Assignment 4

anonymous

1 General information

2 Bioassay model

2.1 (a)

2.2 (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

3.1 (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)
```

```
    }
```

3.2 (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)
}
```

3.3 (e)

Write your answers and code here!

3.4 (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
}
```

3.5 (g)

3.6 (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)
}
```