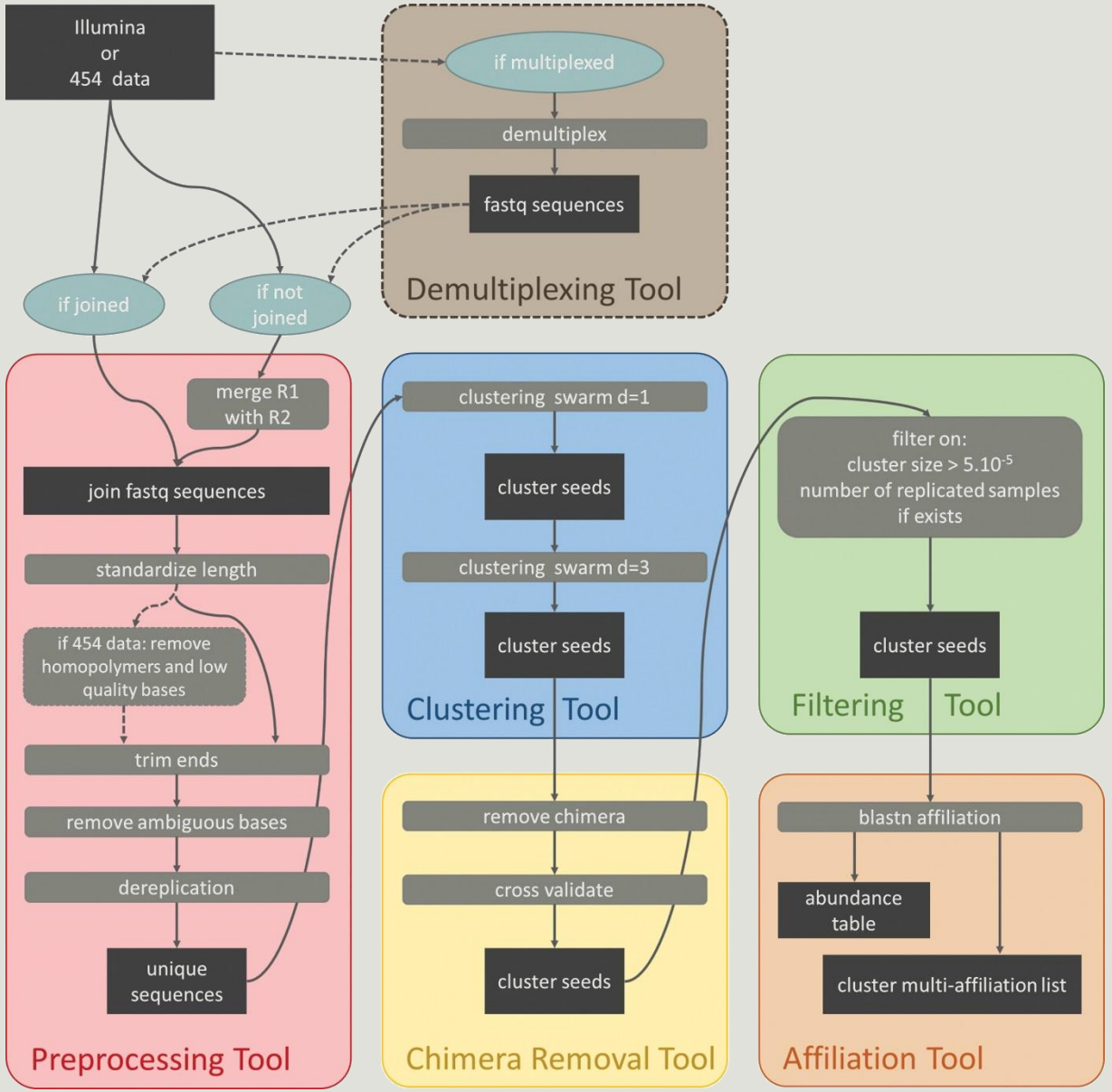
→ unlike QIIME or mothur, FROGS never produced Supernumerary OTUs, which further validates the FROGS OTU picking strategy.

Conclusions

Why Use FROGS ?

- User-friendly
- Fast
- 454 data and Illumina data
  - sequencing methods change but same tool
  - easier for comparisons
- Clustering without global threshold and independent of sequence order
- New chimera removal method (Vsearch + cross-validation)
- Filters tool
- Multi-affiliation with 2 taxonomy affiliation procedures
- Cluster Stat and Affiliation Stat tools
- A lot of graphics
- Independant tools
- Few FPs and few FNs

Our recommended guideline:



How to cite FROGS

In waiting for the publication:

Pipeline FROGS on http://sigenae-workbench.toulouse.inra.fr/

Github: https://github.com/geraldinepascal/FROGS.git

Poster FROGS: Escudie F., Auer L., Bernard M., Cauquil L., Vidal K., Maman S., Mariadassou M., Combes S., Hernadez-Raquet G., Pascal G., 2016. FROGS: Find Rapidly OTU with Galaxy Solution. In: ISME-2016 Montreal, CANADA,

http://bioinfo.genotoul.fr/wp-content/uploads/FROGS_ISME2016_poster.pdf

To contact

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Next training sessions

9th to 12th April 2018 - 4 days

0.5 Galaxy day
2 FROGS days
1.5 Statistics phyloseq days