EPA-ng·····

·····RAxML-NG·····EPA-ng·····jplace···likelihood weight·····
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EPA-ng·····RAxML-NG·····evaluate·····.bestModel····EPA-ng··
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```
#!/usr/bin/env bash
set -euo pipefail
ref=/data/reference.msa.fasta
tree=/data/reference.tree
query=/data/query.msa.fasta
root="$PWD/epa-pilot-001"
for f in "$ref" "$tree" "$query"; do test -s "$f"; done
test ! -e "$root" || { echo "output exists: $root" >&2; exit 2; }
mkdir -p "$root"
raxml-ng --evaluate --msa "$ref" --tree "$tree"   --prefix "$root/model" --model GTR+G+F --threads 4   > "$root/model.log" 2>&1
test -s "$root/model.raxml.bestModel"
epa-ng --ref-msa "$ref" --tree "$tree" --query "$query"   --model "$root/model.raxml.bestModel" --outdir "$root/placement"   --threads 4 > "$root/epa.log" 2>&1
find "$root/placement" -maxdepth 1 -type f -name '*.jplace'   -print -quit | grep -q .
sha256sum "$ref" "$tree" "$query" > "$root/inputs.sha256"
```

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EPA-ng··README····· https://raw.githubusercontent.com/pierrebarbera/epa-ng/master/README.md

EPA-ng····· https://doi.org/10.1093/sysbio/syy054