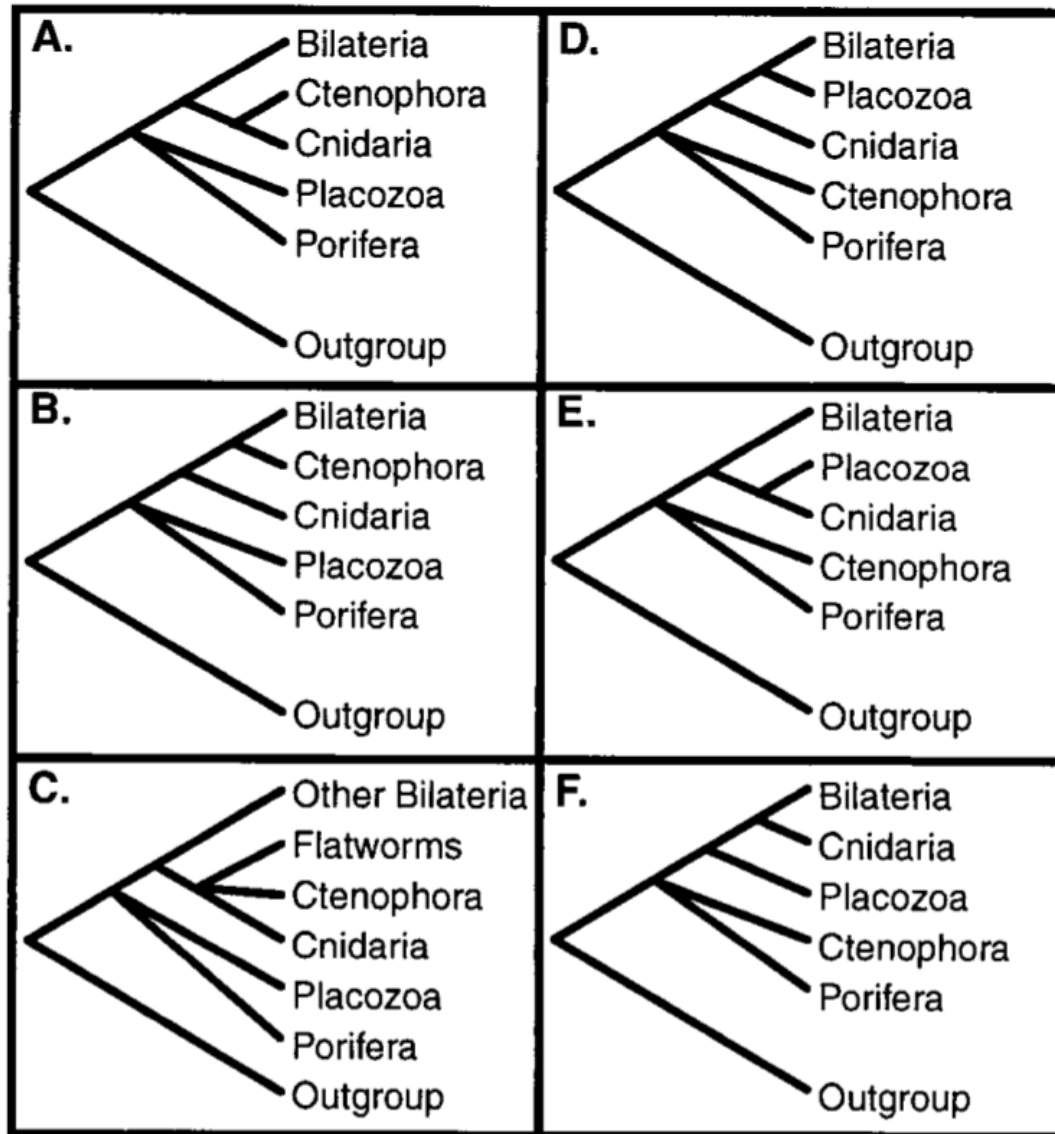# BI694
Bioinformatics & Phylogenetics

FIG. 1. Six alternative hypotheses for the origin of the Bilateria.
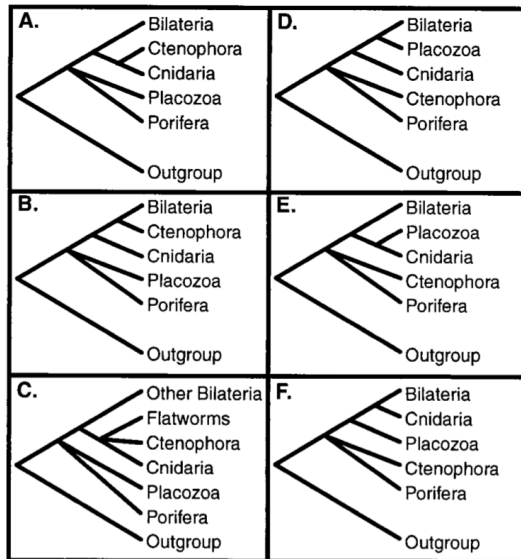
Maximum likelihood

FIG. 1.   Six alternative hypotheses for the origin of the Bilateria.

Bootstrapping ML phylogenies: RAxML implements fast algorithm for ML search

```
$ raxmlHPC    -f a \ # rapid bootstrap and search for best ML tree
              -m GTRGAMMA \ # model of evolution
              -p 12345 \ # random no seed for tree search
              -x 12345 \ # random number seed for bootstrap
              -# 100 \ # no of bootstrap replicates
              -s RootOfBilateria_RAxML.phy \ # alignment file
              -n Bilatria_RAxML # name of run
```
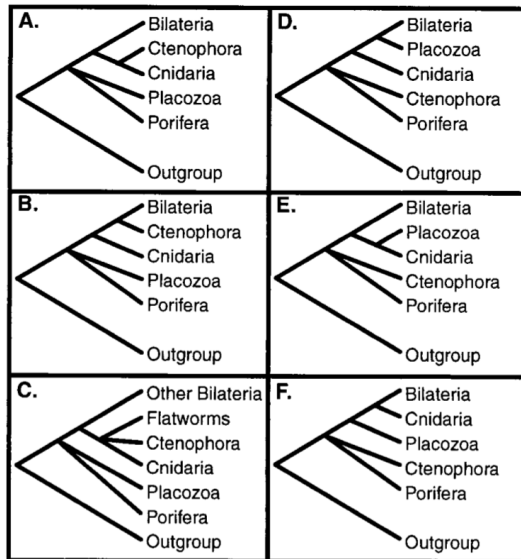
Bayesian

FIG. 1. Six alternative hypotheses for the origin of the Bilateria.

MrBayes:

```
lset nst=6 rates=gamma # set the model
prset statefreqpr=fixed(equal) # set the prior
mcmcp \
    ngen=100000 \ # number of generations to run sampler for
    printfreq=100 \ # How often will output be printed to screen
    samplefreq=100 \ # set frequency for sampling trees and their likelihoods
    nruns=2 nchains=4 \ # How many chains and runs are conducted?
    savebrlens=yes \ # save the branch lengths of tree
    mcmcdiagn=yes # save diagnostics of run
mcmc # start MCMC sampler
sump # calculate summary statistics
sumt # calculate consensus tree
```