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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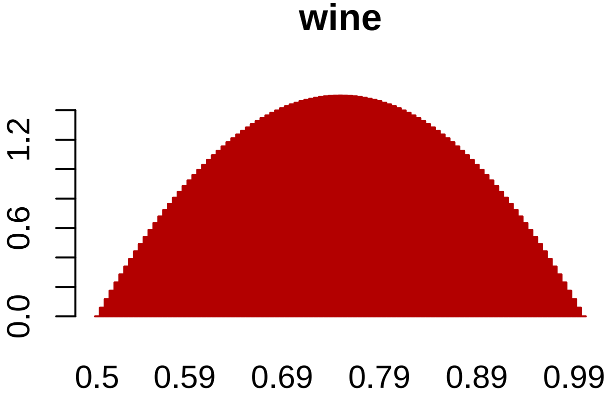

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  - $p(x) = Kx^{\alpha-1}(1-x)^{\beta-1} = B(x|\alpha,\beta)$
  - Beta distribution, say $\alpha = \beta = 2$
  - Likelihood is the same: $p(\#R, \#W|P_R) = CP_R^{\#R}(1-P_R)^{\#W}$
  - So the posterior must be: $p(P_R|\#R,\#W) \propto \left(\frac{P_R+1}{2}\right)^{\alpha-1}\left(1-\frac{P_R+1}{2}\right)^{\bet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

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) }
```

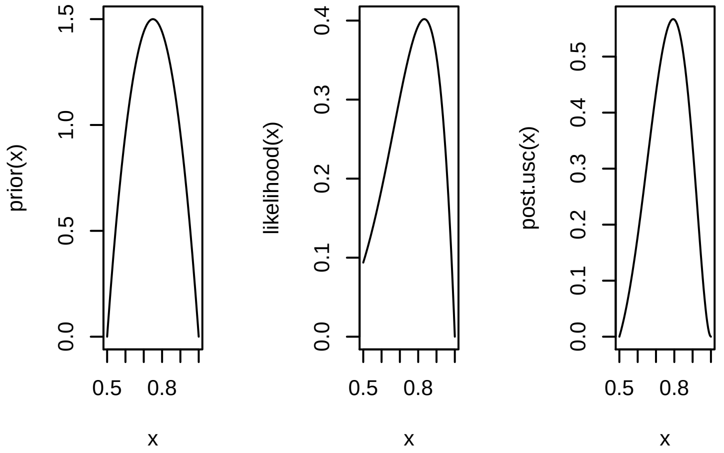
Given those, building the posterior is trivial:

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

Exercise: implement this, plot the three functions

Functional programming

```r
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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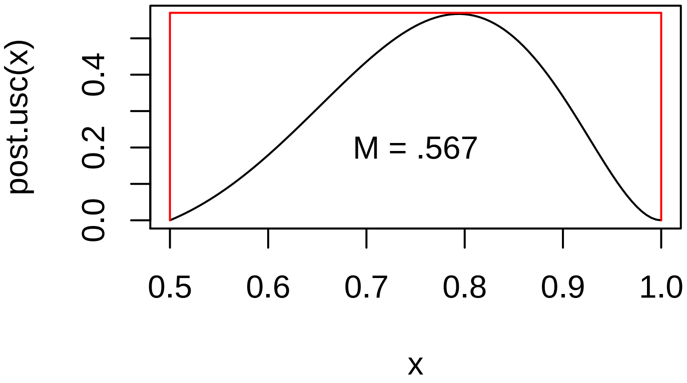
- How do we determine the mean of an arbitrary, somewhat complicated function?
- As it turns out, drawing random samples from a distribution is an efficient way to do that
  - Methods for doing this are called Monte Carlo methods
  - Math win: Monte Carlo methods don't need those hard-to-compute K and C scaling constants

Posterior sampling

One Monte Carlo method is the rejection sampler:

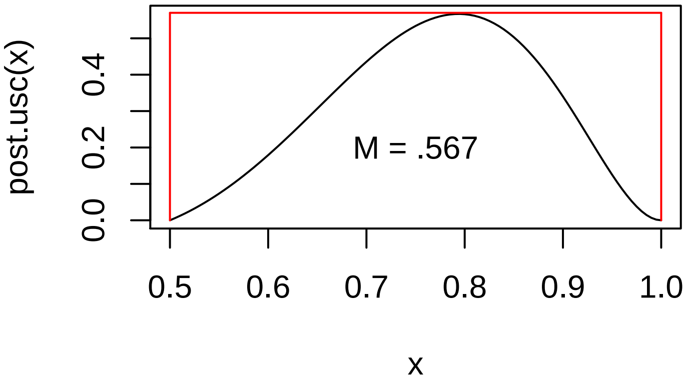
1) Draw a sample from some basic distribution $S(x|...)$



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 $q = \frac{f x}{M \times S(x)}$, where M is chosen so that this is always ≤ 1 (but ideally sometimes close to 1)



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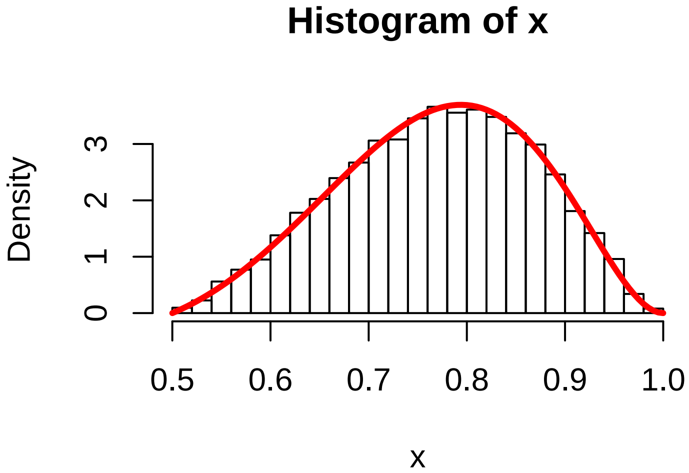
    - Otherwise, reject the value and draw a new sample
3. Repeat many times to get a few thousand samples
4. Make a histogram and compare the shapes of the distribution

Posterior sampling

```
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: 0.7687995
  - ... or the proportion of samples that are $> .85$: 0.2329
  - ... or indeed any quality we fancy

Generative model representation

- Basic unit of a Bayesian model is a distribution function

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- Basic unit of a Bayesian model is a distribution function
- 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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Notice how every statement is a distributional assumption! (Either priors on parameters or likelihoods on data.)

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

JAGS code is (almost) perfect

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

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)
 }
```

Signal detection theory ∼ implementation

```
library(rjags)

data <- list( h = 32 ,  sigtrials  = 39 ,
              f = 12 ,  noistrials = 60 )

modelString = "
    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)
     }
"
```

Signal detection theory ~ implementation

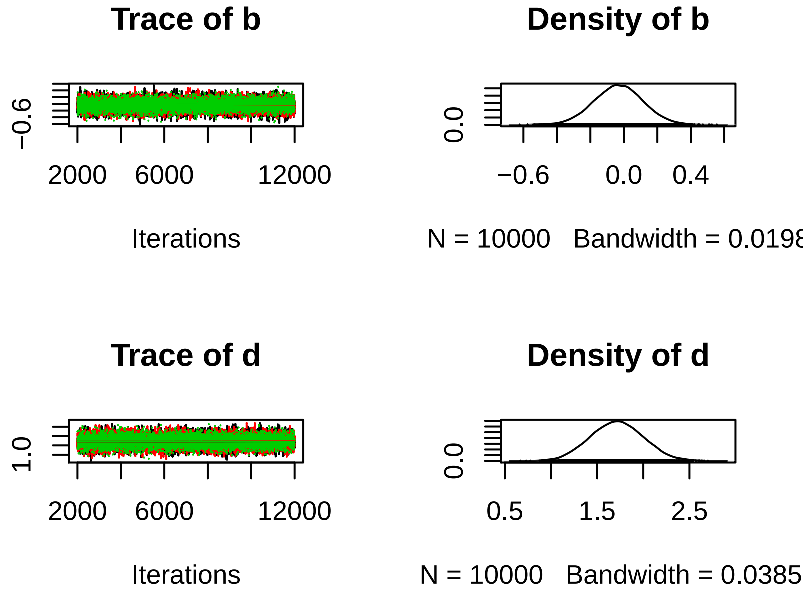
```
writeLines( modelString , con = "sdt.txt" )

jagsModel = jags.model( file     = "sdt.txt" ,
                        data     =     data   ,
                        n.chains =        3   ,
                        n.adapt  =     1000   )

set.seed(0)
update( jagsModel , n.iter = 1000 )  # burn-in

samples = coda.samples( jagsModel ,
                        variable.names = c("d", "b") ,
                        n.iter         =      10000 )
```

Signal detection theory ∼ results



Signal detection theory ~ summary statistics

```
summary(samples)$statistics
```

```
##          Mean        SD     Naive SE Time-series SE
## b -0.03170489 0.1469896 0.0008486449    0.001141949
## d  1.71504253 0.2856798 0.0016493731    0.002172923
```

```
summary(samples)$quantiles
```

```
##         2.5%        25%         50%       75%     97.5%
## b -0.3213127 -0.1300397 -0.03126564 0.0667394 0.2572163
## d  1.1652033  1.5187961  1.71335391 1.9072853 2.2788937
```

Signal detection theory ~ convergence

```
effectiveSize(samples)
```

```
##        b        d
## 16584.75 17313.84
```

```
gelman.diag(samples)
```

```
## Potential scale reduction factors:
##
##   Point est. Upper C.I.
## b          1          1
## d          1          1
##
## Multivariate psrf
##
## 1
```

Summary and conclusion

The outcome of a Bayesian analysis is a probability distribution over parameters of interest

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

Monte Carlo methods provide such a method

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