



MrBayes를 이용한 데이터 분석



MrBayes: Bayesian Inference of Phylogenetics


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MrBayes is a program for Bayesian inference across a wide range of models for discrete data. MrBayes uses Markov Chain Monte Carlo (MCMC) to estimate the posterior probability of a phylogenetic tree.

Program features:

- A common interface for Windows, macOS, and Linux.
- Extensive handling of missing data.
- Analysis of morphological and molecular data.
- Mixing of discrete and continuous characters.
- Easy linking of partitions.
- An abundant set of priors, including a doublet, and the standard priors.
- Estimation of Bayesian factors.



MrBayes: Bayesian Inference of Phylogeny

MrBayes may be downloaded as a pre-compiled executable or in source form (recommended).

Current release

The most recent release version of MrBayes is [3.2.7a](#), released March 6, 2019.

The 3.2.7a [source code](#) is available for compilation on Unix machines.

Pre-compiled (provisional) executables are available for Windows ([MrBayes-3.2.7-WIN.zip](#)). These are, however, serial versions compiled without the [Beagle](#) library. The serial version works well for smaller analyses but if you plan to run large analyses using many parallel chains, you should use the MPI version instead. Refer to the [User Manual](#), and the [INSTALL](#) document on GitHub for help with installation of the program.

MrBayes may also be installed through the Homebrew package manager on macOS, Linux, and Windows Subsystem for Linux (WSL). Please see the [INSTALL](#) document for instructions.

Older releases

You can get access to older releases (from release 3.2.0 onwards), by browsing [the following links](#).

(1) 명령프롬프트를 열어 MrBayes프로그램을 실행한다

```
C:\temp>mb.3.2.7-win64.exe
```

```
MrBayes 3.2.7a x86_64
(Bayesian Analysis of Phylogeny)
Distributed under the GNU General Public License

Type "help" or "help <command>" for information
on the commands that are available.

Type "about" for authorship and general
information about the program.
```

```
MrBayes > exec cynmix.nex
```

(2) cynmix.nex 데이터를 exec
명령어를 사용하여 읽어들인다.

```
MrBayes > exec cynmix.nex
```

```
Executing file "cynmix.nex"
DOS line termination
Longest line length = 217
Parsing file
Expecting NEXUS formatted file
Reading data block
  Allocated taxon set
  Allocated matrix
  Defining new matrix with 32 taxa and 3246 characters
  Data is Mixed
    Data for partition 1 is Standard
    Data for partition 2 is Dna
  There are a total of 2 default data divisions
  Data matrix is interleaved
  Gaps coded as -
```

(본 자료는 MrBayes 매뉴얼
Chapter 3 Tutorial: A
partitioned analysis 의 일부
내용 + α 입니다. 보다
자세한 내용은 매뉴얼을
참조해주세요)

(3) cynmix.nex 파일을 메모장위에 drag/drop 하여 내용을 살펴보자.

각진 괄호('[' 와 ']')는 주석부분이라 프로그램 실행시 무시된다.

Dimensions 명령어를 이용하여 taxa의 수 character 수를 지정한다.

Format 명령어를 이용하여 데이터의 종류를 설정한다. Standard는 Morphological character를 지정하는 명령어이다. Interleave, gap, missing의 설정방식을 눈여겨 보자.

```
#NEXUS

[ Data from: Nylander JAA, Ronquist F, Huelsenbeck JP, Nieves-Aldrey JL. 2004. Bayesian phylogenet

Begin data;
  Dimensions ntax=32 nchar=3246;
  Format datatype=mixed(Standard:1-166,DNA:167-3246) interleave=yes gap=- missing=?;
  Matrix
Ibalia      0000000000000002-0000000000000?00000000000000100{01}0100001-00100000-000000000000100
Synergus    1-1-100000000202110201011010110100000000010121001120101010101000000001100020000000
Periclistus 1-1-100000000202110201011110110100000000010100101000101010011000000001100021001000
Ceroptres   1-1-1000100002021002010111101001000000000111000???10101010010000000000100021001000
Synophromorpha 1-1-00001000021-1001010011111010000000001010010100010001001000000000100001200000
Xestophanes 1-1-00001000011-10-110001011010100000000010110101000100010010101000000100001201000
Diastrophus 011-10101000021-10-210001011010100000100000011101000100010012000000000001101201100
Gonaspis    1-1-10001000011-10-210001011010100000100000021101000100010012000000000000101201000
Liposthenes_gle 0100003000010102202000001011011100000100100010110000100010012000000001000011201100
Liposthenes_ker 0000102000000101????????????????????????????????110????0?10001001000000??00000011101100
Antistrophus 1-010120000?01001010000110110001000001020000101?000101111110021000000000221001110
Rhodus      1-0100000000000000????????????????????????????0????1010000?10101111000000??000000121001110
Hedickiana  1-0101000000000000?????0??10101??????1????0????0010000110101111000000??000000121001100
Neaylax     1-01010000000000001000000110100001000100000000000{01}???01100011110000000000000021001
Isocolus    01000010000001001001000111100001000000000000010110001101010110000000000000020000010
Aulacidea   0000000000000010010020001101000010000000000000101???011010101100000000000000021000000
Panteliella 0000003000100200??17000????0??010700????????200???17101010111020?0??00000121001010
Barbotinia  1-010100000?0100002000000011000100010200000020010021101010111001000000000021001000
```

(4) cynmix.nex 파일의 하단 부분을 살펴보자.

{ begin data; end; } 로 지정한 데이터 블록이 표시된 이후에 { begin mrbayes; end; } 블록에 MrBayes 실행을 위한 설정이 나열된다.

각진 괄호는 주석 부분이라 프로그램 실행 시 무시된다(주석부분을 살린 후, 즉, 각진 괄호를 삭제한 후, cynmix.nex 파일을 읽어 들이면 설정이 자동으로 실행된다).

```
begin mrbayes;

  [This block defines several different character sets that could be used in partitioning the
  and then defines and enforces a partition called favored.]


  charset morphology = 1-166;
  charset COI = 167-1244;
  charset EF1a = 1245-1611;
  charset LWRh = 1612-2092;
  charset 28S = 2093-3246;
  partition favored = 5: morphology, COI, EF1a, LWRh, 28S;

  [The following lines set up a particular model (the one discussed in the MrBayes manual). U
  if you want to set up the model when executing this file instead of specifying it yourself.

  [
  set partition=favored;
  lset app=(1) rates=gamma;
  lset app=(2,3,4,5) rates=invgamma nst=6;
  unlink revmat=(all) pinvar=(all) shape=(all) statefreq=(all);
  prset ratepr=variable;
  ]

end;
```

(참고) 서열데이터의 포맷 변환 사이트



HIV Sequence Database

DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS INFO

Format Converter

Purpose: Convert an input sequence or alignment to a user-specified format. See [Explanation](#).

Input

Paste your sequences here [\[Sample Input\]](#)

Or upload your file: 선택된 파일 없음

Options

Select input format ☒ Automatic

Select output format ☒ Fasta

Output line width ☒ 50 characters ☐ as wide as possible

Enforce sequence name uniqueness ☐

Convert Genbank to GFF3 ☐

Replace IUPAC codes with Ns ☐

https://www.hiv.lanl.gov/content/sequence/FORMAT_CONVERSION/form.html

(5) 결과의
재현가능성을
위해 seed=1
swapseed=1을
설정한다(다른
양의 정수도
무방).

서열데이터를
읽어 들인다.

partition=favored
설정한다.

```
MrBayes > set seed=1 swapseed =1
```

```
Setting seed to 1  
Setting swapseed to 1
```

```
MrBayes > exec cynmix.nex  
      (.....)  
      (화면 출력 부분 생략)  
      (.....)
```

```
MrBayes > set partition = favored
```

```
Setting favored as the partition, dividing characters into 5  
parts.  
Setting model defaults  
Seed (for generating default start values) = 1911300560  
Expecting command
```

```
MrBayes >
```

(6) showmodel
 명령어로 설정을
 확인해보자.
 partition 1은
 morphological
 character,
 partition2-5는
 DNA 로 동일

```
MrBayes > showmodel
```

```
Model settings:
```

```
Settings for partition 1 --
```

```
Datatype = Standard
```

```
Coding = Variable
```

```
# States = Variable, up to 10
```

```
State frequencies are fixed to be equal
```

```
Rates = Equal
```

```
(.....)
```

```
(화면 출력 부분 생략)
```

```
(.....)
```

```
Active parameters:
```

Parameters	Partition(s)				
	1	2	3	4	5
Statefreq	1	2	2	2	2
Ratemultiplier	3	3	3	3	3
Topology	4	4	4	4	4
Brlens	5	5	5	5	5

```
(.....)
```

```
(화면 출력 부분 생략)
```

```
(.....)
```

(7) lset 명령어로 파티션
1-5의 모형을 설정한다
(DNA 모형에 관한
사항은 서태건2022 논문
참조).

```
MrBayes > lset applyto=(1) rates=gamma;
```

```
Setting Rates to Gamma for partition 1  
Successfully set likelihood model parameters to  
partition 1 (if applicable)  
Expecting command
```

```
MrBayes > lset applyto=(2,3,4,5) rates=invgamma nst=6;
```

```
Setting Rates to Invgamma for partition 2  
Setting Rates to Invgamma for partition 3  
Setting Rates to Invgamma for partition 4  
Setting Rates to Invgamma for partition 5  
Setting Nst to 6 for partition 2  
Setting Nst to 6 for partition 3  
Setting Nst to 6 for partition 4  
Setting Nst to 6 for partition 5  
Successfully set likelihood model parameters to  
partitions 2, 3, 4, and 5 (if applicable)  
Expecting command
```

```
MrBayes >
```


(8) showmodel
명령어로 설정을
확인해보자.
partition 1은
morphological
character,
partition2-5는
DNA 로 동일

```
MrBayes > showmodel;
```

```
Model settings:
```

```
Settings for partition 1 --
```

```
Datatype = Standard
```

```
Coding = Variable
```

```
# States = Variable, up to 10
```

```
State frequencies are fixed to be equal
```

```
(.....)
```

```
(화면 출력 부분 생략)
```

```
(.....)
```

```
Active parameters:
```

	Partition(s)				
Parameters	1	2	3	4	5

Revmat	.	1	1	1	1
Statefreq	2	3	3	3	3
Shape	4	5	5	5	5
Pinvar	.	6	6	6	6
Ratemultiplier	7	7	7	7	7
Topology	8	8	8	8	8
Brlens	9	9	9	9	9

```
(.....)
```

```
(화면 출력 부분 생략)
```

```
(.....)
```

(9) unlink 명령어로
파티션별로 다른
모수를 할당하도록
설정 후 showmodel
명령어로 설정을
확인해보자.

앞페이지의
showmodel 결과와
비교해보자.

```
MrBayes > unlink revmat=(all) pinvar=(all) shape=(all)
statefreq=(all);
```

```
Unlinking
Expecting command
```

```
MrBayes > showmodel;
```

```
(.....)
(화면 출력 부분 생략)
(.....)
```

Active parameters:

	Partition(s)				
Parameters	1	2	3	4	5

Revmat	.	1	2	3	4
Statefreq	5	6	7	8	9
Shape	10	11	12	13	14
Pinvar	.	15	16	17	18
Ratemultiplier	19	19	19	19	19
Topology	20	20	20	20	20
Brlens	21	21	21	21	21

```
(.....)
(화면 출력 부분 생략)
(.....)
```

(10) prset 명령어로
ratepr의 설정을
바꾼다.

showmodel 명령어로
설정을 확인한다.
그림의 붉은색 부분이
prset설정 이전과
어떻게 다른지
살펴보자.

```
19 -- Parameter = Ratemultiplier{all}
      Type      = Partition-specific rate multiplier
      Prior     = Fixed(1.0)
      Partitions = All
```

(화면 출력 생략)

```
MrBayes > prset ratepr=variable;
```

(화면 출력 생략)

```
MrBayes > showmodel
```

(화면 출력 부분 생략)

```
19 -- Parameter = Ratemultiplier{all}
      Type      = Partition-specific rate multiplier
      Prior     = Dirichlet(1.00,1.00,1.00,1.00,1.00)
      Partitions = All
```

(11) 『help lset』 명령으로 likelihood setting 확인. 그림은 파티션 5의 예시이다. 파티션 1과는 어떻게 다른지 살펴보자.

```
MrBayes > help lset;
```

(화면 출력 생략)

Model settings for partition 5:

Parameter	Options	Current Setting
Nucmodel	4by4/Doublet/Codon/Protein	4by4
Nst	1/2/6/Mixed	6
Code	Universal/Vertmt/Invermt/Yeast/Mycoplasma/ Ciliate/Echinoderm/Euplotid/Metmt	Universal
Ploidy	Haploid/Diploid/Zlinked	Diploid
Rates	Equal/Gamma/LNorm/Propinv/ Invgamma/Adgamma/Kmixture	Invgamma
Ngammacat	<number>	4
Nlnormcat	<number>	4
Nmixtcat	<number>	4
Nbetacat	<number>	5
Omegavar	Equal/Ny98/M3	Equal
Covarion	No/Yes	No
Coding	All/Variable/Informative/Nosingletons Noabsencesites/Nopresencesites/ Nosingletonabsence/Nosingletonpresence	All
Parsmodel	No/Yes	No

```
MrBayes >
```

(12) 『help prset』명령으로 prior setting 확인. 그림은 파티션 5의 예시이다.

```
MrBayes > help prset;
```

(화면 출력 생략)

Model settings for partition 5:

Parameter	Options	Current Setting
Tratioopr	Beta/Fixed	Beta(1.0,1.0)
Revmatpr	Dirichlet/Fixed	Dirichlet(1.0,1.0,1.0,1.0,1.0,1.0)
Aamodelpr	Fixed/Mixed	Fixed(Poisson)
Aarevmatpr	Dirichlet/Fixed	Dirichlet(1.0,1.0,...)
Omegapr	Dirichlet/Fixed	Dirichlet(1.0,1.0)

(화면 출력 생략)

TK02varpr	Fixed/Exponential/Uniform	Exponential(1.00)
Igrvarpr	Fixed/Exponential/Uniform	Exponential(10.00)
Ratepr	Fixed/Variable=Dirichlet	Dirichlet(...,1.0,...)
Generatepr	Fixed/Variable=Dirichlet	Fixed

```
MrBayes >
```

(13) 『help mcmcp』명령으로 MCMC parameter setting 확인. 디폴트 세팅이다.

```
MrBayes > help mcmcp;
```

```
mcmcp
```

```
-----  
Mcmcp
```

This command sets the parameters of the Markov chain Monte Carlo (MCMC) analysis without actually starting the chain. This command is identical in all respects to Mcmc, except that the analysis will not start after this command is issued. For more details on the options, check the help menu for Mcmc.

Parameter	Options	Current Setting
Ngen	<number>	1000000
Nruns	<number>	2
Nchains	<number>	4
Temp	<number>	0.100000
Reweight	<number>, <number>	0.00 v 0.00 ^
Swapfreq	<number>	1
Nswaps	<number>	1
Samplefreq	<number>	500
Printfreq	<number>	1000
Printall	Yes/No	Yes

(화면 출력 생략)

```
-----  
MrBayes >
```

(14) MCMC 설정을 바꾸려면 아래와 같이 mcmcp 명령으로 바꿀 수 있다. 『help mcmcp』명령으로 MCMC parameter setting 확인하고 어느 부분이 바뀌었는지 살펴보자.

```
MrBayes > mcmcp ngen=1000000 samplefreq=500 printfreq=100 diagnfreq=1000;  
          (화면 출력 생략)
```

```
MrBayes > help mcmcp;
```

```
mcmcp
```

```
-----  
Mcmcp
```

This command sets the parameters of the Markov chain Monte Carlo (MCMC) analysis without actually starting the chain. This command is identical in all respects to Mcmc, except that the analysis will not start after this command is issued. For more details on the options, check the help menu for Mcmc.

Parameter	Options	Current Setting
Ngen	<number>	1000000
Nruns	<number>	2
Nchains	<number>	4
Temp	<number>	0.100000
Reweight	<number>, <number>	0.00 v 0.00 ^
Swapfreq	<number>	1
Nswaps	<number>	1
Samplefreq	<number>	500
Printfreq	<number>	100
Printall	Yes/No	Yes

```
(화면 출력 생략)
```

```
-----  
MrBayes >
```

(15) 『mcmc』를 입력하여 MCMC를 실행한다. 설정한대로 2개의 MCMC run (가운데 ‘*’로 구분) 각 run당 chain 4개 (cold 1, hot 3)가 실행됨을 볼 수 있다. 설정한 100만세대에 도달하면 계속 진행할지 종료할지 물어온다. No를 입력.

MrBayes > **mcmc**

Chain results (1000000 generations requested):

```

0 -- [-36420.775] (-36612.898) (-36521.562) (-36315.410) * [-36398.170] (-36535.731) (-36347.760) (-36231.370)
100 -- [-33056.218] (-33453.289) (-34107.536) (-34076.557) * (-33764.603) (-33392.604) [-32423.715] (-32517.073) -- 2:46:39
200 -- [-31774.765] (-32229.865) (-32461.079) (-32043.488) * (-31670.658) (-31390.711) (-31251.369) [-31072.383] -- 2:46:38
300 -- [-30321.925] (-31283.716) (-31156.318) (-31389.299) * (-30856.835) (-30666.852) (-30596.379) [-29999.069] -- 2:46:37
400 -- [-29977.023] (-30688.639) (-30607.615) (-30533.192) * (-29903.261) (-30231.651) (-30199.993) [-29381.049] -- 2:46:36
500 -- [-29035.889] (-29767.380) (-29943.057) (-29817.365) * (-29423.371) (-29873.605) (-30000.738) [-28721.935] -- 2:46:35
600 -- [-28667.397] (-29342.569) (-29331.651) (-29442.260) * (-28927.953) (-29207.586) (-29742.622) [-28528.715] -- 2:46:34
700 -- [-28331.464] (-28718.483) (-29086.234) (-28989.418) * (-28727.895) (-28890.244) (-29191.674) [-28460.043] -- 3:10:20
800 -- [-28196.837] (-28321.949) (-28999.631) (-28779.440) * (-28395.527) (-28482.847) (-28850.931) [-28227.453] -- 3:07:21
900 -- [-27
1000 -- [-27
Average standard deviation of split frequencies: 0.005460
Average stand 998100 -- (-26550.291) [-26526.585] (-26533.179) (-26548.298) * [-26535.568] (-26538.489) (-26532.042) (-26544.724) -- 0:00:19
998200 -- (-26544.423) [-26532.126] (-26535.483) (-26543.154) * [-26529.331] (-26536.281) (-26526.384) (-26545.223) -- 0:00:18
998300 -- (-26546.771) [-26532.941] (-26536.762) (-26554.364) * (-26532.636) [-26534.869] (-26528.616) (-26545.230) -- 0:00:17
998400 -- (-26553.216) [-26533.143] (-26546.007) (-26553.919) * [-26528.170] (-26550.687) (-26530.388) (-26540.282) -- 0:00:16
1100 -- [-27
1200 -- [-27
998500 -- (-26546.576) [-26533.058] (-26544.599) (-26559.953) * (-26538.783) (-26546.102) (-26528.781) [-26540.176] -- 0:00:15
1300 -- [-27
998600 -- (-26539.610) [-26531.967] (-26541.835) (-26555.832) * (-26543.522) (-26551.674) [-26526.860] (-26547.567) -- 0:00:14
1400 -- [-27
998700 -- (-26533.468) [-26523.269] (-26544.875) (-26552.799) * (-26537.804) (-26554.226) [-26531.164] (-26547.811) -- 0:00:13
1500 -- [-27
998800 -- (-26532.194) [-26521.952] (-26550.870) (-26551.396) * (-26534.674) [-26553.409] (-26541.061) (-26544.463) -- 0:00:12
1600 -- [-27
998900 -- (-26532.885) [-26522.219] (-26548.156) (-26551.624) * [-26534.607] (-26550.197) (-26540.621) (-26547.552) -- 0:00:11
1700 -- [-27
1800 -- [-27
999000 -- (-26539.707) [-26522.163] (-26547.147) (-26548.942) * (-26534.987) (-26548.281) (-26546.160) [-26550.281] -- 0:00:10
1900 -- [-27
2000 -- [-27
Average standard deviation of split frequencies: 0.005402
Average stand 999100 -- (-26543.177) [-26517.502] (-26547.697) (-26546.545) * [-26522.247] (-26546.231) (-26548.351) (-26550.283) -- 0:00:09
999200 -- (-26534.871) [-26515.092] (-26555.376) (-26537.982) * [-26523.955] (-26546.769) (-26563.648) (-26543.853) -- 0:00:08
999300 -- (-26541.478) [-26512.130] (-26552.697) (-26532.226) * (-26523.747) [-26542.773] (-26562.142) (-26549.338) -- 0:00:07
999400 -- (-26538.384) (-26518.928) (-26555.241) [-26535.862] * [-26522.047] (-26546.667) (-26567.006) (-26543.911) -- 0:00:06
999500 -- (-26535.859) [-26519.030] (-26552.608) (-26540.379) * [-26522.902] (-26549.997) (-26562.522) (-26546.062) -- 0:00:05
999600 -- (-26532.493) (-26524.546) (-26545.202) [-26537.017] * [-26526.572] (-26552.777) (-26562.637) (-26544.703) -- 0:00:04
999700 -- [-26527.338] (-26528.291) (-26539.300) (-26530.230) * [-26526.252] (-26554.610) (-26563.025) (-26546.465) -- 0:00:03
999800 -- [-26532.021] (-26531.298) (-26542.708) (-26534.073) * [-26523.469] (-26553.909) (-26561.622) (-26544.778) -- 0:00:02
999900 -- (-26539.992) (-26532.001) (-26532.497) [-26530.797] * [-26529.949] (-26550.553) (-26559.568) (-26537.877) -- 0:00:01
1000000 -- (-26534.265) (-26533.214) (-26543.286) [-26531.268] * [-26523.106] (-26545.323) (-26554.454) (-26540.410) -- 0:00:00
Average standard deviation of split frequencies: 0.005449
Continue with analysis? (yes/no): no

```

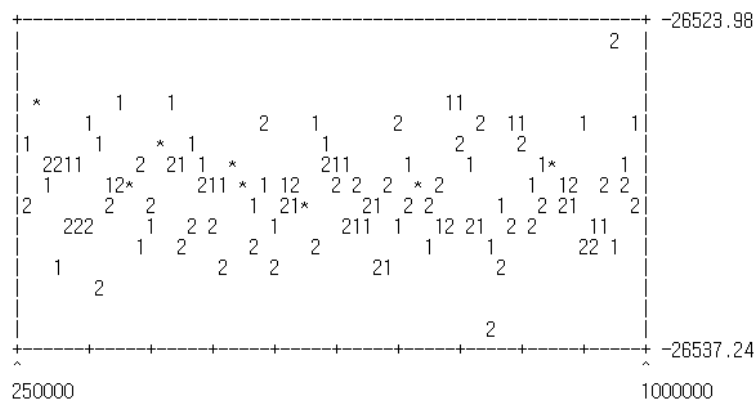

(16) Burn-in step의 비율을 적절히 설정하고 sump 명령을 실행한다. 텍스트 모드로 보여진 로그가능도 plot과 산술/조화 평균을 보면 1번,2번 run이 비슷한 듯 보인다. 보다 자세히는 Tracer 프로그램을 실행시켜 『*.p』파일을 열어보면 알 수 있다(18번 참조).

(17) Burn-in step의 비율을 적절히 설정하고 sumt 명령을 실행한다. 이는 tree를 summary 하는 명령어이다.

```
MrBayes > sump relburnin=yes burninfrac=0.25 ;
```

```
MrBayes > sumt relburnin=yes burninfrac=0.25 conformat=simple;
```

Overlay plot for both runs:
(1 = Run number 1; 2 = Run number 2; * = Both runs)



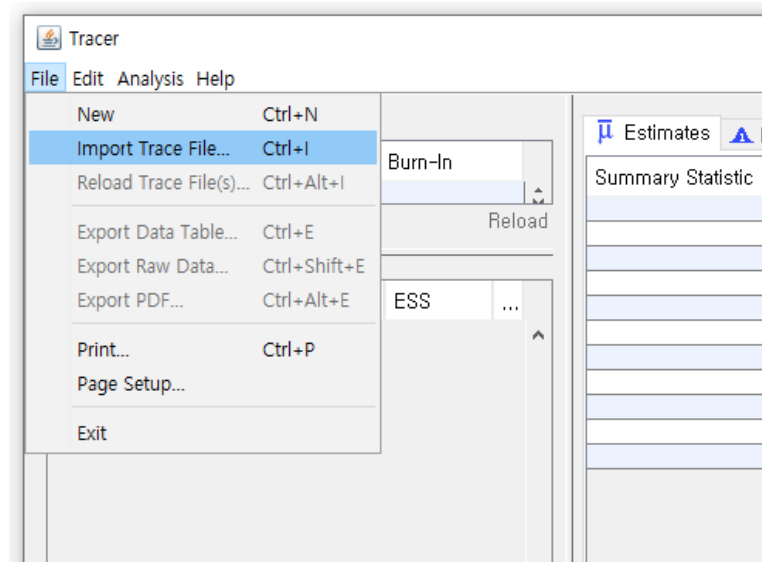
Overwriting file "cynmix.nex.lstat"

Estimated marginal likelihoods for runs sampled in files
"cynmix.nex.run1.p" and "cynmix.nex.run2.p":
(Use the harmonic mean for Bayes factor comparisons of models)

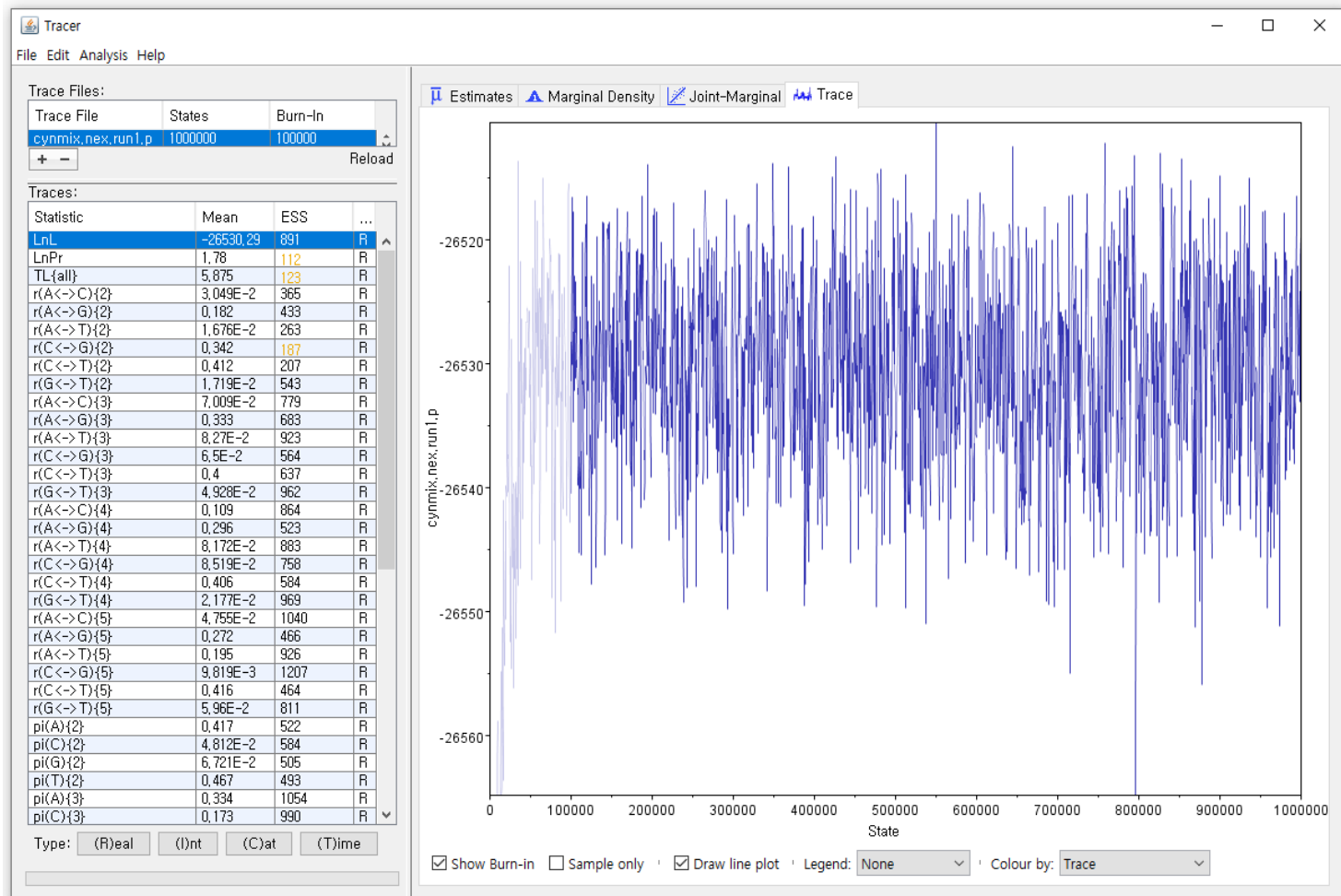
(Values are saved to the file cynmix.nex.lstat)

Run	Arithmetic mean	Harmonic mean
1	-26517.19	-26557.46
2	-26517.36	-26550.41
TOTAL	-26517.27	-26556.76

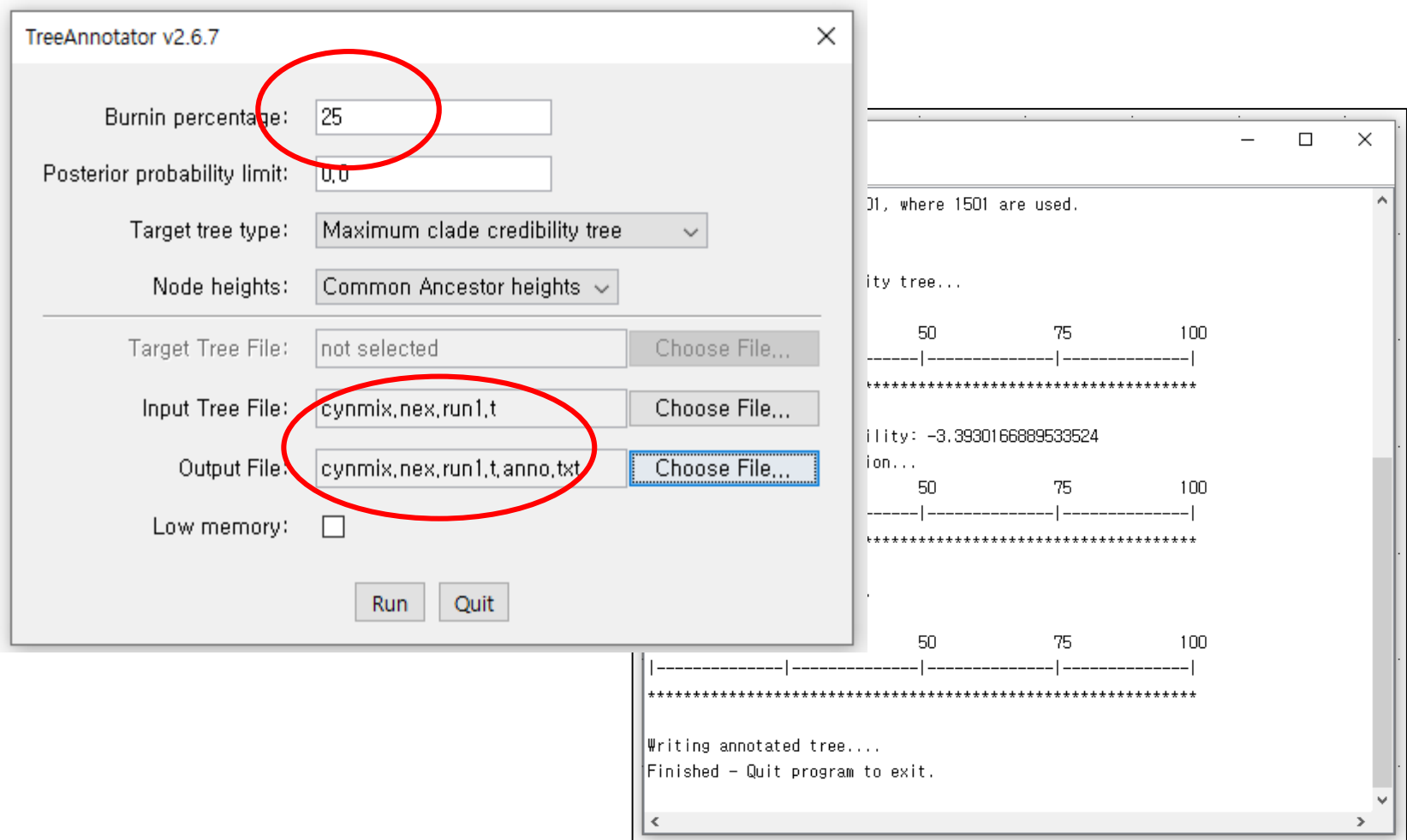
(18) Tracer 프로그램을 실행시켜
cynmix.nex.run1.p 파일을 연다



(18 계속) 왼쪽 패널에서 항목을 선택해서 오른쪽 패널에서 Trace 탭을 누른다. 비교적 랜덤한 패턴이 보이면 총세대수와 sampling interval이 적절하다고 볼 수 있다.
ESS(Effective Sample Size) 값은 일부 항목에서 다소 부족한 듯 보인다.



(19) sumt 명령어로 생성된 『*.t』 파일에는 사후분포로부터 샘플링된 개별적인 계통수가 저장되어 있다. 이를 이용하여 각 노드별 사후확률을 계산하기 위해서는 TreeAnnotator(BEAST 프로그램 패키지의 일부)의 실행이 필요하다. Burn-in 비율과 입출력 파일명을 적절히 선택하여 실행한다.



(참고) TreeAnnotator와 FigTree를 이용한 노드별 사후확률 확인

- (1) “figtree phylogeny”로 검색
- (2) 최신버전을 다운로드 및 FigTree***.exe 실행
 - (2-1) 자바가 설치되어 있지 않거나 오래된 버전이면 안내에 따라 최신 자바를 설치
- (3) File -> open선택하여 TreeAnnotator 로 생성한 파일 (cynmix.nex.run1.t.anno.txt)을 읽어 들임
- (4) 좌측패널에서 Trees/Order nodes(increasing)에 체크, Tree/Transform branches(cladogram)에 체크
- (5) 좌측패널에서 node label에 체크 display에 posterior 선택
- (6) 기타 폰트 사이즈를 적절히 조정. Root 노드의 위치를 적절히 조정.

