

A

NeMu pipeline

The pipeline for neutral mutation spectra evaluation based on evolutionary data

Inputs

Job Title

Test Run (optional)

0/100

Sampling type* ?

☒ Auto

☐ Manual


Level of analysis* ?

☒ Species-specific

Genetic code* ?

2. The Vertebrate Mitochondrial Code

Query protein sequence* ?

 Drag and drop file here

Limit 2MB per file • FASTA, FAA, FA

Browse files

Query protein sequence* ?

>optional name

TSKHHFGFQAAAWYWHFVDVWVWLFVSYWWGS...

0/1000

Species name* ?

mtDNA gene database* ?

0/100

Choose a database

* - required parameters

Advanced pipeline parameters

email ?

test@example.com

Run pipeline!

B

Advanced pipeline parameters

Phylogenetic inference

Substitution model for IQTREE2 phylogeny

GTR+FO+G6+I

Model for IQTREE2 ancestor reconstruction

GTR+FO+G6+I

☒ Use tree shrinking ?

Quantile for TreeShrink

0.05

- +

Mutation types

☒ Synonymous ?

☐ Synonymous fourfold ?

☐ Synonymous and nonsynonymous ?

Branch selection

☐ Branch-specific spectra ?

☐ Terminal tree branches spectra ?

☐ Internal tree branches spectra ?

Mutation filtration

☒ Use probabilities ?

☐ Use uncertainty coefficient ?

Mutation probability cutoff ?

0.30

- +

Mutation types cutoff ?

16

- +

☐ Run site rates estimation in phylogenetic inference ?

☐ Run simulation of neutral evolution ?