

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
```