

# Markov Chain Monte Carlo

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# Markov Chain Monte Carlo

- This class introduces estimation of posterior probability distributions using a stochastic process known as **Markov chain Monte Carlo** (MCMC).
- Here we'll produce samples from the joint posterior without maximizing anything.
- We will be able to sample directly from the posterior without assuming a Gaussian, or any other, shape.
- The cost of this power is that it may take much longer for our estimation to complete.
- But the benefit is escaping multivariate normality assumption of the Laplace approximation.
- More advanced models such as the generalized linear and multilevel models tend to produce non-Gaussian posterior distributions.
- In most cases they cannot be estimated at all with the techniques of earlier classes.
- This class is based on Chapter 9 of [McElreath, 2020] and Chapter 7 of [Kruschke, 2014].

# Markov Chain Monte Carlo

- The essence of MCMC is to produce samples from the posterior  $f(\theta|d)$  by only accessing a function that is proportional to it.
- This proportional function is the product of the likelihood and the prior  $f(d|\theta) * f(\theta)$ , which is always available in a Bayesian model.
- So, merely by evaluating  $f(d|\theta) * f(\theta)$ , without normalizing it by  $f(d)$ , MCMC allows us to generate random representative values from the posterior distribution.
- This property is wonderful because the method obviates direct computation of the evidence  $f(d)$ , which, as you'll recall, is one of the most difficult aspects of Bayesian inference.
- It has only been with the development of MCMC algorithms and software that Bayesian inference is applicable to complex data analysis.
- And it has only been with the production of fast and cheap computer hardware that Bayesian inference is accessible to a wide audience.
- The question then becomes this: How does MCMC work? For an answer, let's ask a politician.

# A politician stumbles upon the Metropolis algorithm

- Suppose an elected politician lives on a long chain of islands.
- He is constantly traveling from island to island, wanting to stay in the public eye.
- At the end of a day he has to decide whether to:
  - 1 stay on the current island
  - 2 move to the adjacent island to the left
  - 3 move to the adjacent island to right
- His goal is to visit all the islands **proportionally** to their **relative population**.
- But, he doesn't know the total population of all the islands.
- He only knows the population of the current island where he is located.
- He can also ask about the population of an adjacent island to which he plans to move.

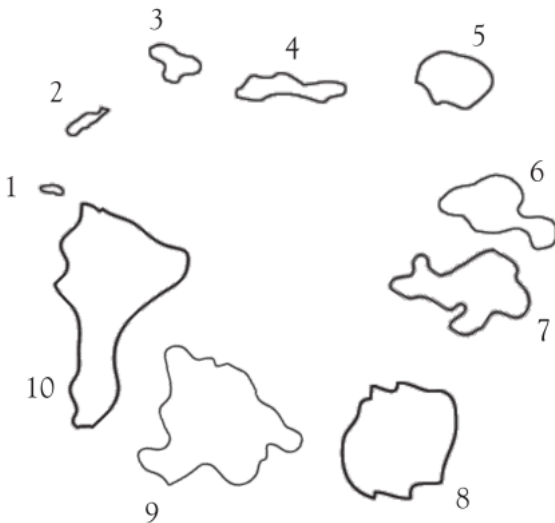
# The Metropolis algorithm

- The politician has a simple heuristic for travelling accross the islands called the **Metropolis** algorithm [Metropolis et al., 1953].
- First, he flips a (fair) coin to decide whether to propose the adjacent island to the left or the adjacent island to the right.
- If the proposed island has a larger population than the current island ( $P_{proposed} > P_{current}$ ), then he goes to the proposed island.
- If the proposed island has a smaller population than the current island ( $P_{proposed} < P_{current}$ ), then he goes to the proposed island with probability  $p_{move} = P_{proposed} / P_{current}$ .
- In the long run, the probability that the politician is on any one of the islands exactly matches the relative population of the island!

# The Metropolis algorithm

- Let's analyze the Metropolis algorithm in more detail.
- Suppose there are 10 islands in total.
- Each island is neighbored by two others, and the entire archipelago forms a ring.
- The islands are of different sizes, and so had different sized populations living on them.
- The second island is twice as populous as the first, the third three times as populous as the first.
- And so on, up to the largest island, which is 10 times as populous as the smallest.

# The Metropolis algorithm



# The Metropolis algorithm

- We are going to show an implementation of this algorithm in R.
- But before that, we will combine the two possibilities for the probability of moving into a single expression: the proposed island having a 1) higher or 2) lower population than the current island.

$$p_{\text{move}} = \min(1, P_{\text{proposed}}/P_{\text{current}}). \quad (1)$$

- So, if  $P_{\text{proposed}} > P_{\text{current}}$ ,  $P_{\text{proposed}}/P_{\text{current}} > 1$  and  $p_{\text{move}} = 1$ .
- For example,  $\text{current} = 4$  and  $\text{proposed} = 5$ ,  $5/4 > 1$  so we move to the proposed island (with probability 1).
- On the other hand, if  $P_{\text{proposed}} < P_{\text{current}}$ ,  $P_{\text{proposed}}/P_{\text{current}} < 1$ , and  $p_{\text{move}} = P_{\text{proposed}}/P_{\text{current}}$ .
- For example,  $\text{current} = 4$  and  $\text{proposed} = 3$ ,  $3/4 < 1$  so we move to the proposed island with probability  $3/4$ .

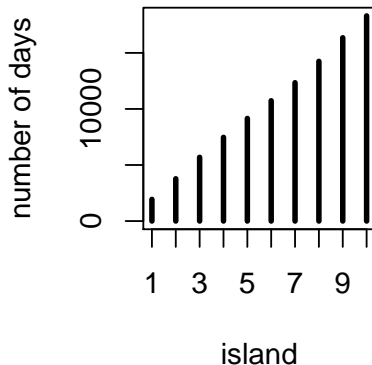


# The Metropolis algorithm

```
num_days <- 1e5
positions <- rep(0,num_days)
current <- 10
for ( i in 1:num_days ) {
  # record current position
  positions[i] <- current
  # flip coin to generate proposal
  proposal <- current + sample( c(-1,1) , size=1 )
  # now make sure he loops around the archipelago
  if ( proposal < 1 ) proposal <- 10
  if ( proposal > 10 ) proposal <- 1
  # move?
  prob_move <- min(proposal/current,1)
  decision <- rbinom(1,1,prob_move)
  current <- ifelse( decision == 1 , proposal , current )
}

library(rethinking)
simplehist(positions,xlab="island",ylab="number of days")
```

# The Metropolis algorithm



The time spent on each island is proportional to its population size.

# The Metropolis algorithm

- The first three lines of the method just define the number of days to simulate, an empty history vector, and a starting island position (the biggest island, number 10).
- Then the for loop steps through the days.
- Each day, it records the politician's current position.
- Then it simulates a coin flip to nominate a proposal island.
- The only trick here lies in making sure that a proposal of "11" loops around to island 1 and a proposal of "0" loops around to island 10.
- Finally, a random binary number is generated with a Bernoulli distribution (Binomial with 1 trial) with probability of success (or moving) =  $\min(1, P_{proposed} / P_{current})$ .
- If this random number is 1 we move, otherwise we stay.

# The Metropolis algorithm

- In real applications, the goal is not to help a politician, but instead to draw samples from an unknown and usually complex posterior probability distribution.
- The “islands” in our objective are parameter values  $\theta$ , and they need not be discrete, but can instead take on a continuous range of values as usual.
- The “population sizes” in our objective are the posterior probabilities (or densities) at each parameter value:  $f(\theta|d)$
- The “days” in our objective are samples taken from the posterior distribution.
- The Metropolis algorithm will eventually give us a collection of samples from the posterior.
- We can then use these samples just like all the samples we have already used in this course.

# Why it works

- Now, let's try to understand why the algorithm works.
- Consider two adjacent positions and the probabilities of moving from one to the other.
- We'll see that the relative transition probabilities, between adjacent positions, exactly match the relative values of the target distribution.
- Extrapolate that result across all the positions, and you can see that, in the long run, each position will be visited proportionally to its target value.
- Suppose we are at position  $\theta$ .
- The probability of moving to  $\theta + 1$ , denoted  $P(\theta \rightarrow \theta + 1)$ , is the probability of proposing that move times the probability of accepting it if proposed, which is:

$$P(\theta \rightarrow \theta + 1) = 0.5 \times \min(P(\theta + 1)/P(\theta), 1)$$

# Why it works

- On the other hand, if we are presently at position  $\theta + 1$ , the probability of moving to  $\theta$  is:

$$P(\theta + 1 \rightarrow \theta) = 0.5 \times \min(P(\theta)/P(\theta + 1), 1)$$

- The ratio of the transition probabilities is:

$$\begin{aligned}\frac{p(\theta \rightarrow \theta + 1)}{p(\theta + 1 \rightarrow \theta)} &= \frac{0.5 \min(P(\theta + 1)/P(\theta), 1)}{0.5 \min(P(\theta)/P(\theta + 1), 1)} \\ &= \begin{cases} \frac{1}{P(\theta)/P(\theta + 1)} & \text{if } P(\theta + 1) > P(\theta) \\ \frac{P(\theta + 1)/P(\theta)}{1} & \text{if } P(\theta + 1) < P(\theta) \end{cases} \\ &= \frac{P(\theta + 1)}{P(\theta)}\end{aligned}$$

# Why it works

- The last equation tells us that during transitions back and forth between adjacent positions, the relative probability of the transitions exactly matches the relative values of the target distribution.
- That might be enough to get the intuition that, in the long run, adjacent positions will be visited proportionally to their relative values in the target distribution.
- If that's true for adjacent positions, then, by extrapolating from one position to the next, it must be true for the whole range of positions.
- In more mathematical terms, this means that the transition probabilities form a Markov chain that has the target distribution as its equilibrium or stationary distribution. [Wikipedia, 2021]
- Hence, one can obtain a sample of the desired distribution by recording states from the chain.

# The Metropolis Algorithm more Generally

- So far, we have only considered the case with a single discrete parameter  $\theta$  that can only move to the left or right.
- The general Metropolis algorithm allows working with multiple continuous parameters  $\theta_1, \theta_2, \dots, \theta_n$  and more general proposal distributions.
- The essentials of the general method are the same as for the simple case.
- First, we have some target distribution  $P(\theta)$  ( $\theta$  can be a vector of parameters) from which we would like to generate representative sample values.
- We must be able to compute the value of  $P(\theta)$  for any candidate value of  $\theta$ .
- The distribution,  $P(\theta)$ , does not have to be normalized, however.
- Just needs needs to be nonnegative.



# The Metropolis Algorithm more Generally

- In our Bayesian inference application  $P(\theta)$  is the unnormalized posterior distribution on  $\theta$ , which is the product of the likelihood and the prior:  $f(d|\theta) * f(\theta)$ .
- This is a very important property of MCMC, as it allows us to draw samples from the posterior without having to calculate the evidence  $f(d)$ .
- Sample values from the target distribution are generated by taking a random walk through the parameter space.
- Proposal distributions can take many different forms, the goal being to use a proposal distribution that efficiently explores the regions of the parameter space where  $P(\theta)$  has most of its probability area.
- The generic case is using a Gaussian distribution centered at the current position.
- So the proposed move will typically be near the current position, with the probability of proposing a more distant position dropping off according to the normal curve.
- For multivariate target distributions, we can use a Multi-variate Gaussian to propose multi-dimensional points in each step.

# Gibbs Sampling

- The Metropolis algorithm works whenever the probability of proposing a jump to B from A is equal to the probability of proposing A from B, when the proposal distribution is symmetric (such as a Gaussian distribution).
- There is a more general method, known as Metropolis-Hastings, that allows asymmetric proposals.
- This would mean, that the politician's coin were biased to lead him clockwise on average.
- Asymmetric proposal distributions allows us to explore the posterior distribution more efficiently (i.e., acquire a good image of the posterior distribution in fewer steps).
- Gibbs sampling is a variant of the Metropolis-Hastings algorithm that uses clever proposals and is therefore more efficient.
- The improvement arises from adaptive proposals in which the distribution of proposed parameter values adjusts itself intelligently, depending upon the parameter values at the moment.

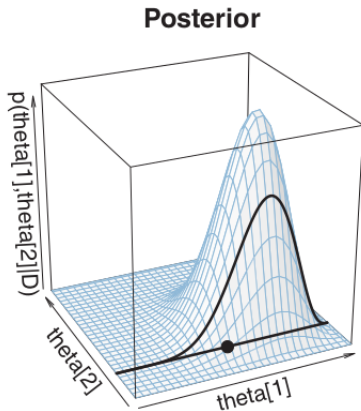
# Gibbs Sampling

- How Gibbs sampling computes these adaptive proposals depends upon using conjugate combinations of priors and likelihoods (such as the Beta and the Binomial).
- As previously presented, conjugate combinations have analytical solutions for the posterior distribution of an individual parameter.
- And these solutions are what allow Gibbs sampling to make smart jumps around the joint posterior distribution of all parameters.
- The algorithm works as follows:
- At each point in the walk, the parameters are selected in an iterative cycle:  
 $\theta_1, \theta_2, \theta_3, \dots \theta_1, \theta_2, \theta_3, \dots$
- Suppose that parameter  $\theta_i$  has been selected.
- Gibbs sampling then chooses a new value for that parameter by generating a random value directly from the conditional probability distribution of that parameter given all the others and  $d$ :

$$f(\theta_i | \theta_1, \dots, \theta_{i-1}, \theta_{i+1}, \dots, \theta_n, d)$$

# Gibbs Sampling

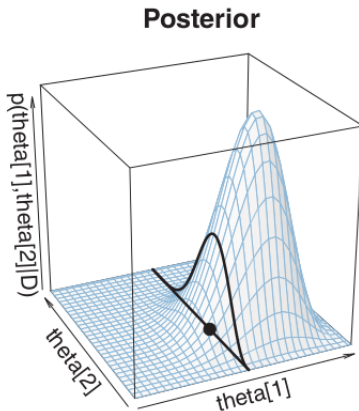
- Since we are using conjugate combinations, this conditional distribution has a closed form that facilitates the sampling of random numbers from it.
- The new value for  $\theta_j$ , combined with the unchanged values of  $\theta_1, \dots, \theta_{j-1}, \theta_{j+1}, \dots, \theta_n$ , constitutes the new position in the random walk.
- The process then repeats: select the next parameter  $\theta_{j+1}$  and select a new value for that parameter from its conditional posterior distribution.
- Let's illustrate this process for a two-parameter example:  $\theta_1, \theta_2$ .
- In the first step, we want to select a new value for  $\theta_1$ .
- We conditionalize on the values of all the other parameters from the previous step in the chain.
- In this example, there is only one other parameter, namely  $\theta_2$ .



- The figure shows a slice through the joint distribution at the current value of  $\theta_2$ .
- The heavy curve is the posterior distribution conditional on this value of  $\theta_2$ , which is  $f(\theta_1 | \theta_2, d)$  in this case because there is only one other parameter.

# Gibbs Sampling

- Because we are using conjugate distributions a computer can directly generate a random value of  $\theta_1$  from  $f(\theta_1|\theta_2, d)$ .
- Having generated a new value for  $\theta_1$ , we then conditionalize on it and determine the conditional distribution of the next parameter,  $\theta_2$  using  $f(\theta_2|\theta_1, d)$  as shown below:



- We generate a new value of  $\theta_2$ , and the cycle repeats.

# Gibbs Sampling

- Because the proposal distribution exactly mirrors the posterior probability for that parameter, the proposed move is always accepted.
- Hence, the algorithm is more efficient than the standard Metropolis algorithm in which proposals are rejected in many cases.
- But there are some limitations to Gibbs sampling.
- First, there are cases when we don't want to use conjugate priors.
- Second, it can become inefficient with complex models containing hundreds, thousands or tens of thousands of parameters.

# Hamiltonian Monte Carlo

- The Metropolis algorithm and Gibbs sampling are both highly random procedures.
- They try out new parameter values and see how good they are, compared to the current values.
- But Gibbs sampling gains efficiency by reducing this randomness and exploiting knowledge of the target distribution.
- Hamiltonian Monte Carlo (or Hybrid Monte Carlo, HMC) is another sampling method that is much more computationally costly than the others but its proposals are much more efficient.
- As a result, it doesn't need as many samples to describe the posterior distribution.
- And as models become more complex (thousands or tens of thousands of parameters) HMC can really outshine other algorithms.



# Hamiltonian Monte Carlo

- HMC is a very complex algorithm and we won't get into the details of its inner workings
- Let's try to understand it in a very superficial way by using again the politician's tale.
- Suppose the politician has moved to the mainland now.
- Now, instead of moving over a set of discrete islands, it has to move through a continuous territory stretched out along a narrow valley, running north-south.
- The obligations are the same: to visit his citizens in proportion to their local density.
- And again, the politician doesn't know the population of each area in advance.

# Hamiltonian Monte Carlo

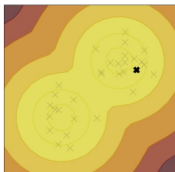
- The strategy of the politician is the following:
- He drives his car across the narrow valley back and forth along its length.
- In order to spend more time in densely settled areas, he slows down his vehicle when houses grow more dense.
- Likewise, he speeds up when houses grow more sparse.
- This strategy requires knowing how quickly population density is changing, at their current location.
- But it doesn't require remembering where they've been or knowing the population distribution anywhere else.
- This story is analogous to how Hamiltonian Monte Carlo works.

# Hamiltonian Monte Carlo

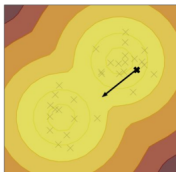
- In statistical applications, the politician's vehicle is the current vector of parameter values.
- HMC really does run a physics simulation, pretending the vector of parameters gives the position of a little frictionless particle.
- The log-posterior provides a surface for this particle to glide across.
- Then the job is to sweep across this surface, adjusting speed (momentum) in proportion to how high up we are.
- When the log-posterior is very flat, then the particle can glide for a long time before the slope (gradient) makes it turn around.
- When instead the log-posterior is very steep, then the particle doesn't get far before turning around.

# Hamiltonian Monte Carlo

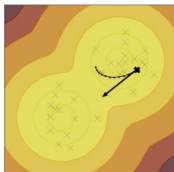
start at prev. sample



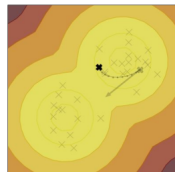
random momentum



simulate dynamics



accept / reject



source: [Izmailov et al., 2021]

# Hamiltonian Monte Carlo

- A big limitation of HMC is that it needs to be tuned to a particular model and its data.
- Stan<sup>1</sup> is a very popular platform for statistical modeling and high-performance statistical computation.
- Stan automates much of that tuning.
- Next, we will see how to use Stan to fit a linear model with an interaction.
- Make sure that the **rstan** package is installed to access Stan from within R.



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<sup>1</sup><https://mc-stan.org/>

- Stan provides its own language to declare models.
- The rethinking package provides a convenient interface, **ulam**, to compile lists of formulas, like the lists we've been using so far to construct quap estimates, into Stan HMC code.
- All that ulam does is translate formulas into Stan models, and then Stan defines the sampler and does the hard part.
- Stan models look very similar, but require some more explicit definitions.
- We will show them later.
- Before using ulam we must preprocess any variable transformations (log, exp, etc).
- We also must construct a clean data list with only the variables we will use.

# A model of ruggedness

- We are going to work with the **rugged** dataset from the rethinking package.
- Each row in these data is a country, and the various columns are economic, geographic, and historical features.
- The variable rugged is a Terrain Ruggedness Index that quantifies the topographic heterogeneity of a landscape.
- The outcome variable of our regression model will be the logarithm of real gross domestic product per capita, from the year 2000, **rgdppc\_2000**.
- Ruggedness is usually associated with poorer countries, in most of the world.
- Rugged terrain usually means transport is difficult, which means market access is hampered, which means reduced gross domestic product.
- However, this association is not valid for African countries.

# A model of ruggedness

- Let's load and explore the data:

```
library(rethinking)
data(rugged)
d <- rugged
d$log_gdp <- log(d$rgdppc_2000)
#remove rows with missing values
dd <- d[ complete.cases(d$rgdppc_2000) , ]
# discard columns we are not going to use
dd.trim <- dd[ , c("log_gdp","rugged","cont_africa") ]
summary(dd.trim)
```

```
> summary(dd.trim)
```

log_gdp	rugged	cont_africa
Min. : 6.146	Min. : 0.0030	Min. : 0.0000
1st Qu.: 7.539	1st Qu.: 0.4422	1st Qu.: 0.0000
Median : 8.578	Median : 0.9795	Median : 0.0000
Mean : 8.517	Mean : 1.3332	Mean : 0.2882
3rd Qu.: 9.480	3rd Qu.: 1.9572	3rd Qu.: 1.0000
Max. : 10.965	Max. : 6.2020	Max. : 1.0000

- Note that we do not convert `cont_africa` into a factor because that produces numerical problems with the rethinking methods.



# A model of ruggedness

- We end up with a `data.frame` formed by the countries as rows and the following 3 columns:
  - 1 `log_gdp`: the log GDP of the country in year 2000.
  - 2 `rugged`: the Terrain Ruggedness Index of the country
  - 3 `cont_africa`: a binary variable (1 for African countries and 0 for non-African ones).

- Let's compute the correlation between `log_gdp` and `rugged`:

```
> cor(dd.trim$rugged, dd.trim$log_gdp)
[1] 0.002833496
```

- It is very low. Now let's calculate them separately for African and non-African countries:

```
> dd.A<-dd.trim[dd.trim$cont_africa==1,]
> cor(dd.A$rugged, dd.A$log_gdp)
[1] 0.2607532
>
> dd.NA<-dd.trim[dd.trim$cont_africa==0,]
> cor(dd.NA$rugged, dd.NA$log_gdp)
[1] -0.2307945
```

- We now observe a stronger relationship between the two variables that is reversed for African and non-African countries.

# A model of ruggedness

- We will now construct a Bayesian Linear Regression between log GDP ( $y$ ) and terrain ruggedness ( $x$ ) capable of incorporating the different relationships for these two groups of countries encoded by the variable  $A$ .
- As we learned in a previous lecture, interactions are a convenient way to include different slopes for different categories in our data.
- Our model will be as follows:

$$\begin{array}{ll} y_i \sim N(\mu_i, \sigma) & [\text{likelihood}] \\ \mu_i = \beta_0 + \beta_1 x_i + \beta_2 A_i + \beta_3 * x_i * A_i & [\text{linear model}] \\ \beta_0 \sim N(0, 100) & [\beta_0 \text{ prior}] \\ \beta_1 \sim N(0, 10) & [\beta_1 \text{ prior}] \\ \beta_2 \sim N(0, 10) & [\beta_2 \text{ prior}] \\ \beta_3 \sim N(0, 10) & [\beta_3 \text{ prior}] \\ \sigma \sim \text{Cauchy}(0, 2) & [\sigma \text{ prior}] \end{array}$$

- We put Gaussian priors on all  $\beta$  coefficients and a Cauchy prior for  $\sigma$  (a t-student with 1 degree of freedom).
- The Cauchy distribution is heavy-tailed and has proven to be a useful prior for standard deviations (especially when restrained to positive values, taking the name of half-Cauchy).

# A model of ruggedness

- The R code for the model would be:

```
model<-alist(  
  log_gdp ~ dnorm( mu , sigma ) ,  
  mu <- b0 + b1*rugged + b2*cont_africa  
  + b3*rugged*cont_africa,  
  b0 ~ dnorm(0,100),  
  b1 ~ dnorm(0,10),  
  b2 ~ dnorm(0,10),  
  b3 ~ dnorm(0,10),  
  sigma ~ dcauchy(0,2)  
)
```

- Let's try to fit this model using Laplace Approximation:

```
> b.reg3<-quap(model,data=dd.trim)  
Error in quap(model, data = dd.trim) :  
  initial value in 'vmmin' is not finite  
The start values for the parameters were invalid.
```

- The optimizer is having a hard time finding the MAP estimates for this model!
- This can sometimes be corrected by using start values (declared with the **start** parameter), but in many models even this does not help.

# A model of ruggedness

- After trying to fit `b.reg3` with `quap` many times, it worked!

```
> precis(b.reg3)
      mean    sd  2.5% 97.5%
b0      9.22 0.14   8.95  9.49
b1     -0.20 0.08  -0.35 -0.05
b2     -1.95 0.22  -2.39 -1.51
b3      0.39 0.13   0.14  0.65
sigma   0.93 0.05   0.83  1.03
```

- Let's interpret the mean values for the posterior marginals of each  $\beta$  coefficient:
  - `mean(b0) = 9.22`: this is the intercept for non-African countries.
  - `mean(b1) = -0.20`: this is the slope for non-African countries, which is clearly negative.
  - `mean(b2) = -1.95`: this is the difference between the intercept for African and non-African countries, which indicates that African countries have a lower GDP than non-African countries when ruggedness is zero.
  - `mean(b3) = 0.39`: this is the difference between the slopes for African and non-African countries, which indicates that the slope for non-African countries is positive ( $0.39 - 0.2$ ).

- Now, let's fit the same model using Stan HMC with **ulam**:

```
m.reg1 <- ulam(model ,data=dd.trim)
```

- After messages about compiling, and sampling, ulam returns an object that contains a bunch of summary information, as well as samples from the posterior distribution.
- This process takes much longer than **quap**.
- We can summarize just like with quap:

```
> precis(m.reg1, prob=0.95 )
```

	mean	sd	2.5%	97.5%	n_eff	Rhat4
b0	9.21	0.15	8.89	9.51	169	1.03
b1	-0.20	0.09	-0.37	-0.01	163	1.04
b2	-1.95	0.23	-2.37	-1.48	241	1.01
b3	0.39	0.13	0.10	0.66	243	1.03
sigma	0.95	0.05	0.85	1.06	348	1.00

- These estimates are very similar to the Laplace approximation.

- A report of the chain can be obtained with command **show**:

```
> show(m.reg1)
Hamiltonian Monte Carlo approximation
500 samples from 1 chain
```

```
Sampling durations (seconds):
      warmup sample total
chain:1      0.2   0.17  0.37
```

```
Formula:
log_gdp ~ dnorm(mu, sigma)
mu <- b0 + b1 * rugged + b2 * cont_africa +
b3 * rugged * cont_africa
b0 ~ dnorm(0, 100)
b1 ~ dnorm(0, 10)
b2 ~ dnorm(0, 10)
b3 ~ dnorm(0, 10)
sigma ~ dcauchy(0, 2)
```

We can also get the Stan code with: `stancode(m.reg1):`

```
data{
  vector[170] log_gdp;
  int cont_africa[170];
  vector[170] rugged;
}
parameters{
  real b0;
  real b1;
  real b2;
  real b3;
  real sigma;
}
```

```
model{  
  vector[170] mu;  
  sigma ~ cauchy( 0 , 2 );  
  b3 ~ normal( 0 , 10 );  
  b2 ~ normal( 0 , 10 );  
  b1 ~ normal( 0 , 10 );  
  b0 ~ normal( 0 , 100 );  
  for ( i in 1:170 ) {  
    mu[i] = b0 + b1 * rugged[i] + b2 * cont_africa[i]  
      + b3 * rugged[i] * cont_africa[i];  
  }  
  log_gdp ~ normal( mu , sigma );  
}
```

This is Stan code, not R code. It is essentially the formula list we provided to `ulam`, but in reverse order.



## Additional Ulam Parameters

- **iter**: the number of samples from the chain. The default is 1000.
- **warmup**: the number of tuning samples. These samples are used to adapt sampling, and so are not actually part of the target posterior distribution. The default value is  $\text{iter}/2$ , which gives us 500 warmup samples and 500 real samples to use for inference.
- **chains**: the number of independent Markov chains to sample from. All of the non-warmup samples from each chain will be automatically combined in the resulting inferences.
- **cores**: the number of procesors over which the chains will be distributed.

- Let's fit the same model sampling 4 different chains distributed over 4 CPU cores with 3000 iterations and 1000 warmups.

```
> m.reg2 <- ulam(model ,data=dd.trim, iter=3000,  
                warmup =1000, chains=4, cores=4)
```

```
> show(m.reg2)
```

Hamiltonian Monte Carlo approximation

8000 samples from 4 chains

Sampling durations (seconds):

	warmup	sample	total
chain:1	0.62	1.08	1.70
chain:2	0.54	1.06	1.60
chain:3	0.60	0.89	1.49
chain:4	0.37	0.82	1.19

# Diagnostic criteria: $n_{\text{eff}}$ and $R_{\text{hat}}$

- Note that **precis** reported two new columns:  $n_{\text{eff}}$  and  $R_{\text{hat}}$ , which provide MCMC diagnostic criteria.
- They help us tell how well estimation worked.
- The column  $n_{\text{eff}}$  is a crude estimate of the number of independent samples we managed to get.
- When  $n_{\text{eff}}$  is much lower than the actual number of iterations (minus warmup) of your chains, it means the chains are inefficient, but possibly still okay.
- $R_{\text{hat}}$  is the Gelman Rubin convergence diagnostic, which estimates the convergence of the Markov chains to the target distribution.
- It should approach 1.00 from above, when all is well.
- When  $R_{\text{hat}}$  is above 1.00, it usually indicates that the chain has not yet converged, and probably we shouldn't trust the samples.
- If we draw more iterations, it could be fine, or it could never converge.

- We can extract samples from the posterior in the usual way:

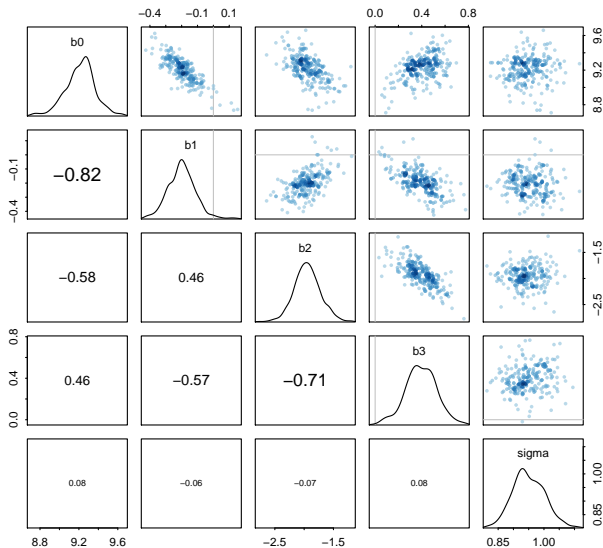
```
post <- extract.samples( m.reg1 )
```

- We also use **link** and **sim** functions to get posterior predictions.
- We can plot the correlations between samples using the function **pairs**:

```
pairs( m.reg1)
```

- This will show a pairs plot: a matrix of bivariate scatter plots.
- Along the diagonal the smoothed histogram of each parameter is shown, along with its name.
- In in the lower triangle of the matrix, below the diagonal, the correlation between each pair of parameters is shown, with stronger correlations indicated by relative size.

# Ulam Pairs



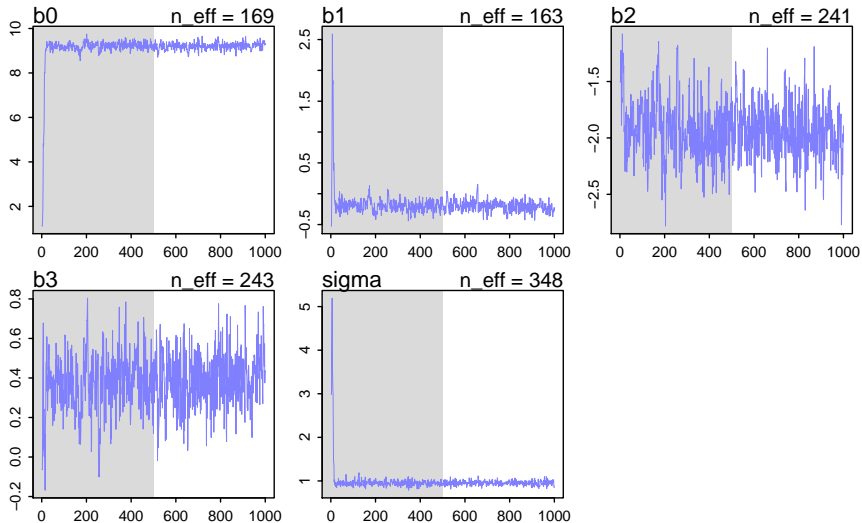
- For this model and these data, the resulting posterior distribution is quite nearly multivariate Gaussian.
- The density for sigma is certainly skewed in the expected direction.
- But otherwise the Laplace approximation does almost as well as Hamiltonian Monte Carlo.
- This is a very simple kind of model structure of course, with Gaussian priors, so an approximately Gaussian posterior should be no surprise.
- For more complex models, posterior distributions can take more exotic shapes.

# Checking the Chain

- If the Markov chain is defined correctly then it is guaranteed to converge in the long run to the right posterior distribution.
- But the machine can sometimes fail.
- We won't study these cases in detail.
- A trace plot is a very useful tool for diagnosing malfunction.
- It basically plots the samples in sequential order, joined by a line.
- In the terrain ruggedness example, the trace plot shows a very healthy chain.
- We can obtain it with the following command:

```
traceplot( m.reg1 )
```

# Trace Plot





# Checking the Chain

- The plot shows the zig-zagging trace of each parameter as the path the chain took through each dimension of parameter space.
- The gray region in each plot, the first 500 samples, marks the warmups samples.
- During adaptation, the Markov chain is learning to more efficiently sample from the posterior distribution.
- So these samples are not necessarily reliable to use for inference.
- They are automatically discarded by **extract.samples**, which returns only the samples shown in the white regions.
- Typically we look for two things in these trace plots: stationarity and good mixing.

# Checking the Chain

- Stationarity refers to the path staying within the posterior distribution.
- Notice that these traces, all stick around a very stable central tendency.
- Another way to think of this is that the mean value of the chain is quite stable from beginning to end.
- A well-mixing chain means that each successive sample within each parameter is not highly correlated with the sample before it, which is known as **autocorrelation**.
- Visually, we can see this by the rapid zig-zag motion of each path, as the trace traverses the posterior distribution without getting mired anywhere.

# Conclusions

- This class has been an introduction to Markov chain Monte Carlo (MCMC) estimation.
- The goal has been to introduce the purpose and approach MCMC algorithms.
- The major algorithms introduced were the Metropolis, Gibbs sampling, and Hamiltonian Monte Carlo algorithms.
- Each has its advantages and disadvantages.
- A function in the rethinking package, **ulam**, was introduced that uses the Stan Hamiltonian Monte Carlo engine to a linear model with an interaction.

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