Assignment 6

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.

This is the template for assignment 6. You can download the broken stan-file and the qmd-file or copy the code from this rendered document after clicking on </> Code in the top right corner.

Please replace the instructions in this template by your own text, explaining what you are doing in each exercise.

2 Stan warm-up: linear model of BDA retention with Stan (2 points)

2.1 (b)

Write your answers/code here!

Plotting happens here:

```
ggplot() +
  # scatter plot of the training data:
  geom_point(
    aes(x, y, color=assignment),
    data=data.frame(x=assignment, y=propstudents, assignment="1-8")
) +
  # scatter plot of the test data:
  geom_point(
    aes(x, y, color=assignment),
    data=data.frame(x=no_assignments, y=propstudents9, assignment="9")
) +
  # you have to tell us what this plots:
  geom_line(aes(x,y=value,linetype=pct), data=mu_quantiles_df, color='grey', linewidth=1.5) +
  # you have to tell us what this plots:
  geom_line(aes(x,y=value,linetype=pct), data=y_quantiles_df, color='red') +
```

```
    # adding xticks for each assignment:
    scale_x_continuous(breaks=1:no_assignments) +
    # adding labels to the plot:
    labs(y="assignment submission %", x="assignment number") +
    # specifying that line types repeat:
    scale_linetype_manual(values=c(2,1,2)) +
    # Specify colours of the observations:
    scale_colour_manual(values = c("1-8"="black", "9"="blue")) +
    # remove the legend for the linetypes:
    guides(linetype="none")
```

```
Error in fortify(data): object 'mu_quantiles_df' not found
```

2.2 (c)

Write your answers/code here!

3 Generalized linear model: Bioassay with Stan (4 points)

3.1 (d)

Write your answers/code here!

```
data("bioassay")
```

3.2 (e)

Write your answers/code here!

3.3 (f)

Write your answers/code here!

3.4 (g)

Write your answers/code here!