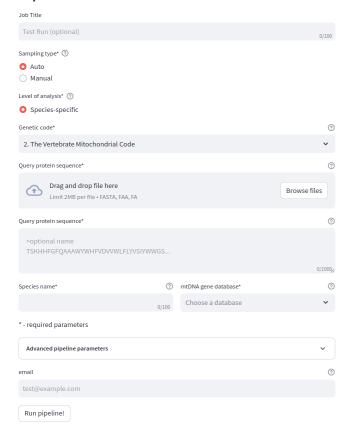
A NeMu pipeline

The pipeline for neutral mutation spectra evaluation based on evolutionary data

Inputs



Advanced pipeline parameters Phylogenetic inference **Mutation types** Substitution model for IQTREE2 phylogeny Synonymous ③ Synonymous fourfold ③ ☐ Synonymous and nonsynonymous ② Model for IQTREE2 ancestor reconstruction GTR+FO+G6+I **Branch selection** ✓ Use tree shrinking ② ☐ Branch-specific spectra ③ Quantile for TreeShrink ☐ Terminal tree branches spectra ③ ☐ Internal tree branches spectra ② **Mutation filtration** ✓ Use probabilities ② Run site rates estimation in ? phylogenetic inference Use uncertainty coefficient ② Run simulation of neutral evolution ② Mutation probability cutoff 0.30 ? Mutation types cutoff

В