

Phylogenetic Inference using RevBayes

A Simple Binomial Model

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1 Overview

This very basic tutorial provides an introduction to Bayesian inference and Markov chain Monte Carlo (MCMC) algorithms. The tutorial explains the fundamental concepts of an MCMC algorithm, such as *moves* and *monitors*, which are ubiquitous in every other tutorial. After the tutorial you should be somewhat familiar with Bayesian inference (*e.g.*, what is a prior distribution, posterior distribution, and likelihood function) and MCMC simulation (*e.g.*, what are moves and monitors and why do we need them).

2 A Coin Flipping (Binomial) Model

We'll begin our exploration of Bayesian inference with a simple coin-flipping model. In this model, we imagine flipping a coin n times and count the number of heads, x ; each flip comes up heads with probability p . This model gives rise to the Binomial probability distribution, with parameters n and p :

$$P(x | n, p) = \binom{n}{x} p^x (1 - p)^{n-x}$$

Simple intuition suggests that, given that we observe x heads in n coin tosses, the maximum-likelihood estimate (MLE) of p is simply $\frac{x}{n}$: if we flip a coin 100 times and observe 70 heads, we assume the probability the coin comes up heads is $\frac{70}{100} = 0.7$. This is indeed the maximum likelihood estimate!

From Bayes' theorem, the *posterior distribution* of p given x , $P(p | x)$, is:

$$\underbrace{P(p | x)}_{\text{posterior distribution}} = \frac{\overbrace{P(x | p)}^{\text{likelihood}} \times \overbrace{P(p)}^{\text{prior}}}{\underbrace{P(x)}_{\text{marginal likelihood}}}$$

The take-home message here is that, if we're interested in doing Bayesian inference for the coin flipping model, we need to specify a *likelihood function* and a *prior distribution* for p . In virtually all practical cases, we cannot compute the posterior distribution directly and instead use numerical procedures, such as a Markov chain Monte Carlo (MCMC) algorithm. Therefore, we will also have to write an MCMC algorithm that samples parameter values in the frequency of their posterior probability.

We'll use a simple beta distribution as a prior on the parameter of the model, p . The beta distribution has two parameters, α and β (Figure 1). Different choices for α and β represent different prior beliefs.

Figure 2 shows the graphical model for the binomial model. This nicely visualizes the dependency structure in the model. We see that the two parameters α and β are drawn in solid squares, representing that these

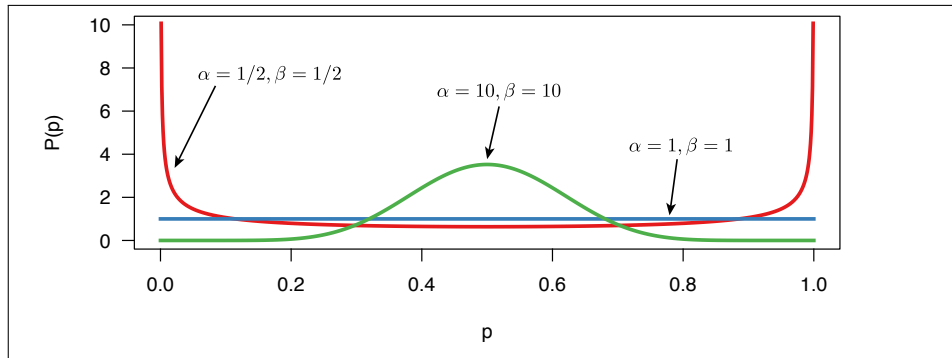


Figure 1: A beta distribution with two parameters, α and β . This distribution is used as a prior distribution on the probability parameter p of observing a head. Here we show different curves for the beta distribution when using different parameters.

variables are constant. From these two variables, we see arrows going into the variable p . That simply means that p depends on α and β . More specifically, p is a stochastic variable (shown as a solid circle) and drawn from a beta distribution with parameters α and β . Then, we have another constant variable, n . Finally, we have the observed data x which is drawn from a Binomial distribution with parameters p and n , as can be seen by the arrows going into x . Furthermore, the solid circle of x is shaded which means that the variable has data attached to it.

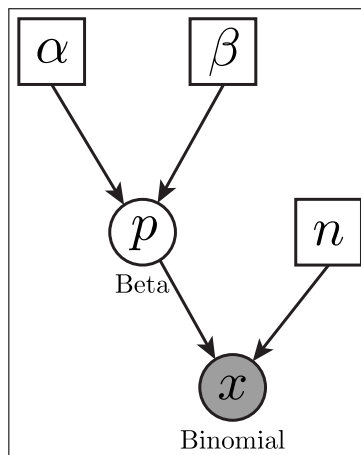


Figure 2: A graphical model for the binomial model.

3 Writing an MCMC from Scratch

3.1 The Metropolis-Hastings Algorithm

Though `RevBayes` implements efficient and easy-to-use Markov chain Monte Carlo algorithms, we'll begin by writing one ourselves to gain a better understanding of the moving parts. The Metropolis-Hastings MCMC algorithm ([Metropolis et al. 1953](#); ?) proceeds as follows:

1. Generate initial values for the parameters of the model (in this case, p).

2. Propose a new value (which we'll call p') for some parameters of the model, (possibly) based on their current values
3. Calculate the acceptance probability, R , according to:

$$R = \min \left\{ 1, \frac{P(x | p')}{P(x | p)} \times \frac{P(p')}{P(p)} \times \frac{q(p)}{q(p')} \right\}$$

4. Generate a uniform random number between 1 and 0. If it is less than R , accept the move (set $p = p'$). Otherwise, keep the current value of p .
5. Store the values of the parameters in
6. Return to step 2 many many times, keeping track of the value of p .

3.2 Reading in the data

Actually, in this case, we're just going to make up some data on the spot. Feel free to alter these values to see how they influence the posterior distribution

```
# Make up some coin flips!  
# Feel free to change these numbers  
n <- 100 # the number of flips  
x <- 63 # the number of heads
```

3.3 Initializing the Markov chain

We have to start the MCMC off with some initial parameter values. One way to do this is to randomly draw values of the parameter (just p , in this case) from the prior distribution. We'll assume a "flat" beta prior distribution; that is, one with parameters $\alpha = 1$ and $\beta = 1$.

```
# Initialize the chain with starting values  
alpha <- 1  
beta <- 1  
p <- rbeta(n=1,alpha,beta)[1]
```

3.3.1 Likelihood function

We also need to specify the likelihood function. We use the binomial probability for the likelihood function:

```
# specify the likelihood function  
function RealPos likelihood(p) {  
  l = dbinomial(x,p,n,log=false)  
  return l  
}
```

3.3.2 Prior distribution

Similarly, we need to specify a function for the prior distribution. Here, we use the beta probability distribution for the prior on p :

```
# specify the prior function
function RealPos prior(p) {
  pp = dbeta(p,alpha,beta,log=false)
  return pp
}
```

3.3.3 Monitoring parameter values

Additionally, we are going to monitor, *i.e.*, store, parameter values into a file during the MCMC simulation. For this file we need to write the column headers:

```
# Prepare a file to log our samples
write("iteration","p","\n",file="binomial_MH.log")
write(0,p,"\n",file="binomial_MH.log",append=TRUE)
```

(You may have to change the newline characters to `"\r\n"` if you're using a Windows operating system.)

3.4 Writing the MH Algorithm

At long last, we can write our MCMC algorithm. First, let us define the frequency how often we print to file (*i.e.*, monitor), which is also often called thinning. If we set the variable `printgen` to 1, then we will store the parameter values every single iteration; if we choose `clprintgen=10` instead, then only every 10th iteration.

```
printgen = 10
```

We will repeat this resampling procedure many times (here, 10000), and iterate the MCMC using a `for` loop:

```
# Write the MH algorithm
reps = 10000
for(rep in 1:reps){
```

(remember to close your `for` loop at the end).

The first thing we do in the first generation is generate a new value of p' to evaluate. We'll propose a new value of p from a uniform distribution between 0 and 1. Note that in this first example we do not condition new parameter values on the current value.

```
# Propose a new value of p
p_prime <- runif(n=1,0.0,1.0)[1]
```

Next, we compute the proposed likelihood and prior probabilities, as well as the acceptance probability, R :

```
# Compute the acceptance probability
R <- ( likelihood(p_prime) / likelihood(p) ) * ( prior(p_prime) / prior(p) )
```

Then, we accept the proposal with probability R and reject otherwise:

```
# Accept or reject the proposal
u <- runif(1,0,1)[1]
if(u < R){
  # Accept the proposal
  p <- p_prime
}
```

Finally, we store the current value of p in our log file. Here, we actually check if we want to store the value during this iteration.

```
if ( (rep % printgen) == 0 ) {
  # Write the samples to a file
  write(rep,p,"\n",file="binomial_MH.log",append=TRUE)
}
} # end MCMC
```

3.5 Exercise 1

Write and execute this script (there is also an example file called *Binomial_MH_algorithm.Rev*). The `.log` file will contain samples from the posterior distribution of the model! We can open the file in **Tracer** to learn about various features of the posterior distribution, for example: the posterior mean or the 95% credible interval. Pretty awesome, right?

Below we show an example of the obtained output in **Tracer**. Specifically, Figure 3 shows the sample trace (left) and the estimated posterior distribution of p (right). There are other parameters, such as the posterior mean and the 95% HPD (highest posterior density) interval, that you can obtain from **Tracer**.

4 More on Moves: Tuning and weights

In the previous example we hard coded a single move updating the variable p by drawing a new value from a `uniform(0,1)` distribution. There are actually many other ways how to propose new values; some of which are more efficient than others.

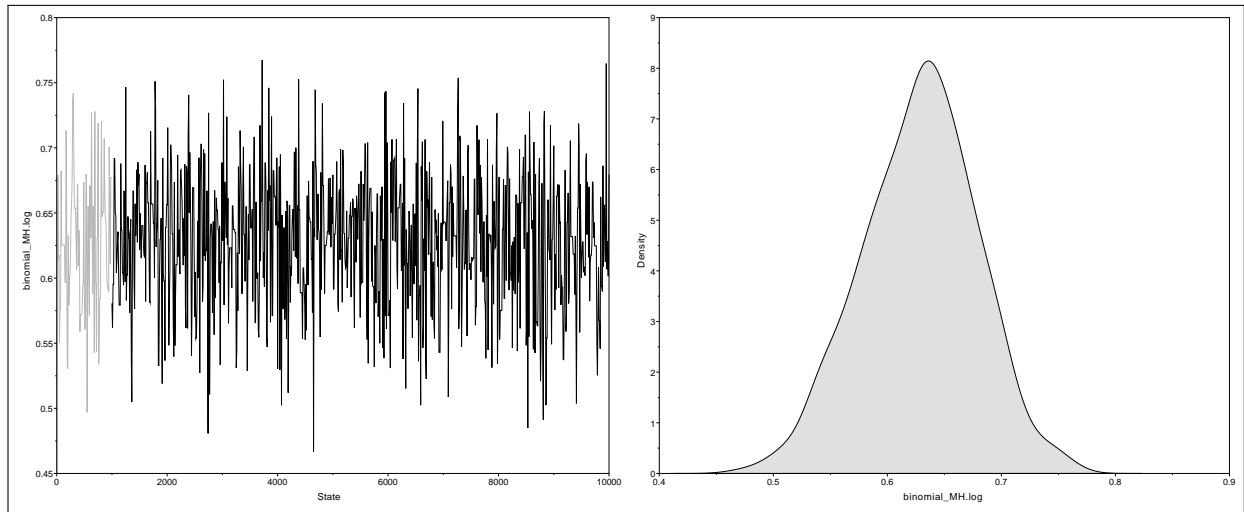


Figure 3: Left: The *Trace* of sample from an MCMC simulation. Right: The approximated posterior probability distribution for p .

First, let us rewrite the MCMC loop so that we use instead a function, which we call `move_uniform` for simplicity, that performs the move:

```
for (rep in 1:reps){

  # call uniform move
  move_uniform(1)

  if ( (rep % printgen) == 0 ) {
    # Write the samples to a file
    write(rep,p,"\n",file="binomial_MH.log",append=TRUE)
  }

} # end MCMC
```

This loop looks already much cleaner.

4.1 Uniform move

Now we need to actually write the `move_uniform` function. We mostly just copy the code we had before into a dedicated function

```
function move_uniform( Natural weight) {

  for (i in 1:weight) {
    # Propose a new value of p
    p_prime <- runif(n=1,0.0,1.0)[1]
```

```
# Compute the acceptance probability
R <- ( likelihood(p_prime) / likelihood(p) ) * ( prior(p_prime) / prior(p) )

# Accept or reject the proposal
u <- runif(1,0,1)[1]
if (u < R){
  # Accept the proposal
  p <- p_prime
} else {
  # Reject the proposal
  # (we don't have to do anything here)
}
}
```

There are a few things to consider in the function `move_uniform`. First, we do not have a return value because the move simply change the variable p if the move is accepted. Second, we expect an argument called `weight` which will tell us how often we want to use this move. Otherwise, this function does exactly the same what was inside the for loop previously.

(Note that you need to define this function before the for loop in your script).

4.2 Sliding-window move

As a second move we will write a sliding-window move. The sliding-window moves propose an update by drawing a random number from a normal distribution and then adds this random number to the current value (*i.e.*, centered on the previous value).

```
function move_slide( RealPos delta, Natural weight) {

  for (i in 1:weight) {
    # Propose a new value of p
    p_prime <- p + rnormal(n=1,0.0,delta)[1]

    # Compute the acceptance probability
    R <- ( likelihood(p_prime) / likelihood(p) ) * ( prior(p_prime) / prior(p) )

    # Accept or reject the proposal
    u <- runif(1,0,1)[1]
    if (u < R) {
      # Accept the proposal
      p <- p_prime
    } else {
      # Reject the proposal
      # (we don't have to do anything here)
    }
  }
}
```

```

    }
  }
}
```

This move has another argument, **delta**, additionally to the weight of the move. The argument **delta** defines the standard deviation of the normal distribution from which we draw new values. Thus, if **delta** is large, then the proposed values are more likely to be very different from the current value of p . Conversely, if **delta** is small, then the proposed values are more likely to be very close to the current value of p .

→ Experiment with different values for **delta** and check how the effective sample size (ESS) changes.

There is, a priori, no good method on knowing what values of **delta** are most efficient. However, there are some algorithms implemented in **RevBayes**, called *auto-tuning*, that will estimate good values for **delta**.

Note that you could, in principle, use other distributions instead of the normal distribution too. For example, a `uniform(-delta,delta)` distribution would be similarly applicable.

4.2.1 Reflecting proposal

One thing we have to be careful about is making sure p (being a probability) stays between 0 and 1. We can do that by reflecting any proposals outside of that region back into the valid region. (One of the nice things about the real MCMC algorithms implemented in **RevBayes** is that it takes care of this for us).

```

if (p_prime < 0) {
  p_prime <- abs(p_prime)
} else if (p_prime > 1) {
  p_prime <- 2 - p_prime
}
```

However, this reflection procedure would have to be repeated until the values fall inside the acceptable range. Another alternative, as implicitly used here, is that the prior and/or likelihood will return *nan* if the parameter values are outside the allowed range. There are just more rejected, and thus wasted, proposal.

4.3 Scaling move

As a third and final move we will write a scaling move. The scaling move proposes an update by drawing a random number from a `uniform(-0.5,0.5)` distribution, exponentiates the random number, and then multiplies this scaling factor to the current value. An interesting feature of this move is that it is not symmetrical and thus needs a Hastings ratio. The Hastings ratio is rather trivial in this case and one only needs to multiply the scaling factor to the acceptance rate.


```
function move_scale( RealPos lambda, Natural weight) {

  for (i in 1:weight) {
    # Propose a new value of p
    sf <- exp( lambda * ( runif(n=1,0,1) - 0.5 ) )
    p_prime <- p * sf

    # Compute the acceptance probability
    R <- ( likelihood(p_prime) / likelihood(p) ) * ( prior(p_prime) / prior(p) ) *
      sf

    # Accept or reject the proposal
    u <- runif(1,0,1)[1]
    if (u < R){
      # Accept the proposal
      p <- p_prime
    } else {
      # Reject the proposal
      # (we don't have to do anything here)
    }
  }
}
```

As before, this move has a tuning parameter called *lambda*.

The sliding-window and scaling moves are very common and popular moves in **RevBayes**. The code examples here are actually showing the exact same equation as implemented internally, with some minor performance difference. It will be very useful if you understand these moves.

4.4 Exercise 2

Rewrite your previous script to include these three different moves now. Then, run the script to estimate the posterior distribution of p again. Look at the output in **Tracer**. Are the distributions, mean and credible interval the same? Did the ESS change?

→ Add to each move a counter variable that counts how often the move was accepted. For example:

```
if (u < R){
  # Accept the proposal
  p <- p_prime
  ++num_sliding_move_accepted
}
```

Have a look at how the acceptance rate changes for different values of the tuning parameters.

However, this MCMC algorithm is *very* specific to our binomial model and thus hard to extend (also it's pretty inefficient!).

5 The Metropolis-Hastings Algorithm with the *Real* RevBayes

We'll now specify the exact same model in **Rev** using the built-in modeling functionality. It turns out that the **Rev** code to specify the above model is extremely simple. Again, we start by “reading in” (*i.e.*, making up) our data.

```
# Make up some coin flips!
# Feel free to change these numbers
n <- 100 # the number of flips
x <- 63 # the number of heads
```

Now we specify our prior model.

```
# Specify the prior distribution
alpha <- 1
beta <- 1
p ~ dnBeta(alpha,beta)
```

One difference between **RevBayes** and the MH algorithm that we wrote above is that many MCMC proposals are already built-in, but we have to specify them *before* we run the MCMC. We usually define (at least) one move per parameter immediately after we specify the prior distribution for that parameter.

```
# Define a move for our parameter, p
moves[1] = mvSlide(p,delta=0.1)
```

Next, our likelihood model.

```
# Specify the likelihood model
k ~ dnBinomial(p, n)
k.clamp(x)
```

We wrap our full Bayesian model into one model object (this is a convenience to keep the entire model in a single object, and is more useful when we have very large models):

```
# Construct the full model
my_model = model(p)
```

We use “monitors” to keep track of parameters throughout the MCMC. The two kinds of monitors we use here are the `mnModel`, which writes parameters to a specified file, and the `mnScreen`, which simply outputs some parts of the model to screen (as a sort of progress bar).

```
# Make the monitors to keep track of the MCMC
monitors[1] = mnModel(filename="binomial_MCMC.log", printgen=10, separator = TAB)
monitors[2] = mnScreen(printgen=100, p)
```

Finally, we assemble the analysis object (which contains the model, the monitors and the moves), and execute the run using the `.run` command:

```
# Make the analysis object
analysis = mcmc(my_model, monitors, moves)

# Run the MCMC
analysis.run(100000)
```

Open the resulting `binomial_MCMC.log` file in **Tracer**. Do the posterior distributions for the parameter p look the same as the ones we got from our first analysis?

Hopefully, you’ll note that this **Rev** model is substantially simpler and easier to read than the MH algorithm script we began with. Perhaps more importantly, this **Rev** analysis is *orders of magnitude* faster than our own script, because it makes use of extremely efficient probability calculations built-in to **RevBayes** (rather than the ones we hacked together in our own algorithm).

5.1 Exercise

Play around with various parts of the model to develop on intuition for both the Bayesian model and the MCMC algorithm. For example, how does the posterior distribution change as you increase the number of coin flips (say, increase both the number of flips and the number of heads by an order of magnitude)? How does the estimated posterior distribution change if you change the prior model parameters, α and β (*i.e.*, is the model prior sensitive)? Does the prior sensitivity depend on the sample size? Are the posterior estimates sensitive to the length of the MCMC? Do you think this MCMC has been run sufficiently long, or should you run it longer?

References

Metropolis, N., A. Rosenbluth, M. Rosenbluth, A. Teller, and E. Teller. 1953. Equation of State Calculations by Fast Computing Machines. *Journal of Chemical Physics* 21:1087–1092.

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