

QIIME2 based eDNA App

Select a folder of "fastq.gz" files to process through the eDNA pipeline.

Choose folder	Browse	Process folder
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If you find this App useful please cite us:

Figure S1. The *eDNA-container app* main GUI homepage with the sequencing folder selection buttons.

Please provide key details of the project so the pipeline will run correctly. Note defaults are reasonable settings for most projects. The primers shown are the teleo fish primers.

Project Name:

Primer information required for trimming

Forward primer (5'-3'):

Reverse primer (5'-3'):

For information on these settings for DADA2 see [here](#).

trunc-len-f:

trunc-len-r:

max-ee-f:

max-ee-r:

trunc-q:

chimera-method:

OPTIONAL: The default taxonomic database is based on [MIDORI2](#)

If you want to select another database navigate to the file using this upload button

Optionally choose a compatible QIIME2 taxonomic database *.qza file

Figure S2. The *eDNA-container app* settings screen. The project name will be included in the final PDF report as the project title. The primer sequences are used for trimming using the *cutadapt* plugin. Key *DADA2* parameters can be adjusted to improve the number and quality of ASVs generated. The user can select a compatible a *QIIME2* database (QZA file) or use the default which is based on MIDORI 12S rRNA.

```

Forward read trimming primers
^ACACCGCCCGTCAYYCT...CAYGGTAAGTRTACCGGAAG
Reverse read trimming primers
^CTTCCGGTAYACTTACCRTG...AGRRTGACGGGCGGTGT
Using p-error-rate=0.1 and p-overlap=3
Saved Visualization to: ./qiime2/loci/paired-end-demux-trimmed.qzv
Extracted ./qiime2/loci/paired-end-demux-trimmed.qza to directory fastq_data_trimmed/b993258e-2798-4bce-823b-ab2bfd1c0f
e
[Thu May 18 04:41:06 2023]
Finished job 8.
4 of 12 steps (33%) done
Select jobs to execute...

[Thu May 18 04:41:06 2023]
rule clean_reads:
  input: qiime2/loci/paired-end-demux-trimmed.qza
  output: qiime2/loci/asvs/stats-dada2.qzv
  jobid: 7
  reason: Missing output files: qiime2/loci/asvs/stats-dada2.qzv; Input files updated by another job: qiime2/loci/pai
  resources: tmpdir=/tmp

Using the following DADA2 params:
--p-trunc-len-f 0
--p-trunc-len-r 0
--p-max-ee-f 2
--p-max-ee-r 4
--p-trunc-q 2
--p-chimera-method consensus

```

Figure S3. Outputs from each step of the *Snakemake* pipeline are logged to the Docker terminal window. These outputs are important for troubleshooting any pipeline failures.