

In order to save computational time, this short README just guides you to reproduce a small case (248 genes) I played before.

For a given question, T1 is unconstrained ML $t1((\text{turtles}, \text{crocodiles}), \text{birds})$, whereas T2 $((\text{birds}, \text{crocodiles}), \text{turtles})$ is another hypothesis or incongruent relative to T1.

- 1) Find constrained-based ML tree for $t2((\text{birds}, \text{crocodiles}), \text{turtles})$ on the supermatrix using RAxML or IQ-TREE, which is incongruent with unconstrained ML $t1((\text{turtles}, \text{crocodiles}), \text{birds})$

raxml:

```
raxmlHPC-PTHREADS-SSE3 -T 6 -p 748962402 -# 5 -g t2.tre -s 284genes.fas -n t2_ML -m GTRGAMMA --no-bfgs
```

iq-tree: (the option "-g" was released recently in IQ-TREE 1.5.X, I would recommend you IQ-TREE since it runs much faster than RAxML if your data is pretty huge)

```
iqtree-omp1.5.1 -nt 6 -st DNA -s 284genes.fas -m GTR+G4 -g t2.tre -pre t2_ML
```

- 2) Estimate site-wise loglk for alternative hypothesis (-z trees.tre) using raxml (a) or iqtree (b)
a) Estimate site-wise loglk for alternative hypothesis (-z trees.tre) using raxml with option (-f G)

```
/home/shenx3/tools/standard-RAxML-master_8.2.0/raxmlHPC-PTHREADS-SSE3 -T 6 -f G -m GTRGAMMA -z trees.tre -s 284genes.fas -n turtle_site_lk --no-bfgs
```

- b) Estimate site-wise loglk for alternative hypothesis (-z trees.tre) using iqtree with option (-wsl)

```
/gpfs23/scratch/shenx3/tools/iqtree-1.6.8-Linux/bin/iqtree -nt 6 -st DNA -m GTR+G4 -z trees.tre -wsl -s 284genes.fas -pre turtle_site_lk
```

- 3) Passer sits-wise log-likelihood file by Phylogenetic_signal_parser_v1.1.pl (please make sure PERL has installed on your computer)

```
perl Phylogenetic_signal_parser_v1.1.pl RAxML_perSiteLLs.turtle_site_lk turtle_genes_order.txt No turtle
```

Option Explanations

RAxML_perSiteLLs.turtle_site_lk: Site-wise log likelihood file estimated from RAxML or IQ-TREE (see output in step 2a or 2b)

turtle_genes_order.txt: Gene-based partition file in RAxML-style

Yes/No: Do you want to print out site-wise log likelihood for each gene?

prefix: Prefix for all output files

#####

- 4) What is updated?

Version 1.1 can work on Site-wise log likelihood file from RAxML and IQ-TREE

Note that:

- a) Characters in red are command lines
- b) Phylogenetic_signal_parser.pl only accepts no more than three alternative hypotheses (i.e.,

T1 Vs T2 or T1 Vs T2 VS T3).

- c) If you use this small case in your paper, please cite the original study (Chiari et al., 2012 in BMC Biology; doi: 10.1186/1741-7007-10-65).

Please let me know if you have any questions about them.

Xingxing Shen

shenxingxing2010@gmail.com; xingxingshen@zju.edu.cn