

PICRUST2 Workflow

Contents

1. Installing PICRUST

This was already done and does not need to be done again.

```
mamba create -n picrust2 -c bioconda -c conda-forge picrust2=2.5.2
```

2. Required input file

The input files should be a FASTA of amplicon sequences variants (ASVs; i.e. your representative sequences, not your raw reads) and a tab-delimited table with ASV ids as the first column and sample abundances as all subsequent columns.

Example of both files :

3. Running the full pipeline

Running picrust through command line (not R)

1. Activate the environment

```
mamba activate picrust2
```