

# Two Recursive Simulation Schemes

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# Outline

- 1 Introduction
- 2 Simulating Functionals of Diffusions
- 3 Binary Adaptive Rejection Sampler
- 4 References

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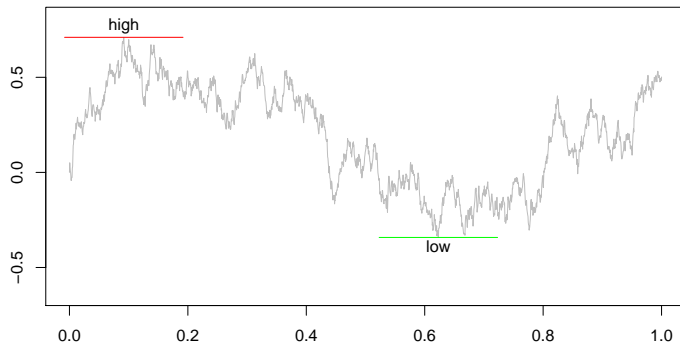
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- About 12 years ago I studied perfect simulation, including Propp and Wilson's CFTP algorithm.
- I realized that CFTP is an example of the following general principle: to simulate from a target density  $f(\cdot)$ , often we can generate a finite sequence of approximations, and be certain that a draw from the final one is drawn exactly from  $f(\cdot)$ .
- Today I will talk about two applications of this principle. This is joint work with Tingting Gou and John Braun.

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# Simulating Extremes of a Diffusion



Given a stochastic differential equation

$$dX_s = \mu(X_s)ds + \sigma(X_s)dW_s$$

our ultimate goal is to simulate functionals such as the high and low points and where they occur, without simulating the entire path.

McLeish (2002) described a simple algorithm to simulate the High or Low values of a Brownian Motion over an interval  $[0;T]$ , conditional on the values at the end points  $W_0 = o; W_T = c$ .

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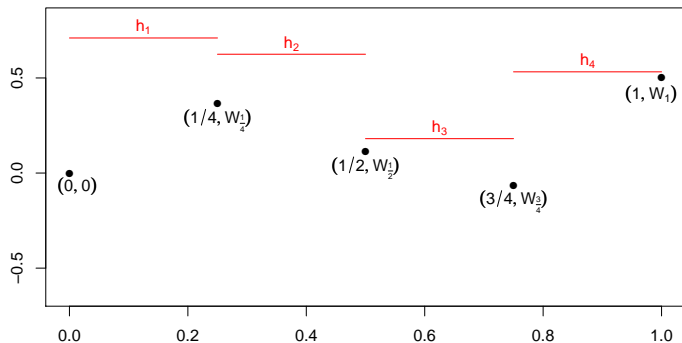
## Algorithm

High( $o; c; T$ )

$Y \sim \text{Unif}(0; \exp[-(c - o)^2 / 2T])$   
Return  $[c + o + \sqrt{-2T \log(Y)}] / 2$

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# Both the high and its time



The Euler method:

- Divide the interval into  $N$  subintervals.
- Discretize and use McLeish on each subinterval, then pick the biggest.



# What is wrong with Euler?

- The Euler method gets the distribution of the high exactly right, but only obtains the time to within an interval of length  $1/N$ .
- This is inaccurate if  $N$  is small, slow if  $N$  is large.
- We can speed it up by a recursive approach...

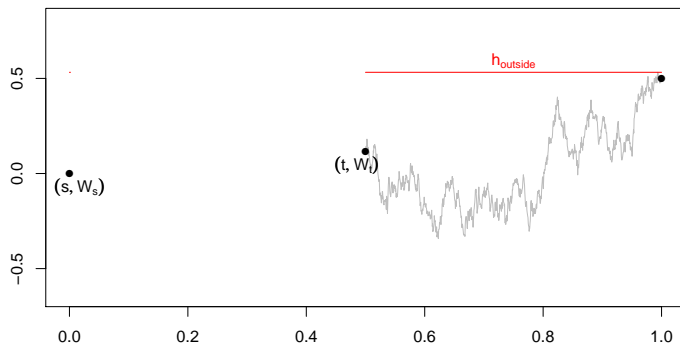
# A Recursive Rejection Algorithm

Principle: Divide the interval into two parts: the “inside”  $[s;t]$  (containing the max) and the “outside”  $[0;1] \setminus [s;t]$ . Recursively shrink the inside part.

- Recursion: At each step, we start with  $(s;t;W_s;W_t;h_{\text{outside}})$ ; use 2-step Euler and apply McLeish twice to choose one half of  $[s;t]$  as the new inside, and to update  $h_{\text{outside}}$ .
- Rejection: The high inside must be bigger than  $h_{\text{outside}}$ . Repeat Euler and McLeish until it is.

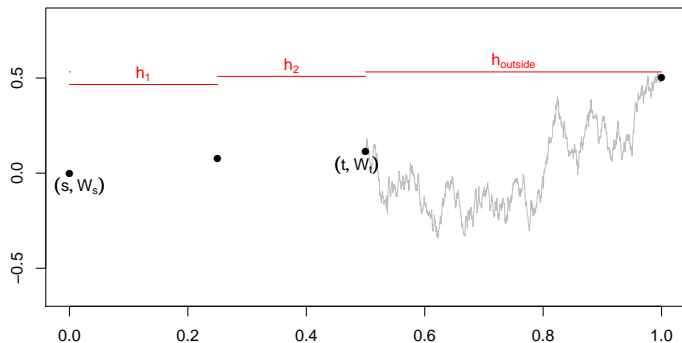
Advantage: Order  $n$  steps for  $2^n$  step accuracy: much more efficient than the Euler Method.

# RRA at step one



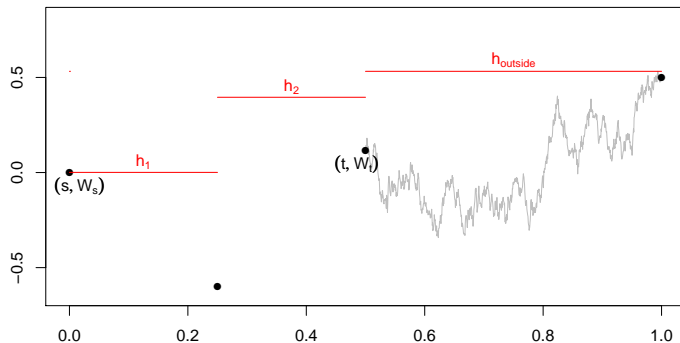
After one step we might have this. (Don't simulate the full path, but consider it fixed...)

# RRA first proposal



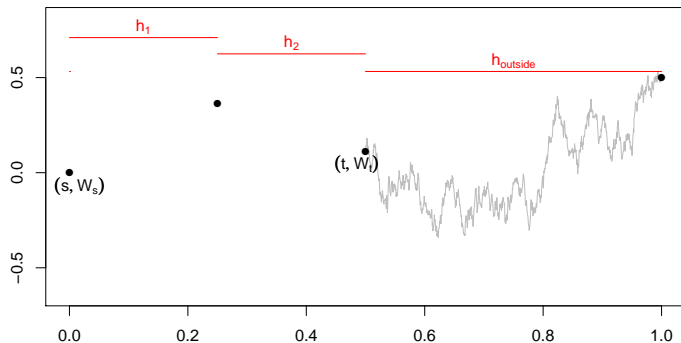
Simulate the inside interval until  $\max(h_1, h_2) > h_{\text{outside}}$ . This one failed!

# RRA second proposal



Try again: failed again!

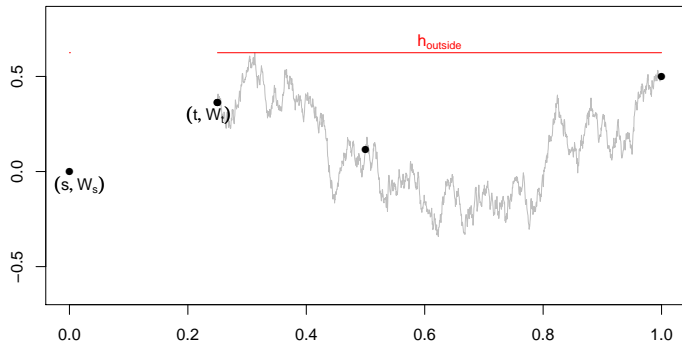
# RRA third proposal



Try again: success!

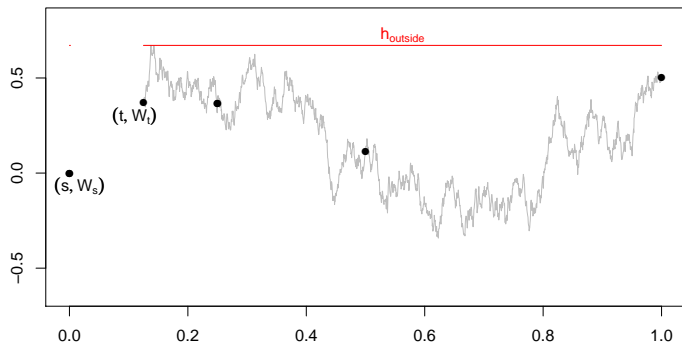
Accept this simulation, set  $h_{\text{outside}} = \max(h_{\text{outside}}; h_2)$ , discard  $h_1$ .

# RRA at step two



Update to the new state.

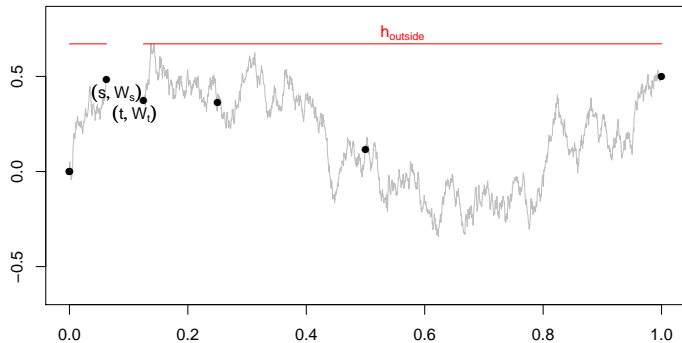
# RRA at step three



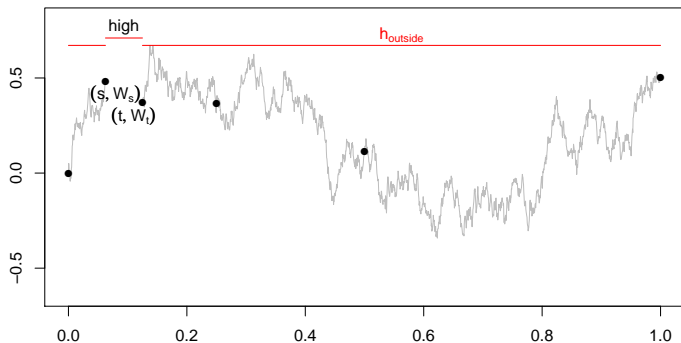
Repeat the whole recursive step to refine the interval. Continue until  $|t - s|$  is small enough.



# RRA at step four



# RRA is done



Apply McLeish one more time at the end (or just use the  $\max(h_1; h_2)$  value from the previous step).

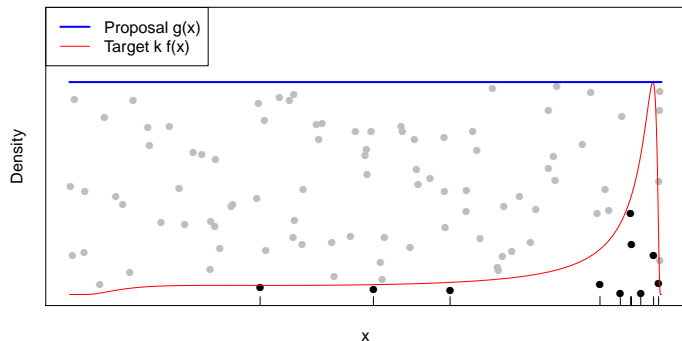
- Simulating lows instead of highs—use mins not maxes.
- Barrier crossing times and other functionals can be simulated in a similar way.
- Simulating both lows and highs and both locations—more complicated:
  - Invert distribution from Billingsley (1999) to simulate high and low simultaneously.
  - In RRA, the “inside” eventually becomes two disjoint intervals, one containing the high, the other containing the low.
  - We maintain both high and low in the “outside”.
- More general diffusions—Beskos and Roberts (2005), Beskos *et al.* (2006) described an exact algorithm (EA) for simulating some diffusions. First generate a random skeleton; conditional on the skeleton, simulate Brownian bridges between.

Our goal was exact simulation, and RRA only gives us the time(s) to within  $2^{-n}$ . Shepp (1979) derived the joint density of the high  $h$ , its time  $\theta$ , and closing value  $c$  for a Brownian motion on  $[0;T]$ , which allows us to derive

$$f(\theta|h;c;T) \propto \frac{1}{\theta^{3=2}(T-\theta)^{3=2}} \exp \left[ -\frac{h^2}{2\theta} - \frac{(h-c)^2}{2(T-\theta)} \right]$$

This is a non-standard density, but we can construct a rejection sampler for it.

# Rejection Sampling



Suppose you want to sample from density  $f(\cdot)$ , and know how to sample from density  $g(\cdot)$ . Find  $k$  such that  $g(x) \geq kf(x)$  for all  $x$ . Then:

- 1 Sample  $Y$  from  $g(\cdot)$ .
- 2 Sample  $U$  from  $\text{Unif}(0; g(Y))$ .
- 3 If  $U < kf(Y)$ , output  $Y$ ; else repeat.

The probability of acceptance is  $k$ .

# The Rejection Sampler Can Be Slow

It is simple to compute the mode (or modes) of the Shepp density, and then use a  $\text{Unif}(0,1)$  proposal in a rejection sampler. But this can be very slow (i.e.  $k$  can be very small). Some solutions:

- 1 Identify the values of  $h$ ,  $c$  and  $T$  that lead to a slow sampler, and use another RRA step in those cases.
- 2 Work out a smarter proposal density.
- 3 Use an adaptive proposal.

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# When does rejection sampling work well?

Rejection sampling works very well in low dimensions:

- We can sample even if we do not know the normalizing constants on the densities.
- We get IID samples from the target, unlike MCMC, which gives correlated values from an approximation to the target.
- It is often not hard to find a bounding function in one dimension.
- Gilks and Wild (1992) presented an adaptive rejection sampler: with each rejection,  $g(\cdot)$  was adjusted to be a better approximation to  $f(\cdot)$ . It produced very tight approximations.



# Why not use rejection sampling?

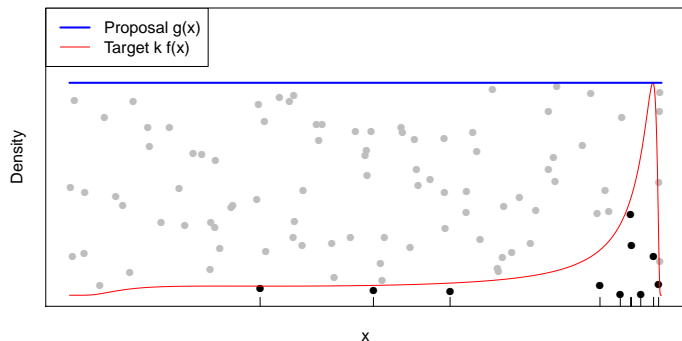
In high dimensions, rejection sampling is not so successful:

- It is hard to find a proposal that gives tight bounds. (Sometimes this is hard even in one dimension.)
- Typically  $k$  will be extremely small, so the sampler will be very inefficient.
- Multidimensional proposal distributions are hard to work with.
- Gilks and Wild (1992) required strong conditions (log-concavity) on  $f(\cdot)$ ; these are not always available and verifiable.

We would like to construct an adaptive sampler, with weak conditions on  $f(\cdot)$ .

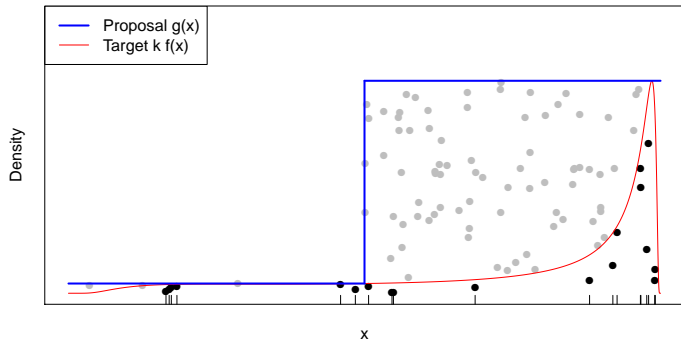
- Start with any bound, one region.
- Split regions where there are a lot of rejections to get tighter bounds.

# Example: Shepp's density



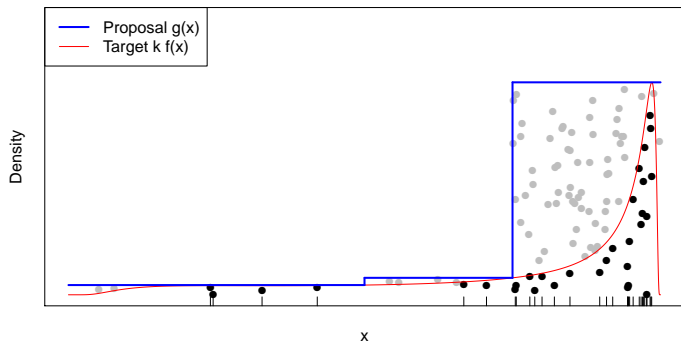
We accepted 10=100 proposals. Can we improve this?

# Split the interval and bound separately



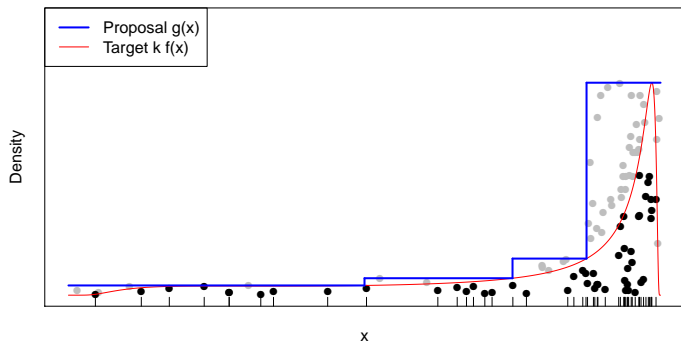
Now we accept 19=100 proposals.

# Split again



We chose to split the region with the highest expected number of rejections.  
Now we accept  $31 = 100$  proposals.

# And again..



We accept  $52=100$  proposals with this approximation. We may now draw a large sample using this sampler, which is very fast.

# How did we choose where to subdivide?

We can estimate the rejection rate in each region in several ways:

- 1 Just count how many rejections there were in each region.
- 2 Better: Find the average of  $P(\text{reject})$  in each region, and multiply by the number sampled in that region.
- 3 Best: Use the computed volume of each region as the multiplier.

# Higher Dimensions

We don't really need the adaptive rejection sampler in one dimension: our first uniform proposal was good enough. But how to handle higher dimensions?

Our strategy:

- Divide the space into rectangular regions, and use the same strategy as before to select regions to subdivide.
- Use a proposal that is independent in the coordinates on each subregion.
- Subdivide the target region one coordinate at a time to improve the bound.
- After choosing the region, try all coordinate choices, and pick the best one.



## Two Dimensional Example



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Try to sample from  $kf(x;y) = 1/(0.01 + |x - 0.9|^4 + |y - 0.1|^6)$ ,  $0 < x < 1$ ,  $0 < y < 1$ , using uniform proposals.

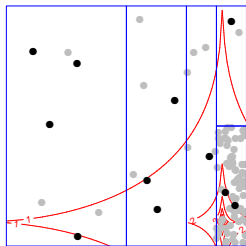
## Finding a bound

If  $x \in [x_0; x_1]$  and  $y \in [y_0; y_1]$ , then an upper bound on  $kf(x; y)$  is  $kf(x^*; y^*)$ , where

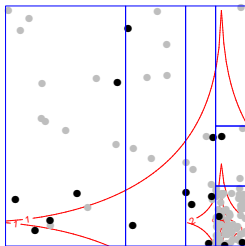
$$x^* = \begin{cases} x_0 & \text{if } x_0 > 0.9 \\ x_1 & \text{if } x_1 < 0.9 \\ 0.9 & \text{otherwise} \end{cases}$$

with a similar formula for  $y^*$ .

# Sampling from $f(x; y)$

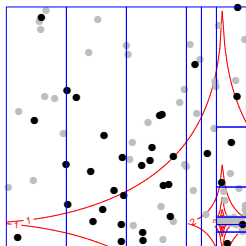


Accepted 11 proposals

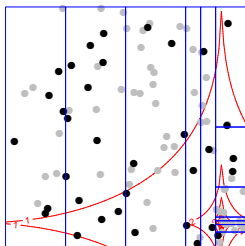


Accepted 16 proposals

# Continuing...

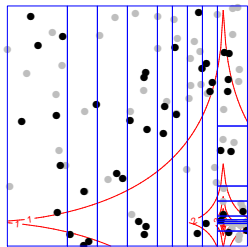


Accepted 35 proposals

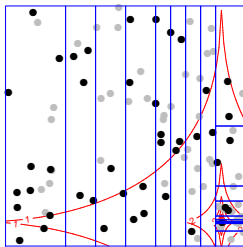


Accepted 35 proposals

# Continuing...



Accepted 43 proposals



Accepted 44 proposals

# Pump Data Example

Gaver and O'Muircheartaigh (1987) described data on pump failures at a nuclear power plant. A number of authors have analyzed this using the following Bayesian hierarchical model:

- $s_1; \dots; s_{10}$  count failures after operation for known times  $t_1; \dots; t_{10}$ .
- $s_k \sim \text{Poisson}(\lambda_k t_k)$ ,  $k = 1; \dots; 10$ .
- $\lambda_k \sim \text{Gamma}(\alpha; \beta)$ ,  $k = 1; \dots; 10$ , with  $\alpha = 1.802$  treated as known.
- $\beta \sim \text{Gamma}(\gamma; \delta)$ , with  $\gamma = 0.01$  and  $\delta = 1$ .

We want to study the joint posterior distribution of  $(\beta; \lambda)$ , where  $\lambda = (\lambda_1; \dots; \lambda_{10})$ .

# The Target Density

The joint posterior is (up to normalizing constants):

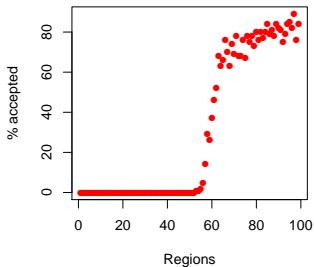
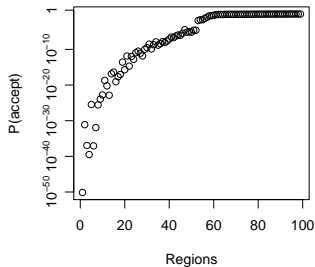
$$f(\beta; \lambda) = \beta^{\gamma+10\alpha-1} e^{-\beta\delta} \prod_{k=1}^{10} \lambda_k^{s_k+\alpha-1} e^{-\lambda_k t_k} e^{-\lambda_k \beta}$$

If  $\beta > \beta_0$  and  $\lambda_k > \lambda_{k0}$  then

$$\begin{aligned} g(\beta; \lambda) &= e^{\beta_0 \sum \lambda_{k0}} \\ &\times \beta^{\gamma+10\alpha-1} e^{-\beta(\delta+\sum \lambda_{k0})} \\ &\times \prod_{k=1}^{10} \lambda_k^{s_k+\alpha-1} e^{-\lambda_k(t_k+\beta_0)} \end{aligned}$$

dominates  $f(\beta; \lambda)$ , so we may use independent truncated Gamma proposals on rectangular regions.

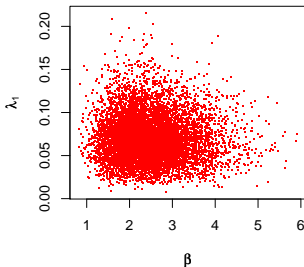
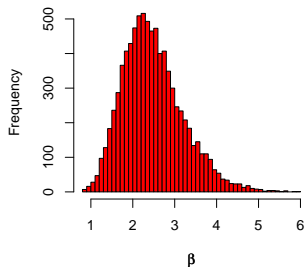
# The Acceptance Rate



The acceptance rate starts out very low (less than  $10^{-50}$ ), but quickly rises to acceptable levels.



# Samples



We obtain IID samples from the posterior, which we can use in whatever further inference we like.

Implementing the pump data example was both easy and difficult:

- Finding the bounds was very easy, because the target density is mainly made up of easy factors. We expect this to be quite common in Bayesian hierarchical models.
- Evaluating the bounds, and implementing the sampler, was a little trickier than we expected:
  - The problem was in evaluating the truncated Gamma proposals. In many cases, the samples come from far out in the tails, and we were experiencing underflows and huge rounding errors.
  - The solution in this case was to work on a log scale, and to evaluate probabilities using *both* the CDF and the survival function.
- Experience has shown that the pump data is unusually well suited to our algorithm. We can't handle general densities with 11 parameters.

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# References

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