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, dmvnorm (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)
```

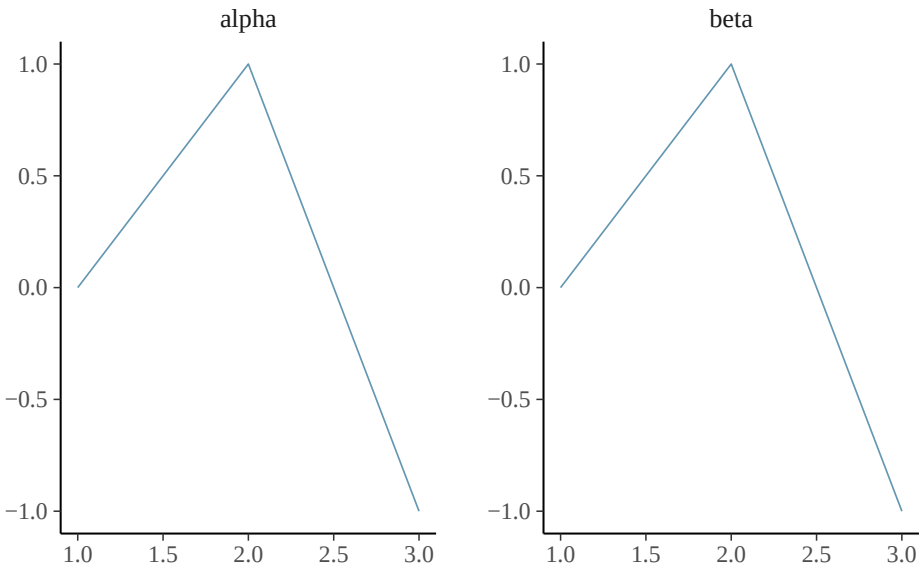
2.2 (b)

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!

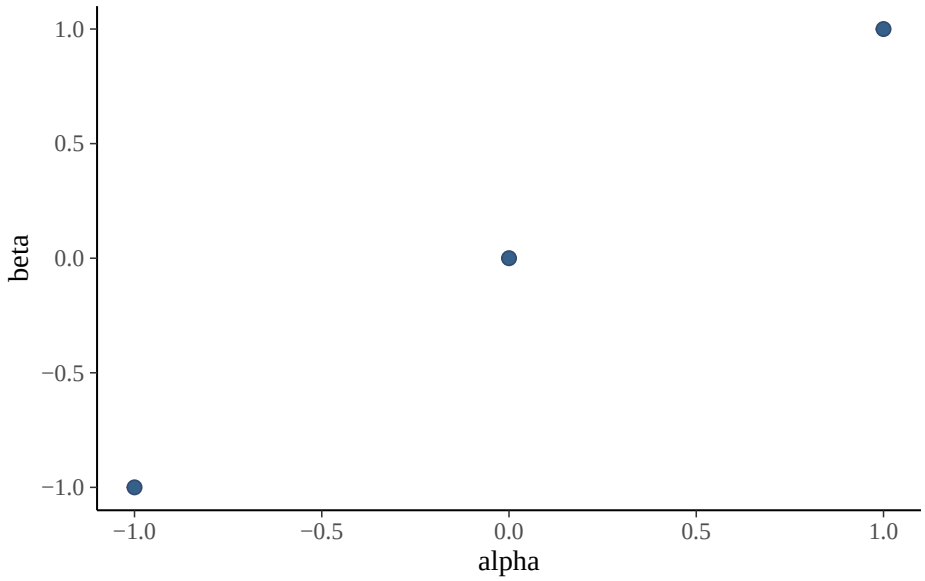
```
# Useful functions: rhat_basic (from posterior)
```

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"))
```


1.0
0.5
0.0
−0.5
−1.0
beta
−1.0
−0.5
0.0
0.5
1.0
alpha