HW6

(a) Assuming a noninformative uniform prior on the parameters in question (α, β), the posterior is $\propto p(y_i|\alpha,\beta,n_i,x_i) \propto [\text{logit}^{-1}(\alpha+\beta x_i)]^{y_i}[1-\text{logit}^{-1}(\alpha+\beta x_i)]^{n_i-y_i}$. For the purposes of HMC, we'll use the log posterior, which is given by $y_i((\alpha+\beta x_i)-\log(1+e^{\alpha+\beta x_i}))-(n_i-y_i)\log(1+e^{\alpha+\beta x_i}) = y_i(\alpha+\beta x_i) - n_i\log(1+e^{\alpha+\beta x_i})$. In code:

```
inv.logit <- function(x){
  exp(x)/(1+exp(x))
}

log_p_th <- function(th, y, n, x){
  alpha <- th[1]
  beta <- th[2]
  log_prior <- 0
  log_likelihood <- sum(log((inv.logit(alpha + beta * x) ^ y)
                            * (1 - inv.logit(alpha + beta * x)) ^ (n-y)))
  return (log_likelihood + log_prior)
}
```

We can now get the gradients $\frac{d\log p(\alpha,\beta|y_i,n_i,x_i)}{d\alpha} = y_i - n_i\frac{e^{\alpha+\beta x_i}}{1+e^{\alpha+\beta x_i}}$ and $\frac{d\log p(\alpha,\beta|y_i,n_i,x_i)}{d\beta} = y_i x_i - n_i x_i\frac{e^{\alpha+\beta x_i}}{1+e^{\alpha+\beta x_i}} = x_i(y_i - n_i\frac{e^{\alpha+\beta x_i}}{1+e^{\alpha+\beta x_i}}$. In code:

```
gradient_th <- function(th, y, n, x){
  alpha <- th[1]
  beta <- th[2]
  d_alpha <- sum(y - n * inv.logit(alpha + beta * x))
  d_beta <- sum(x * (y - n * inv.logit(alpha + beta * x)))
  return (c(d_alpha, d_beta))
}
```

Now we want to check the gradient numerically:

```
gradient_th_numerical <- function(th, y, n, x){
  d <- length(th)
  e <- .0001
  diff <- rep(NA, d)
  for (k in 1:d){
    th_hi <- th
    th_lo <- th
    th_hi[k] <- th[k] + e
    th_lo[k] <- th[k] - e
    diff[k] <- (log_p_th(th_hi, y, n, x) - log_p_th(th_lo, y, n, x))/(2 * e)
  }
  return (diff)
}

setwd("~/Documents/BDA/Homework 6")
bioassay <- read.table("bioassay_data.txt", header=TRUE)
x <- bioassay$x
y <- bioassay$y
```

```r
n <- bioassay$n
gradient_th(c(1, 1), y, n, x)
```

```
## [1] -4.868  3.582
```

```r
gradient_th_numerical(c(1, 1), y, n, x)
```

```
## [1] -4.868  3.582
```