Posterior inference

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- The posterior distribution gives a lot of information
- Ideally, we could just show a graph of it and leave the interpretation to the reader
  - But often the posterior will have many dimensions
  - And also that seems lazy
- We need a way to describe the posterior distribution
  - Mean? SD? Skew? Kurtosis? Mass at or around a certain value? $p(.8 \leq P_R \leq .9 | \#R, \#W)$?

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Here, with the discrete domain of P_R:

$$\begin{aligned} p(.8 \leq P_R \leq .9|\#R, \#W) = \\ p(P_R = .80|\#R, \#W) \\ +p(P_R = .85|\#R, \#W) \\ +p(P_R = .90|\#R, \#W) \end{aligned}$$

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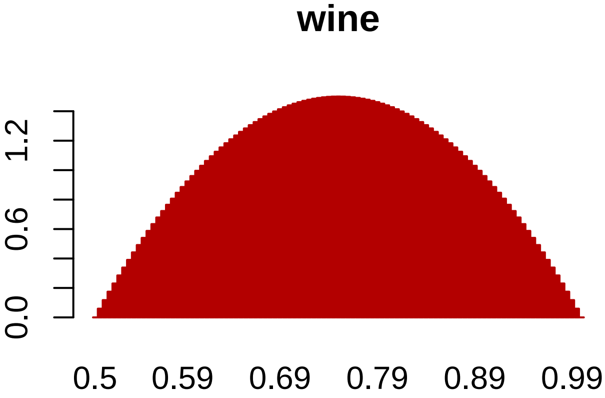

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  - Likelihood is the same: $p(\#R, \#W|P_R) = CP_R^{\#R}(1-P_R)^{\#W}$
  - So the posterior must be:
    $p(P_R|\#R, \#W) \propto \left(\frac{P_R+1}{2}\right)^{\alpha-1}\left(1-\frac{P_R+1}{2}\right)^{\beta-1}$

Functional programming

Sometimes it is useful in R to turn a function into a variable to change it quickly

You can make a function "on the fly" inside a function or script file like this:

```r
funcname <- function(n, x) { rep(x, n) }
```

So that prior and likelihood can be written like:

```r
prior <- function(p) { dbeta(2 * (p-.5), 2, 2) }
likelihood <- function(p) { dbinom(5, 6, p) }
```

Functional programming

Prior and likelihood:

```
prior <- function(p) { dbeta(2 * (p-.5), 2, 2) }
likelihood <- function(p) { dbinom(5, 6, p) }
```

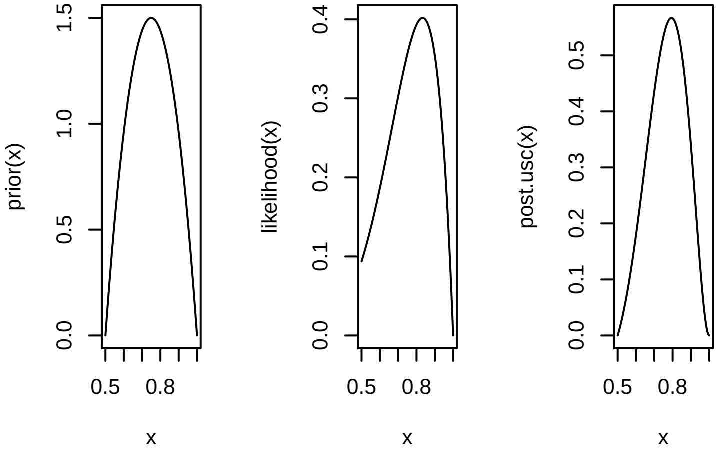
Given those, building the posterior is trivial:

```
post.usc  <- function(p) { prior(p) * likelihood(p) }
```

Exercise: implement this, plot the three functions

Functional programming

```
par(mfrow=c(1,3))
curve(prior, 0.5, 1)
curve(likelihood, 0.5, 1)
curve(post.usc, 0.5, 1)
```



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    - Methods for doing this are called Monte Carlo methods

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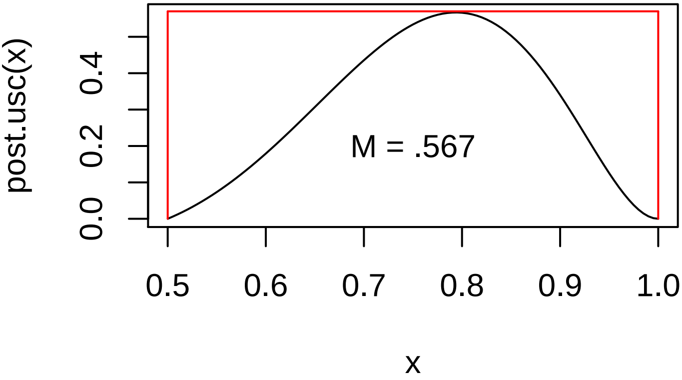
- These graphs don't tell us the mean of the posterior (or any other useful statistic)
- How do we determine the mean of an arbitrary, somewhat complicated function?
- As it turns out, drawing random samples from a distribution is an efficient way to do that
  - Methods for doing this are called Monte Carlo methods
  - Math win: Monte Carlo methods don't need those hard-to-compute K and C scaling constants

Posterior sampling

One Monte Carlo method is the rejection sampler:

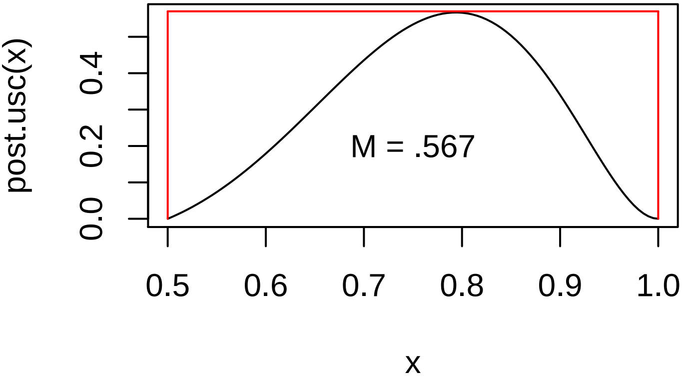
1) Draw a sample from some basic distribution $S(x|...)$



Posterior sampling

One Monte Carlo method is the rejection sampler:

1) Draw a sample from some basic distribution $S(x|...)$
2) Reject the sample with probability $q = \frac{fx}{M \times S(x)}$, where M is chosen so that this is always ≤ 1 (but ideally sometimes close to 1)



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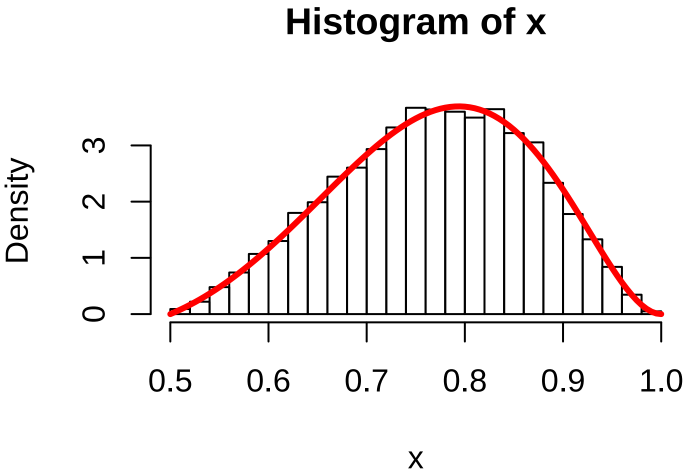
   - Otherwise, reject the value and draw a new sample
3. Repeat many times to get a few thousand samples
4. Make a histogram and compare the shapes of the distribution

Posterior sampling

```r
N <- 10000
x <- vector(,N)
c <- 1
M <- .567
while(c <= N) {
  x[c] <- runif(1, 0.5, 1)
  u <- runif(1, 0, M)
  if (u < post.usc(x[c])) c <- c + 1;
}
hist(x, breaks=25,freq=FALSE)
K <- integrate(post.usc, 0.5, 1)$value
lines(domain, post.usc(domain)/K, lwd=3, col='red')
```

Posterior sampling



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  - Now we can compute the mean of that sample: 0.7682109
  - ... or the proportion of samples that are $> .85$: 0.2267
  - ... or indeed any quality we fancy

Generative model representation

- Basic unit of a Bayesian model is a distribution function

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- The posterior is defined through a *generative model representation*

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- The posterior is defined through a *generative model representation*
    - ... which is basically a sequence of distributional assumptions

Generative model representation

Let's define a really trivial model $\mathcal{M}_t$ in which we estimate the parameters μ and τ $(= 1/\sigma^2)$ of a normal distribution, applied to some data points d_j:

$$\mathcal{M}_t : \begin{cases} \forall j \in (1, \ldots, J) : \; d_j \sim N(\mu, \tau) \\ \mu \sim N(0, 0.1) \\ \tau \sim \Gamma(4, 0.01) \end{cases}$$

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Notice how every statement is a distributional assumption! (Either priors on parameters or likelihoods on data.)

JAGS code is (almost) perfect

$$\mathcal{M}_s : \begin{cases} \forall j \in (1, \dots, J) : d_j \sim N(\mu, \tau) \\ \mu \sim N(0, 0.1) \\ \tau \sim \Gamma(4, 0.01) \end{cases}$$

The program needs to know the specifics of the model:

```
model {
    for (j in 1:J) {
        d[j] ~ dnorm(mu, tau)
    }
    mu ~ dnorm(0,0.1)
    tau ~ dgamma(4,0.01)
}
```

A psychological model: Signal detection theory

$$\mathcal{M}_{sdt}: \begin{cases} \delta \sim N(1,1) & \beta \sim N(0,1) \\ \phi_h = \Phi(\delta/2 - \beta) & \phi_f = \Phi(-\delta/2 - \beta) \\ h \sim B(\phi_h, n_s) & f \sim B(\phi_f, n_n) \end{cases}$$

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```
model {
    d ~ dnorm(1, 1)
    b ~ dnorm(0, 1)

    phih <- phi( d / 2 - b)
    phif <- phi(-d / 2 - b)

    h ~ dbin(phih, sigtrials)
    f ~ dbin(phif, noistrials)
 }
```

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