

# Assignment 4

anonymous

## 1 General information

## 2 Bioassay model

### 2.0.1 (a)

### 2.0.2 (b)

Loading the library and the data.

```
# Useful functions: quantile()
# and mcse_quantile() (from aaltobda)

data("bioassay_posterior")
# The 4000 draws are now stored in the variable `bioassay_posterior`.
# The below displays the first rows of the data:
head(bioassay_posterior)
```

	alpha	beta
1	-0.02050577	10.032841
2	1.21738518	4.504546
3	3.04829407	16.239424
4	1.32272770	4.924268
5	1.36274817	12.880561
6	1.08593225	5.943731

## 3 Importance sampling

### 3.0.1 (c)

```
# Useful functions: bioassaylp (from aaltobda)
alpha_test = c(1.896, -3.6, 0.374, 0.964, -3.123, -1.581)
beta_test = c(24.76, 20.04, 6.15, 18.65, 8.16, 17.4)

log_importance_weights <- function(alpha, beta) {
  # Do computation here, and return as below.
  # This is the correct return value for the test data provided above.
  c(-8.95, -23.47, -6.02, -8.13, -16.61, -14.57)
```

```
}
```

### 3.0.2 (d)

```
normalized_importance_weights <- function(alpha, beta) {  
  # Do computation here, and return as below.  
  # This is the correct return value for the test data provided above.  
  c(0.045, 0.000, 0.852, 0.103, 0.000, 0.000)  
}
```

### 3.0.3 (e)

Write your answers and code here!

### 3.0.4 (f)

```
S_eff <- function(alpha, beta) {  
  # Do computation here, and return as below.  
  # This is the correct return value for the test data provided above.  
  1.354  
}
```

### 3.0.5 (g)

### 3.0.6 (h)

```
posterior_mean <- function(alpha, beta) {  
  # Do computation here, and return as below.  
  # This is the correct return value for the test data provided above.  
  c(0.503, 8.275)  
}
```