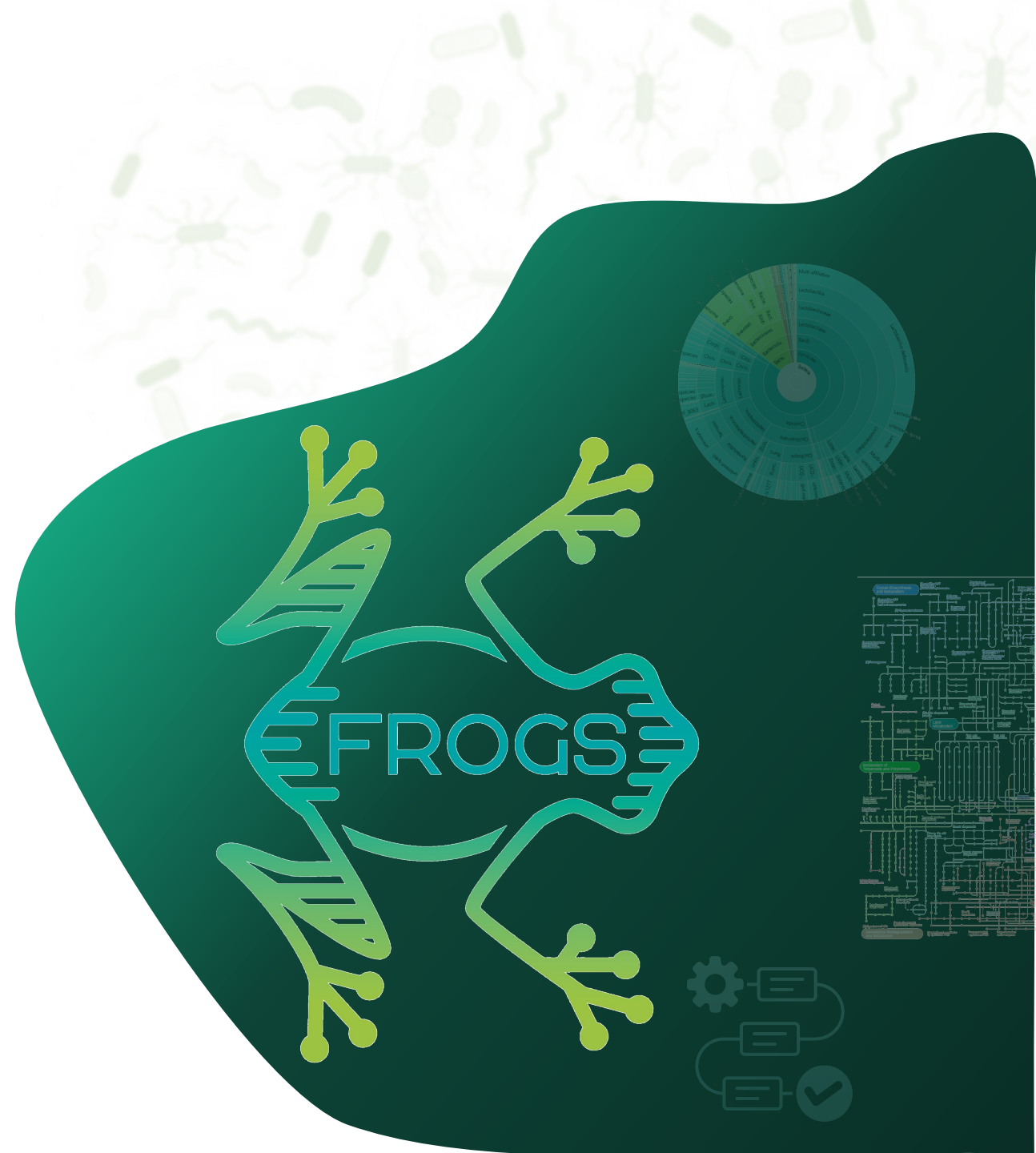


Before starting the training

There are some things to consider.

Lucas AUER, Gabryelle Agoutin,
Maria BERNARD, Géraldine PASCAL,
Maëlle POMIÈS & Olivier RUÉ





9 am (first day 8.45 am)
to 5.30 pm



2 short coffee breaks
morning and afternoon



Lunch
12.30 am to 1.30 pm

J0

Get Started with
Galaxy

To be done
autonomously on
galaxy platform

J1

**Metabarcoding
overview: the key
concepts**

- Barcode
- Technical sources of noise and errors
- Short reads
- Long reads
- Bioinformatics analysis

FROGS Core

- Presentation of the datasets
- 16S short-read processing
- Data analysis
- ASV (Swarm/DADA2)

J2

FROGS Core

- Remove chimera
- ASV filters
- ITSX

FROGS Core

- Taxonomic affiliation
- Phylogenetic tree building
- Companion tools

between
two
croaks

Practical work

application of
acquired
knowledge to a
small dataset

Autonomously

J3

FROGS Stat

- Import data
- Alpha diversity
- Beta diversity

**A stand-alone
application on a
set of long read
data**

- presentation of the datasets
- read processing

J4

FROGS Stat

DesSeq analysis

FROGS Func

Predicting
functional
abundances based
only on marker
gene sequences

Practical work

- Apply all FROGS steps to the long-read dataset
- Find the parameters
- Analyze the outputs
- Understand the processes

FROGS Teams

Developers



Maria BERNARD



OLIVIER RUÉ

Biology and Statistical experts



Lucas AUER

Galaxy support



Patrice DÉHAIS



Gabryelle AGOUTIN

Databank manager



Maelle POMIÈS

Web master



Géraldine PASCAL

Coordinator

FROGS papers

Frédéric Escudié, Lucas Auer, Maria Bernard, Mahendra Mariadassou, Laurent Cauquil, Katia Vidal, Sarah Maman, Guillermina Hernandez-Raquet, Sylvie Combes, Géraldine Pascal.

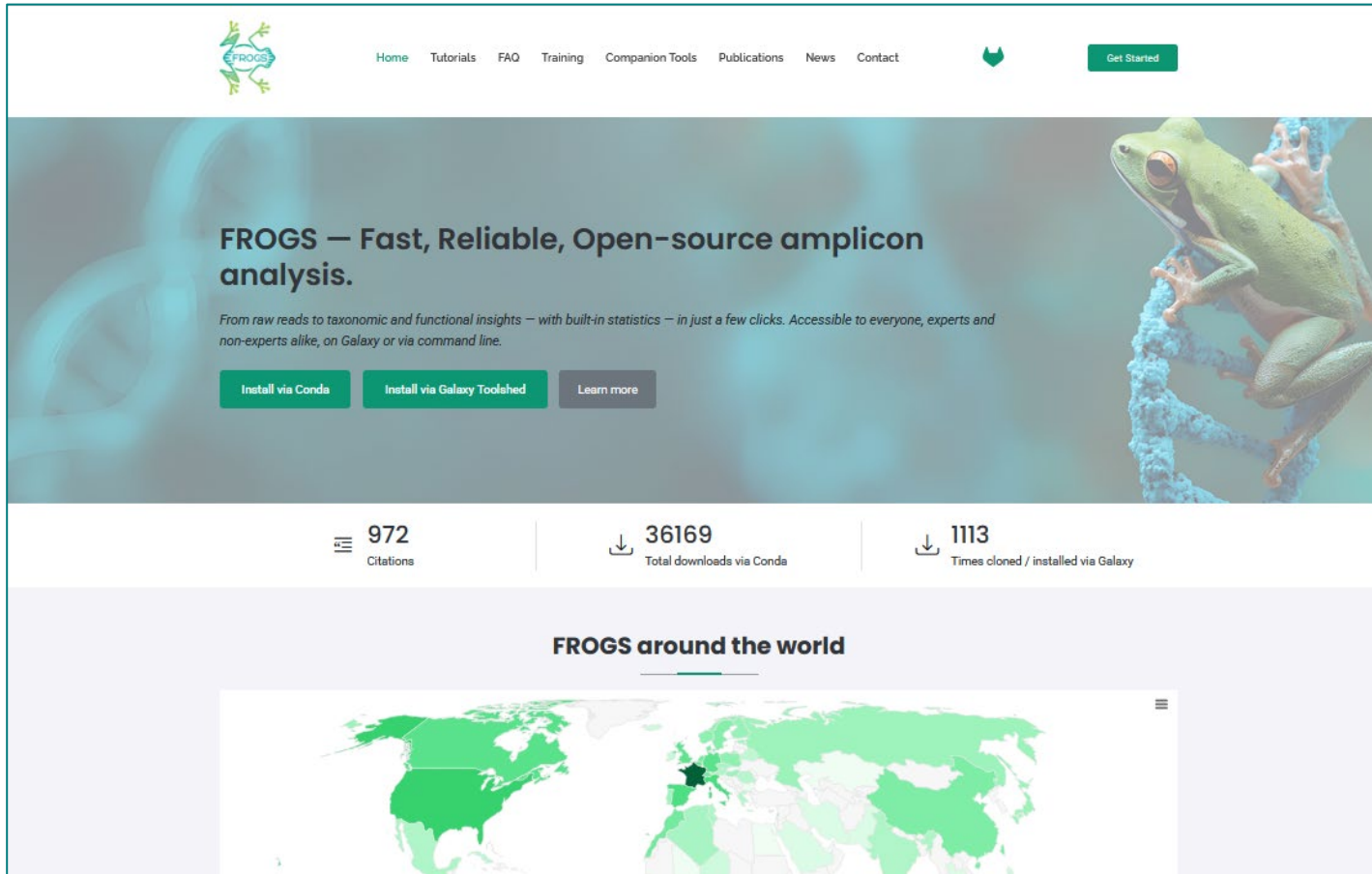
"**FROGS**: Find, Rapidly, OTUs with Galaxy Solution." *Bioinformatics*, Volume 34, Issue 8, 15 April 2018, Pages 1287–1294

Maria Bernard, Olivier Rué, Mahendra Mariadassou and Géraldine Pascal; **FROGS**: a powerful tool to analyse the diversity of fungi with special management of internal transcribed spacers, *Briefings in Bioinformatics* 2021, 10.1093/bib/bbab318



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