

# PyRate exercise

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## Step 1

Prep `Ursidae.txt` to be ready for PyRate by using `extract.ages()` in R utilities:

```
source("pyrate_utilities.r")
extract.ages("example_files/Ursidae.txt")
```

This creates `Ursidae_PyRate.py` in the `example_files/` directory.

## Step 2

Run PyRate on `Ursidae_PyRate.py`:

From PyRate folder in terminal, run the following line-

```
python PyRate.py example_files/Ursidae_PyRate.py
```

Sample output:

```
PyRate 0.600
20151024
```

```
Bayesian estimation of speciation and extinction
rates from fossil occurrence data
```

```
Daniele Silvestro, Jan Schnitzler et al.
pyrate.help@gmail.com
```

Using Gamma priors on the birth-death rates.

```
started at: Thu Oct 29 16:40:02 2015
```

```
initializing chain...
```

```
0* post: -2379.83 lik: -2371.41 prior: -8.42 tot length 209.96
```

```
1000 post: -1242.94 lik: -1234.47 (-862.71, -371.77) prior: -8.46 tot.l: 318.82 k: 2
t.frames: [ 23.748  0. ] (sp.)
t.frames: [ 23.748  0. ] (ex.)
sp.rates: [ 0.244]
ex.rates: [ 0.382]
q.rate: 0.697 Gamma.prm: 1.0
ts: [ 5.494  9.824  6.615  4.088  7.749] ...
te: [ 3.017  6.266  0.491  3.037  5.598] ...
```

### Step 3

After PyRate runs, inspect generated log files.

Output in *Ursidae\_1\_sum.txt*:

```
PyRate 0.600          build          20151024
input: ['example_files/Ursidae_PyRate.py'] output: example_files/pyrate_mcmc_logs/Ursidae_1
PyRate was called as follows:
Namespace(A=2, B=1, BF=[], M=10, N=None, S=1000, T=1.0, a=0.3, b=0, cite=False, d='', dpp_eK=2.0,
dpp_f=500, dpp_grid=1.5, dpp_hp=2.0, fR=1.0, fS=0.7, fU=[0.02, 0.18, 0], fixSE='', fixShift='',
input_data=['example_files/Ursidae_PyRate.py'], j=1, k=10, logT=2, mC=False, mCov=0, mG=False,
mHPP=False, mL=1, mM=1, mProb='', multiR=1, n=10000000, nT=5, ncat=4, out='', p=1000, pC=1,
pL=[1.1, 1.1], pM=[1.1, 1.1], pP=[1.5, 1.1], pS=2.5, plot='', r=1, s=1000, sw=100, t=0.03,
tC=[0.2, 0.2, 0.15], tQ=[1.2, 1.2], tR=1.2, tS=1.0, tT=1.0, tag='', thread=[0, 0], trait=1,
wd='')
```

*Ursidae\_1\_mcmc.log* is a table of MCMC posteriors, priors, likelihoods, and TE and TS for all taxa.

*Ursidae\_1\_marginal\_rates.log*: This file can be opened with Tracer (Figure 1). *Note: I am not really sure what to do with this Tracer output- how can we use this information to determine the appropriate number of burnins?* We can use this information to determine a reasonable burn-in (I will just assume 1000 for now- to be updated after session?), and then use the burnin estimate to create a plot of the logs.

### Step 4

Plotting from the *Ursidae\_1\_marginal\_rates.log*.

We can plot using this command:

```
python PyRate.py -plot ~/full/path/to/pyrate_mcmc_logs/Ursidae_1_marginal_rates.log -b 1000
```

*Note to self*- use full path; otherwise program threw an error.

This step creates two documents in the *pyrate\_mcmc\_logs* folder: the first is an R script (*Ursidae\_1\_marginal\_rates\_RTT.r*); the second is a pdf file made using the R code (*Ursidae\_1\_marginal\_rates\_RTT.pdf*; Figure 2). I kind of want to make a figure that includes both Sppn and Extn rates on the same plot so we can overlay... maybe another day!

From the plot of Speciation Rate over time, we see that the Ursids had experienced a high speciation rate c. 20 MYA; that speciation rate declined rapidly over 3-5 million years to a basal speciation rate. Over this time period, the extinction rate in the clade has remained at a relatively constant basal rate which is approximately equal to the basal speciation rate. There has been a slight upward trend in extinction rate since ~10 MYA. These two sum up to mean that Ursids experienced a rapid diversification from ~20 to ~17 MYA, after which diversity remained constant for ~10 million years. Since then, there has been a slight decline in diversity, as the upward trend of extinction rates has not been counteracted by any change in speciation rates.

We can use this command to test models of how many rates of speciation there have been (alt, how many rate switches there have been).

```
python PyRate.py -mProb ~/full/path/to/Ursidae_1_mcmc.log -b 1000
```

The output is as follows:

First 1000 samples excluded as burnin.

Model	Probability	
	Speciation	Extinction
1-rate	0.0122	0.6791

2-rate	0.645	0.2458
3-rate	0.2686	0.0619
4-rate	0.0631	0.0117
5-rate	0.0103	0.0014
6-rate	0.0008	0.0001

This suggests that a 2-rate model (i.e. one rate switch) is the most probable for speciation, and a 1-rate (i.e. no switch) model for extinction.

Figure 1: Ursidae mcmc log in Tracer

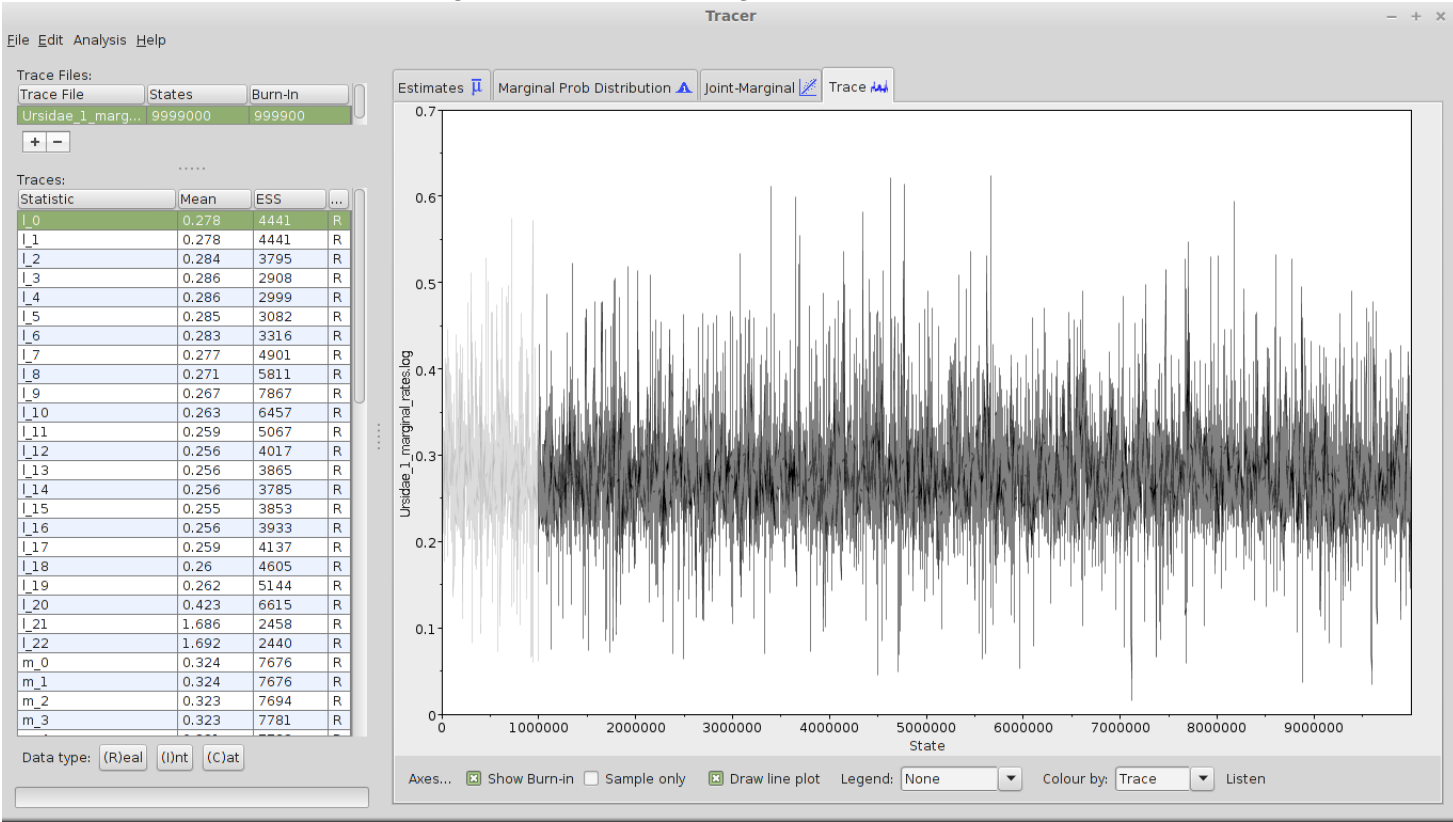


Figure 2: Plot of Sppn, Extn, and Diversification Rates from marginal rates file

