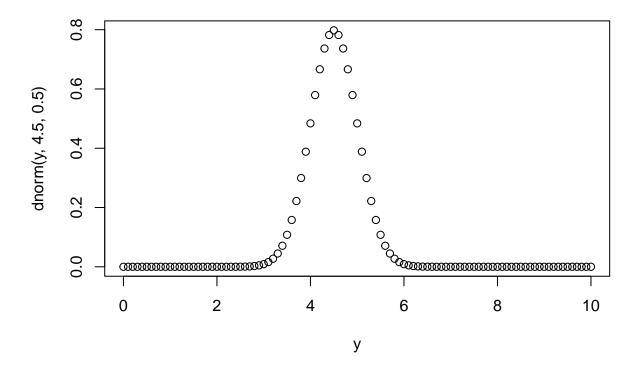
## Bayesian Inference

## David Márquez & Jan Izquierdo

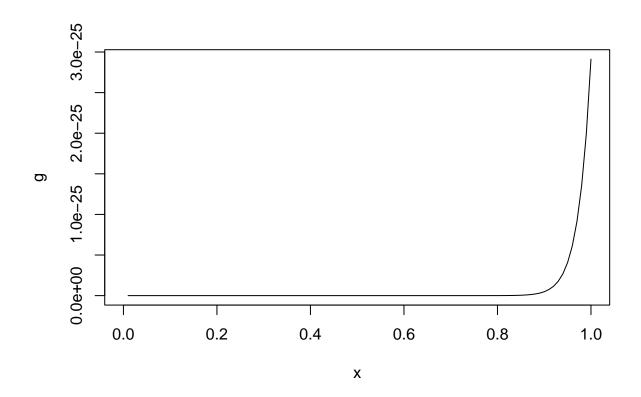
2023-11-15

2. The authors of a paper claim that the mean life expectancy of this bacterium is  $4.5\pm0.5h$  (reading the paper we see that 0.5h is just the standard deviation). Using a Gaussian density for implementing the prior information for parameter , compute the posterior density, the expectation and a 95% credibility interval. You can follow the following steps: #prior normal distribution

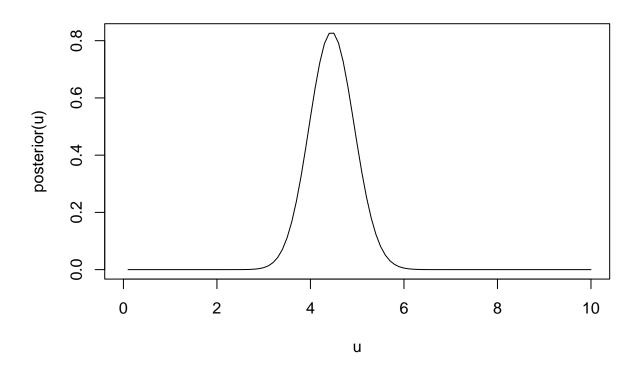
```
Likelihood_Function \leftarrow function(x){(1/(x^8))*exp(-31.77/x)}
y = seq(0,10,0.1)
plot(y, dnorm(y,4.5,0.5))
```



```
#now define f(nu/x) (posterior function)
g = function(x){dnorm(x,4.5,0.5)*(1/x^8)*exp(-31.77/x)}
plot(g)
```

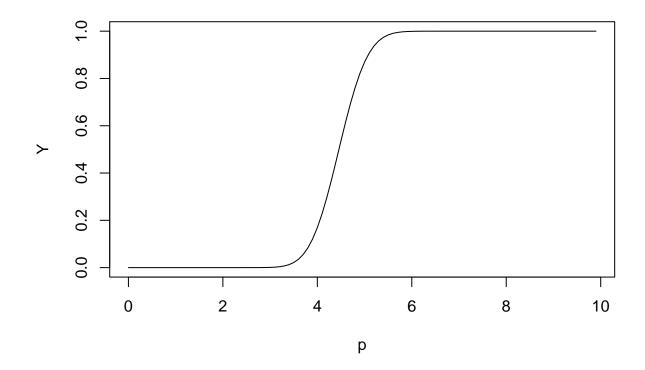


```
#integrate to obtain Constant
c <- integrate(g,0,Inf, rel.tol = 1e-18)$value #rel.tol is to have a lower error and be more sure
help("integrate")
#declare posterior with constant
posterior <- function(x){(dnorm(x,4.5,0.5)*(1/x^8)*exp(-31.77/x))/c}
u = seq(0,10,0.1)
Y = numeric(length(u))
for (i in 1:length(u)){
    Y[i] = posterior(u[i])
}
plot(u,posterior(u), type = 'l')</pre>
```



#it gives a error with seq because seq is a vector an this function does not accept vectors

#define the distribution
h = function(x){integrate(posterior,0,x)\$value}
p = seq(0.000001,10,0.1)
Y = numeric(length(p))
for (i in 1:length(p)){
 Y[i] = h(p[i])
}
plot(p,Y,type = 'l')



```
#F(u) = 0.025
lower_bound <- uniroot(function(x) h(x) - 0.025, interval = c(2, 6))
#F(u) = 0.975
upper_bound <- uniroot(function(x) h(x) - 0.975, interval = c(4, 8))
```

####3. Test if your results agree with those of the authors of the paper. In other words, consider H0: = 4.5 and H1: 4.5. Be non informative for the prior probabilities of H0 and H1, and consider for H1 the same Gaussian prior than in part 2. Compute P(H0|X), P(H1|X), and the Bayes factor. Which are the conclusions?

```
pH0 <- (Likelihood_Function(4.5))/(Likelihood_Function(4.5)+ integrate(g, 0, Inf)$value)
pH1 <- 1 - pH0
#Bayesian factor (in favor of H0):
bayesian <- pH0/pH1
cat('The bayesian factor in favor of H0:',bayesian)</pre>
```

## The bayesian factor in favor of HO: 1.259583

```
#Bayesian factor (in favor of H1):
cat('The bayesian factor in favor of H1:',1/bayesian)
```

## The bayesian factor in favor of H1: 0.7939133

Practical Bayesian interesce

DLifetime of bacterium at certain + follows exponential distribution with desity

(2/56,0'42,3'72,0'64,10'7,1'57,9'62,2'54) William = 1

a) Likelihood function. Estimate men life expectang using classical interacegrordure

L(x1\mu)=\frac{1}{\mu} = \frac{1}{\mu} = \frac

= 1 e -31/77

Estimate mean life expectand pe  $\ell(x|\mu) = h\left(\frac{e^{-\hat{\xi}x_i/\mu}}{\mu^n}\right) = \frac{-\hat{Z}x_i}{\mu} - \ln \mu^n = \frac{-31'77}{\mu} - \ln \mu^8$ 

d (K/μ) = Jy (31'77 - h (μ8)) = 31'77 - 1 8μ2 - 31'77 - 8 μ2 - 31'77 - 8 μ2 - 31'77 - 8

Jμ ((x/μ) =0 > 31/77 -8 = 0 = 31/77 -8μ =0 > 31/77 -8μ=0 > 31/77 = μ2 n= 3'97

a) TILMSL(xlp)