Posterior inference

Joachim Vandekerckhove

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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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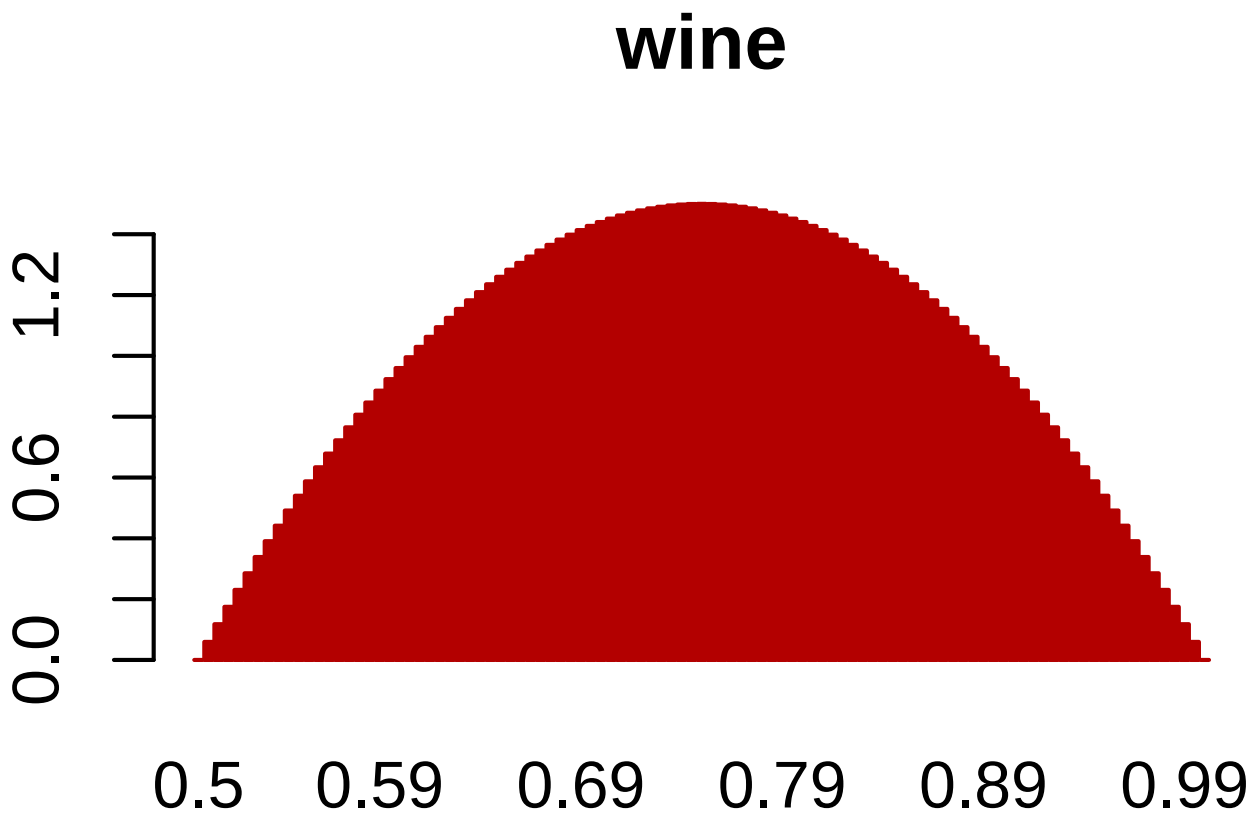

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  - So the posterior must be:
    $p(P_R|\#R, \#W) \propto (2P_R - 1)^{\alpha-1} (1 - (2P_R - 1))^{\beta-1}$
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$$\Rightarrow p(P_R|\#R, \#W) \propto (2P_R - 1)^{\alpha-1} (2 - 2P_R)^{\beta-1} P_R^{\#R}(1-P_R)^{\#W}$$

. . . now what? What's the mean and variance of this?

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:

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

So that prior and likelihood can be written like:

```
prior <- function(p) { dbeta(2*p - 1), 2, 2) }
likelihood <- function(p) { dbinom(5, 6, p) }
```

Functional programming

Prior and likelihood:

```
prior <- function(p) { dbeta(2*p - 1, 2, 2) }
likelihood <- function(p) { dbinom(5, 6, p) }
```

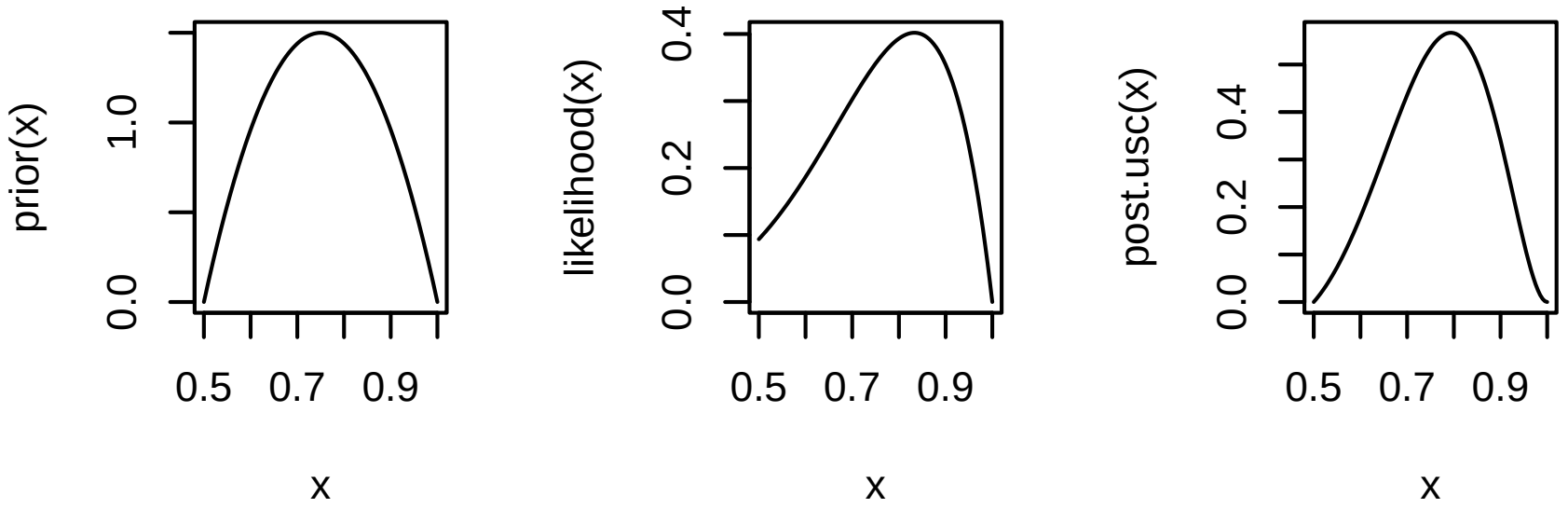
Given those, building the posterior is trivial:

```
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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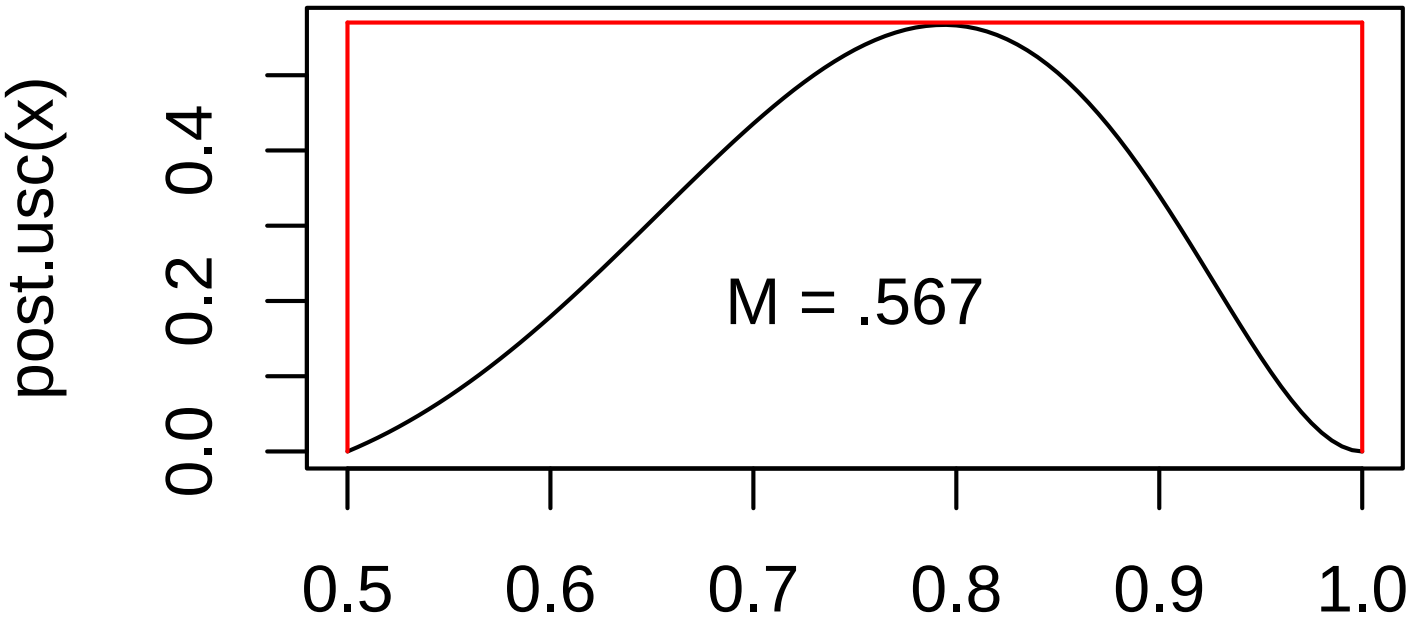
- These graphs still don't tell us the mean of the posterior (or any other useful statistic)
- How do we determine the mean of an arbitrary, somewhat complicated function?
- As it turns out, drawing random samples from a distribution is an efficient way to do that
  - Methods for doing this are called 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 $S(x|...)$



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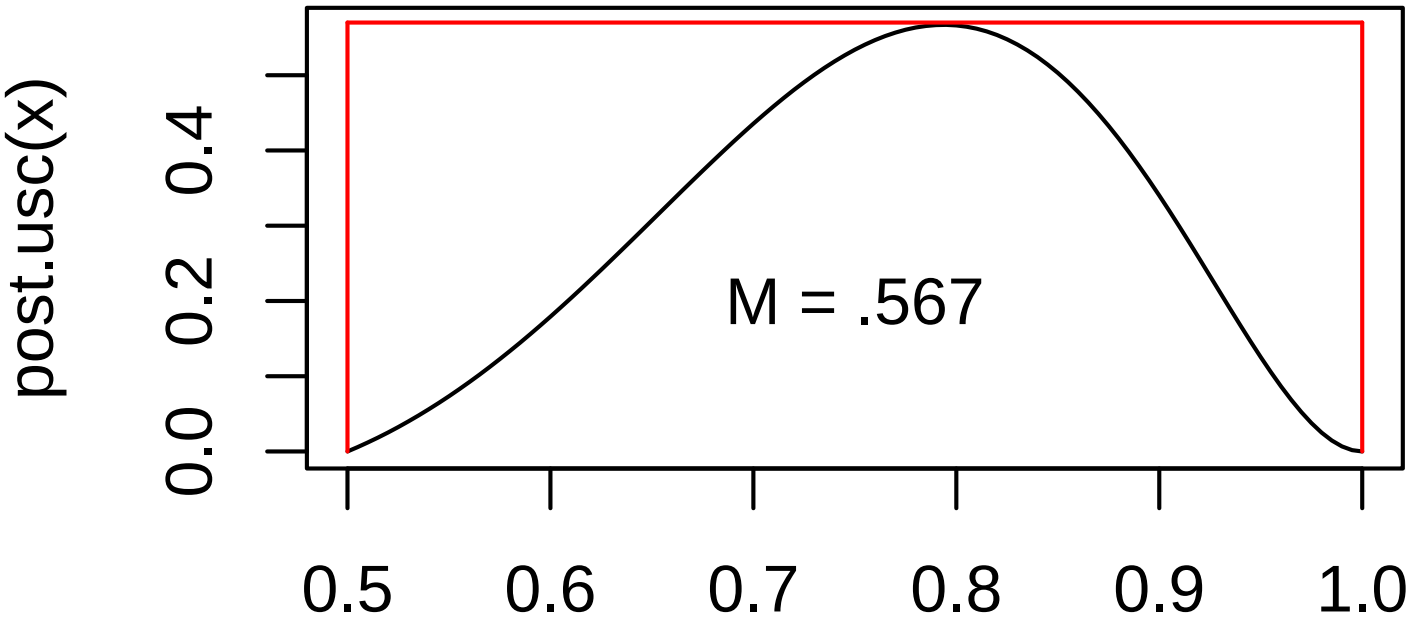
One Monte Carlo method is the rejection sampler:

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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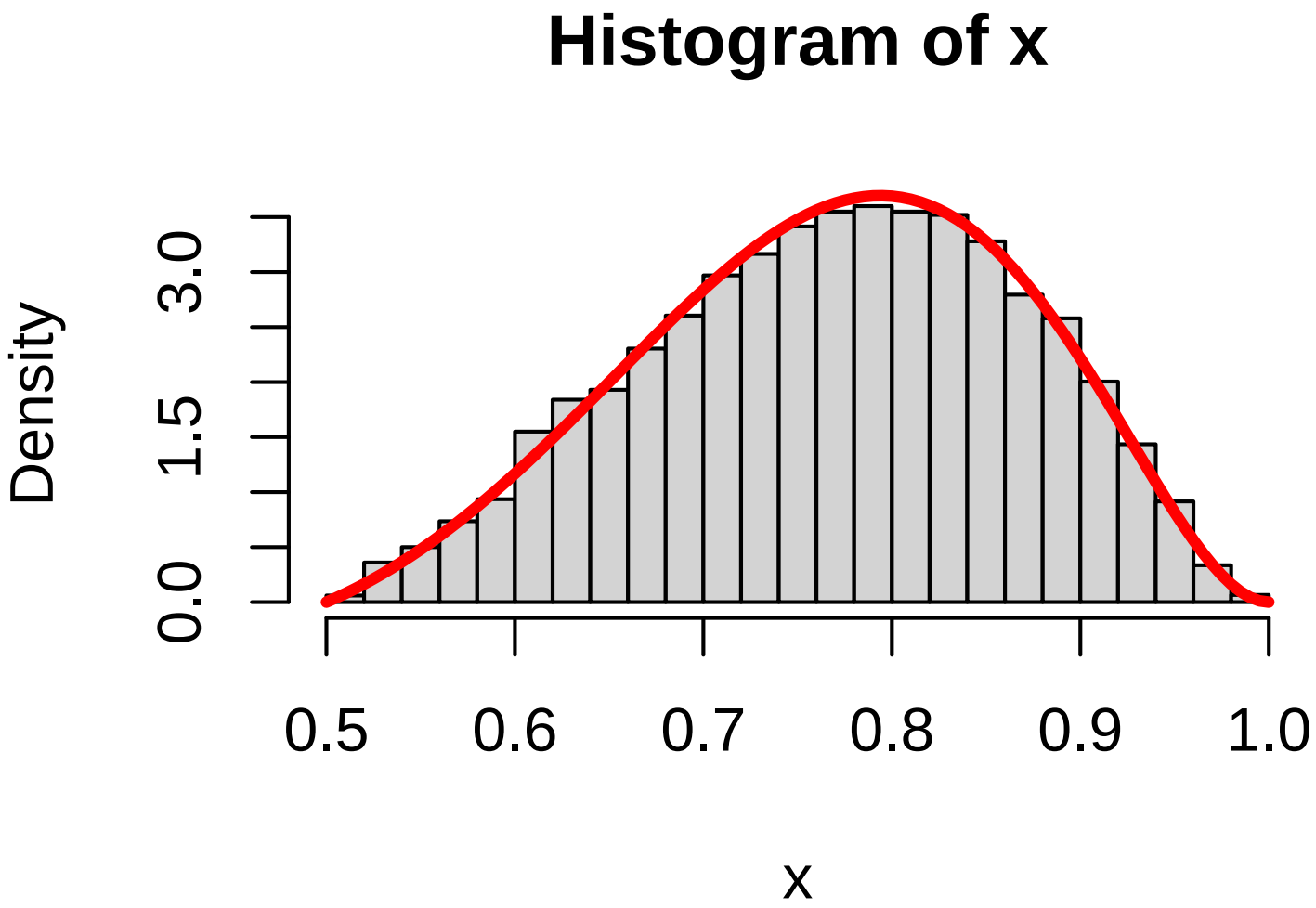
3. Repeat many times to get a few thousand samples
4. Make a histogram and compare the shapes of the distribution

Posterior sampling

```
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: 0.7691061
  - ... or the proportion of samples that are $> .85$: 0.2347
  - ... or indeed any quality we fancy

Generative model representation

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- The posterior is defined through a generative model representation
  - ... which is basically a sequence of distributional assumptions
  - In Bayesian statistics, a "model" is just a special kind of distribution function over parameters and data (and so with possibly very many dimensions)

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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$$\begin{aligned} p(d_1, \ldots, d_J \mid \mathcal{M}_t) &= \left(\prod_{j=1}^{J} N(d_j \mid \mu, \tau) \right) \\ &\times \; N(\mu \mid 0, 0.1) \\ &\times \; \Gamma(\tau \mid 4, 0.01) \end{aligned}$$

JAGS code is (almost) perfect

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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)
}
```

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To communicate results, we needed a method to summarize arbitrary distributions

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JAGS (and Stan) have a straightforward modeling language that lets users specify a model

They then draw samples from the posterior distributions, so we can calculate any summaries we like