

RAxML-ng phylogenetics

RAxML-ng uses maximum likelihood

General usage for RAxML-ng

```
raxml-ng --flag1 [flag1 settings] --flag2 [flag2 settings] ...
```

Example flags:

```
--msa [sequence alignment in Phylip, Fasta, ...]  
--model [sequence evolution model]  
--bs-trees [number of bootstrap replicates]
```

Example call to RAxML-ng:

```
raxml-ng --msa data.phy --model GTR+G --bs-trees 300 --all --tree rand
```

RAxML-ng: output files

RAxML-ng

↘ takes a number of
starting trees - random #
(or you can specify)



***.raxml.startTree**

RAxML-ng: output files

RAxML-ng

→ takes a number of
starting trees - random #
(or you can specify)



→ builds ML trees based
on starting trees



***.raxml.startTree**

RAxML-ng: output files

RAxML-ng

↓ takes a number of
starting trees - random #
(or you can specify)



↓ builds ML trees based
on starting trees



↓ chooses the **best**
ML tree & saves
all ML trees



***.raxml.startTree**

***.raxml.bestTree**

***.raxml.mlTrees**

RAxML-ng: output files

↙ begins bootstrapping
on best ML tree



& saves each bootstrap replicate

`*.raxml.bootstraps`

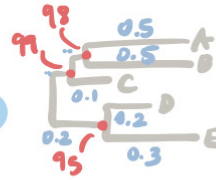
RAxML-ng: output files

↪ begins bootstrapping
on best ML tree



& saves each bootstrap replicate

↪ selects best overall tree
& saves best tree w bootstrap
support values



*.raxml.bootstraps

*.raxml.bestTree

*.raxml.support

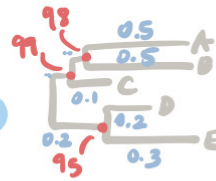
RAxML-ng: output files

↪ begins bootstrapping
on best ML tree



& saves each bootstrap replicate

↪ selects best overall tree
& saves best tree w bootstrap
support values



↪ selects best model

↪ saves all run
info & output

*.raxml.bootstraps

*.raxml.bestTree

*.raxml.support

*.raxml.bestModel

*.raxml.log

RAxML-ng: output files

RAxML-NG v. 0.5.1b BETA released on 01.12.2017 by The Exelixis Lab.
Authors: Alexey Kozlov, Alexandros Stamatakis, Diego Darriba, Tomas Flouri, Benoit Morel.
Latest version: <https://github.com/amkozlov/raxml-ng>
Questions/problems/suggestions? Please visit: <https://groups.google.com/forum/#!forum/raxml>

WARNING: This is a BETA release, please use at your own risk!

RAxML-NG was called as follows:

```
./raxml-ng --msa ./ranaddrad.phy --model GTR+G --all --tree rand --redo --bs-trees 200 --threads 2
```

RAxML-ng

takes a number of
starting trees - random #
(or you can specify)



builds ML trees based
on starting trees



chooses the best
ML tree & saves
all ML trees

+ bootstrapping
0)

ate (linked)

S (2 threads)

ode: existing checkpoints are ignored, and all result files

nt from file: /work/03123/eac3496/lonestar/apr18_all/partiti
t with 12 taxa and 2255590 sites

itions and 53670 patterns

: 2255590 / 53670

Optimized model parameters:

Partition 0: noname

Rate heterogeneity: GAMMA (4 cats, mean), alpha: 0.089241 (ML), weights&rates: (0.250000,0.000000) (0.2

Base frequencies (ML): 0.265350 0.234334 0.235469 0.264847

Substitution rates (ML): 0.993796 3.145209 0.701965 0.726765 3.043371 1.000000

Final LogLikelihood: -3570215.401115

All ML trees saved to: /work/03123/eac3496/lonestar/apr18_all/partitions/phylip_files/full_loci/ranaddrad_t1

Best ML tree saved to: /work/03123/eac3496/lonestar/apr18_all/partitions/phylip_files/full_loci/ranaddrad_t1

Best ML tree with bootstrap support values saved to: /work/03123/eac3496/lonestar/apr18_all/partitions/phylip_files/full_loci/ranaddrad_t1

Optimized model saved to: /work/03123/eac3496/lonestar/apr18_all/partitions/phylip_files/full_loci/ranaddrad_t1

Bootstrap trees saved to: /work/03123/eac3496/lonestar/apr18_all/partitions/phylip_files/full_loci/ranaddrad_t1

Execution log saved to: /work/03123/eac3496/lonestar/apr18_all/partitions/phylip_files/full_loci/ranaddrad_t1

Analysis started: 07-May-2018 18:54:30 / finished: 07-May-2018 20:21:04

Elapsed time: 5194.279 seconds

#16, logLikelihood: -3570215.419053

#17, logLikelihood: -3570215.416867

#18, logLikelihood: -3570215.402859

#19, logLikelihood: -3570215.414789

#20, logLikelihood: -3570215.414698

completed, best tree logLH: -3570215.401115

[00:09:49] Starting bootstrapping analysis with

[00:10:12] Bootstrap tree #1, logLikelihood: -35

[00:10:33] Bootstrap tree #2, logLikelihood: -35

[00:10:55] Bootstrap tree #3, logLikelihood: -35

[00:11:17] Bootstrap tree #4, logLikelihood: -35

[00:11:39] Bootstrap tree #5, logLikelihood: -35

[00:12:02] Bootstrap tree #6, logLikelihood: -35

[00:12:24] Bootstrap tree #7, logLikelihood: -35

[00:12:45] Bootstrap tree #8, logLikelihood: -35

[00:13:10] Bootstrap tree #9, logLikelihood: -35

[00:13:32] Bootstrap tree #10, logLikelihood: -35

[00:13:54] Bootstrap tree #11, logLikelihood: -35

[00:14:18] Bootstrap tree #12, logLikelihood: -35

[00:14:41] Bootstrap tree #13, logLikelihood: -35

[00:15:04] Bootstrap tree #14, logLikelihood: -35

[00:15:26] Bootstrap tree #15, logLikelihood: -35

[00:15:48] Bootstrap tree #16, logLikelihood: -35

[00:15:48] Bootstrap tree #16, logLikelihood: -35

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[00:15:48] Bootstrap tree #16, logLikelihood: -35

[00:15:48] Bootstrap tree #16, logLikelihood: -35