# TreeTuner pipeline workflow

# Online or locally: NCBI BLAST search

#### Files:

BLASTP\_clps.tsv clps\_hits.fasta

#### **Tools:**

- 1.NCBI BLAST server
- 2.BLAST+ package
- 3.Seqkit

# Building\_preliminary\_tree

#### Files:

clps.aligned.fasta
clps.aligned.trimmed.fasta
clps.aligned.trimmed.newick

#### **Tools:**

- 1.MAFFT v7 2.BMGE v1.12 or trimAl v1.4
- 3.FastTree v2.1

# Adjust and Run coarse-tuning

### Files:

clps\_paramer\_input.in
clps.aligned.trimmed.newick
clps\_taxonomic\_info\_clean.txt

#### **Tools:**

1.Ruby v2.5.12.BioRuby v2.0.33.treetrimmer.rb

# Coarse-tuning results

#### Files:

clps\_aligned\_###\_parameter\_input.in.tt 0.0.tre

clps\_aligned\_###\_parameter\_input.in.tt 0.0.tre.png

Tools: 1.Python 3

2.color\_coarse\_tuning\_tree.p

У

#### Renaming the protein ID

#### Files:

renamed\_clps\_hits.fasta clps\_acc2tax\_prot\_all.txt

#### **Tools:**

1.Python 32.rename\_ncbi\_blastdb.py

# Building\_preliminary\_tree

#### Files:

renamed\_clps.aligned.fasta
renamed\_clps.aligned.trimmed.fasta
renamed\_clps.aligned.trimmed.newick

#### **Tools:**

1.MAFFT v7 2.BMGE v1.12 or trimAl v1.4 3.FastTree v2.1

# Adjust and Run fine-tuning

#### Files:

renamed\_clps\_###.fasta.fasttree
renamed\_clps\_###fasta.genus\_trimmed
renamed\_clps\_###fasta\_removedSeq
renamed\_clps\_###.fasta\_sub

#### **Tools:**

1.Perl 5
2.rm\_inparal\_rank.pl
3.trim2untrim.pl

# Fine-tuning results

#### Files:

renamed\_clps\_###.fasta.fasttree.tre
renamed\_clps\_###.fasta.fasttree.png

# **Tools:**

1.Python 32.color\_fine\_tuning\_tree.py



