

Příloha 1

Nastavení programu GARLI pro tvorbu fylogenetického stromu na příkladu rodu *Trebouxia* metodou maximum likelihood se současným provedením bootstrapové analýzy o 100 opakováních.

```
[general]
datafname = Trebouxia_vse.nex
constraintfile = none
streefname = stepwise
attachmentspertaxon = 50
ofprefix = Garli
randseed = -1
availablememory = 512
logevery = 10
saveevery = 100
refinestart = 1
outputeachbettertopology = 0
outputcurrentbesttopology = 0
enforcetermconditions = 1
genthreshfortopoterm = 20000
scorethreshforterm = 0.05
significanttopochange = 0.01
outputphyliptree = 0
outputmostlyuselessfiles = 0
writecheckpoints = 0
restart = 0
outgroup = 1
resampleproportion = 1.0
inferinternalstateprobs = 0
outputsitelikelihoods = 0
optimizeinputonly = 0
collapsebranches = 1

selectionintensity = 0.5
holdoverpenalty = 0
stopgen = 50000
stoptime = 50000

startoptprec = 0.5
minoptprec = 0.01
numberofprecreductions = 10
treerejectionthreshold = 50.0
topoweight = 1.0
modweight = 0.05
brlenweight = 0.2
randnniweight = 0.1
randsprweight = 0.3
limsprweight = 0.6
intervallength = 100
intervalstostore = 5
limsprrange = 6
meanbrlenmuts = 5
gammashapebrlen = 1000
gammashapemodel = 1000
uniqueswapbias = 0.1
distanceswapbias = 1.0

searchreps = 3
bootstrapreps = 100

[model1]
datatype = nucleotide
ratematrix = 2rate
statefrequencies = estimate
ratehetmodel = gamma
numratecats = 4
invariantsites = none

[master]
nindivs = 4
holdover = 1
```