

# Assignment 5

anonymous

## 1 General information

### ! Reporting accuracy

**For posterior statistics of interest, only report digits for which the Monte Carlo standard error (MCSE) is zero.**

*Example:* If you estimate  $E(\mu) = 1.234$  with  $\text{MCSE}(E(\mu)) = 0.01$ , you should report  $E(\mu) = 1.2$ .

See lecture video 4.1, [the chapter notes](#), and [a case study](#) for more information.

## 2 Generalized linear model: Bioassay model with Metropolis

### 2.1 (a)

Write your answers/code here!

```
# Useful functions: runif, rnorm
# bioassaylp, dmnorm (from aaltobda)

data("bioassay")
# Start by implementing a function called `density_ratio` to
# compute the density ratio function,  $r$  in Eq. (11.1) in BDA3:
density_ratio <- function(alpha_propose, alpha_previous, beta_propose, beta_previous, x,
  # Do computation here, and return as below.
  # Below are the correct return values for two different calls of this function:

  # alpha_propose = 1.89, alpha_previous = 0.374,
  # beta_propose = 24.76, beta_previous = 20.04,
  # x = bioassay$x, y = bioassay$y, n = bioassay$n
  1.305179
```

```

# alpha_propose = 0.374, alpha_previous = 1.89,
# beta_propose = 20.04, beta_previous = 24.76,
# x = bioassay$x, y = bioassay$y, n = bioassay$n
0.7661784

}
# Then implement a function called `metropolis_bioassay()` which
# implements the Metropolis algorithm using the `density_ratio()`:
metropolis_bioassay <- function(alpha_initial, beta_initial, alpha_sigma, beta_sigma, no_
# Do computation here, and return as below.
# Below are "wrong" values (unlikely to actually occur)
# in the "correct" format (such that they work with the plotting functions further do
data.frame(
  alpha=c(alpha_initial, alpha_initial+alpha_sigma, alpha_initial-alpha_sigma),
  beta=c(beta_initial, beta_initial+beta_sigma, beta_initial-beta_sigma)
)

}
df = metropolis_bioassay(0, 0, 1, 1, 1000, bioassay$x, bioassay$y, bioassay$n)

```

## 2.2 (b)

**Write your answers/code here!**

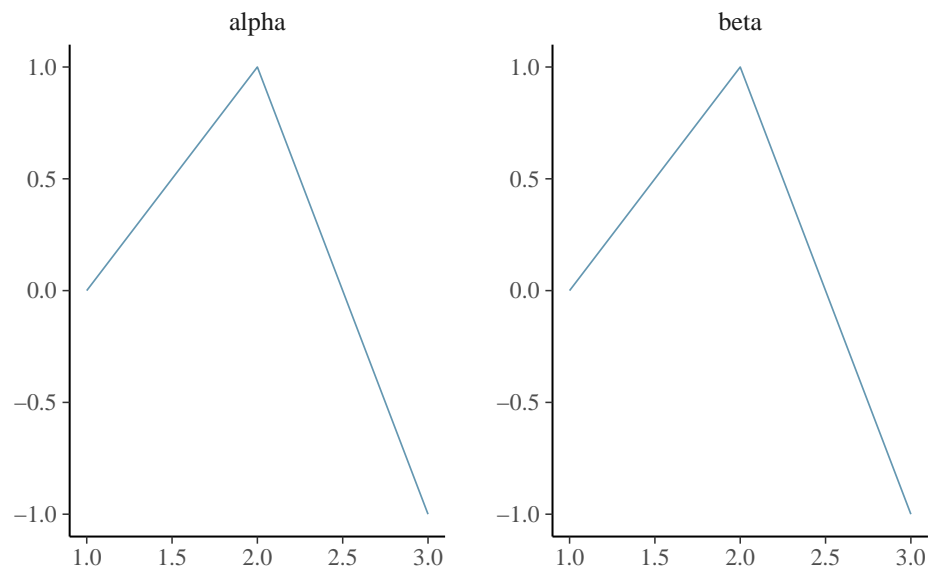
Have a look at [bayesplot trace plot examples](#) and tune your plot if wanted/needed. Don't forget to include a title/caption/description.

**The below example plot only includes a single chain, but your report should include a plot with multiple chains overlayed!**

```

# Useful functions: mcmc_trace (from bayesplot)
mcmc_trace(df, pars=c("alpha", "beta"))

```



### 2.3 (c)

Write your answers/code here!

```
# Useful functions: rhat_basic (from posterior)
```

### 2.4 (c)

Write your answers/code here!

Have a look at [bayesplot scatter plot examples](#) and tune your plot if wanted/needed. Don't forget to include a title/caption/description.

```
# Useful functions: mcmc_scatter (from bayesplot)
mcmc_scatter(df, pars=c("alpha", "beta"))
```

