## Midterm - 2025

## The data

Load the data:

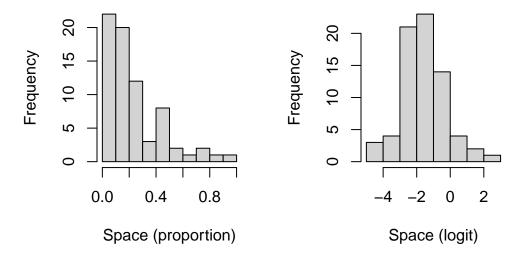
```
library(rethinking)
library(tidyverse)
# Set the web address where R will look for files from this repository
repo_url <- "https://raw.githubusercontent.com/elahi/elahi.github.io/master/"
dat <- read.csv(paste(repo_url, "data/meps_2012_survey_data.csv", sep = ""))
glimpse(dat)</pre>
```

```
Rows: 72
Columns: 9
$ X
             <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,~
             <chr> "ON", "ON", "ON", "ON", "ON", "ON", "ON", "ON", "ON", "ON"~
$ site
             <chr> "ONO", "ONO", "ONO", "ONO", "ON1", "ON1", "ON1", "ON1", "O~
$ transect
             <chr> "ONO_45", "ONO_46", "ONO_48", "ONO_49", "ON1_17", "ON1_84"~
$ quadrat
$ chiton_mean <dbl> 0.0000000, 1.0000000, 0.0000000, 0.0000000, 1.0000000, 0.0~
             <dbl> 0.14213721, 0.22878590, 0.12508222, 0.24288815, 0.73034557~
$ space
$ richness
             <int> 10, 12, 8, 10, 10, 9, 9, 7, 8, 8, 9, 8, 10, 13, 10, 15, 13~
$ simpsondiv <dbl> 0.7004303, 0.7497803, 0.6160904, 0.7580468, 0.7172267, 0.7~
$ urchin mean <dbl> 0.6666667, 0.6666667, 0.6666667, 0.6666667, 1.0000000, 1.0~
```

Transform the proportional cover of space so that we can model it using a normal distribution:

```
# Define logit function
logit <- function(p) log(p / (1 - p))
dat <- dat %>%
   mutate(space_logit = logit(space))
# Plot
```

```
par(mfrow = c(1,2))
hist(dat$space, main = "", xlab = "Space (proportion)")
hist(dat$space_logit, main = "", xlab = "Space (logit)")
```



Importantly, the response is no longer bounded between 0 and 1. It is *not* important that logit(space) appears normally distributed! It just so happens that this is the case here. For now, ignore the effect of site and transect.

## Suggested workflow

You will skip the generative simulation for this exercise. Here is a suggested workflow:

- 1. Visualize the data to make sense of the patterns
- 2. Standardize the predictors
- 3. Come up with sensible priors by plotting prior predictive distributions (see HW4-key or SR2 Fig 5.8 for example). Justify your choice of priors.
- 4. Run the models using ulam. Diagnose your chains what are the criteria you checked to ensure convergence? See SR2 9.4-9.5 for help.
- 5. Compare WAIC for the models.
- 6. Interpret in the context of the DAG and the published results.

