

Command-Line

IQTREE + TreeTime Workflow

```
awk 'BEGIN{while((getline<"delete.txt")>0){if(">$1]=1}/^>/{f=!f[$1]}f' all_208_seq.fasta > out.fasta
```

Align sequences

```
mafft out.fasta > aligned.fasta
```

Run iqtree

```
bin/iqtree -s aligned.fasta
```

Make a names.txt file

Clean combined fasta names:

```
seqkit replace -p "(.*)" -r '{kv}$2' -k names.txt aligned.fasta > modified.fasta
```

Run treetime

```
treetime --tree aligned.fasta.treefile --dates metadata.csv --aln aligned.fasta --outdir timetree
```

TreeTime Workflow

Extract accession numbers from nextstrain metadata file

```
=MID(A1, SEARCH("|",A1) + 1, SEARCH("|",A1,SEARCH("|",A1)+1) - SEARCH("|",A1) - 1)
```

Downloads genomes from GISAID.org

Downloads genomes from Batch Entrez (Genbank)

Clean genbank sequence names:

```
seqkit replace -p "((.+)( +)+)(.*)" genbank.fasta > genbank_modified.fasta
```

Combine fasta files:

```
cat *.fasta > seq.fasta
```

Clean combined fasta names:

```
seqkit replace -p "(.*)" -r '{kv}$2' -k names.txt seq.fasta > output.fasta
```

Copy the Omicron genomes from only omicron.fasta

Align:

```
mafft output.fasta > aligned.fasta
```

Run treetime:

```
treetime --tree nextstrain.nwk --dates metadata.tsv --aln aligned.fasta --outdir 0716_timetree
```

BEAST Workflow

[illegible]

Partitions
Tip Dates
Site Model
Clock Model
Priors
MCMC

Gamma Site Model

Substitution Rate

☒ estimate

Gamma Category Count

Shape

☒ estimate

Proportion Invariant

☒ estimate

Subst Model

GTR

Rate AC

☒ estimate

Rate AG

☒ estimate

Rate AT

☒ estimate

Rate CG

☒ estimate

Rate CT

☐ estimate

Rate GT

☒ estimate

Frequencies

Estimated

Partitions
Tip Dates
Site Model
Clock Model
Priors
MCMC

Random Local Clock
Rates Are Multipliers
Scaling
Include Root
Mean clock rate 1.0 estimate

Partitions
Tip Dates
Site Model
Clock Model
Priors
MCMC

Tree.t:aligned2 Coalescent Constant Population
RRateChanges.c:aligned2 Poisson[0.6931471805599453]
clockrates.c:aligned2 Gamma[0.05,10.0] initial = [1.0] [1.0E-9,∞]
freqParameter.s:aligned2 Dirichlet[4.0, 4.0, 4.0, 4.0] initial = [0.25] [0.0,1.0]
gammaShape.s:aligned2 Exponential[1.0] initial = [1.0] [0.1,∞] Prior on gamma shape for partition s:aligned2
popSize.t:aligned2 1/X initial = [0.3] [0.0,∞] Coalescent population size parameter of partition t:aligned2
proportionInvariant.s:aligned2 Uniform[0.0,1.0] initial = [0.01] [0.0,1.0] Prior on proportion invariant for partition s:aligned2
rateAC.s:aligned2 Gamma[0.05,10.0] initial = [1.0] [0.0,∞] GTR A-C substitution parameter of partition s:aligned2
rateAG.s:aligned2 Gamma[0.05,20.0] initial = [1.0] [0.0,∞] GTR A-G substitution parameter of partition s:aligned2
rateAT.s:aligned2 Gamma[0.05,10.0] initial = [1.0] [0.0,∞] GTR A-T substitution parameter of partition s:aligned2
rateCG.s:aligned2 Gamma[0.05,10.0] initial = [1.0] [0.0,∞] GTR C-G substitution parameter of partition s:aligned2
rateGT.s:aligned2 Gamma[0.05,10.0] initial = [1.0] [0.0,∞] GTR G-T substitution parameter of partition s:aligned2
+ Add Prior

Partitions

Tip Dates

Site Model

Clock Model

Priors

MCMC ?

MCMC ▾

Chain Length100000000 ?

Store Every-1 ?

Pre Burnin0 ?

Num Initialization Attempts10 ?

▶

tracelog

▶

screenlog

▶

treelog.t:aligned2

☐ Sample From Prior ?

Partitions

Tip Dates

Site Model

Clock Model

Priors

MCMC ?

MCMC ▾

Chain Length100000000 ?

Store Every-1 ?

Pre Burnin0 ?

Num Initialization Attempts10 ?

▼

tracelog

File Name\$(filebase).log ?

Log Every10000 ?

Modeautodetect ?

Sortsmart ?

☒ Sanitise Headers ?

☐ posterior

☐ likelihood

☐ prior

☐ treeLikelihood.olr_mv_beast

☐ TreeHeight.t:olr_mv_beast

☐ mutationRate.s:olr_mv_beast

☐ proportionInvariant.s:olr_mv_beast

☐ gammaShape.s:olr_mv_beast

Partitions	Tip Dates	Site Model	Clock Model	Priors	MCMC ?
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MCMC ▾

Chain Length

100000000 ?

Store Every

-1 ?

Pre Burnin

0 ?

Num Initialization Attempts

10 ?

☐ tracelog

☒ screenlog

File Name

 ?

Log Every

10000 ?

Mode

autodetect ▾ ?

Sort

none ▾ ?

☐ Sanitise Headers ?

☐ posterior

☐ likelihood

☐ prior

☒ Ascii

☐ treelog.t:olr_rmv_beast