Easy

E1

2,4

E2

$$Diversity_{animal} = \alpha + \beta_{plant} Diversity_{plant} + \beta_{latitude} Latitude$$

E3

I would expect each slope to be negative.

$$TTD = \alpha + \beta_{funding} Funding + \beta_{size} LabSize$$

E4

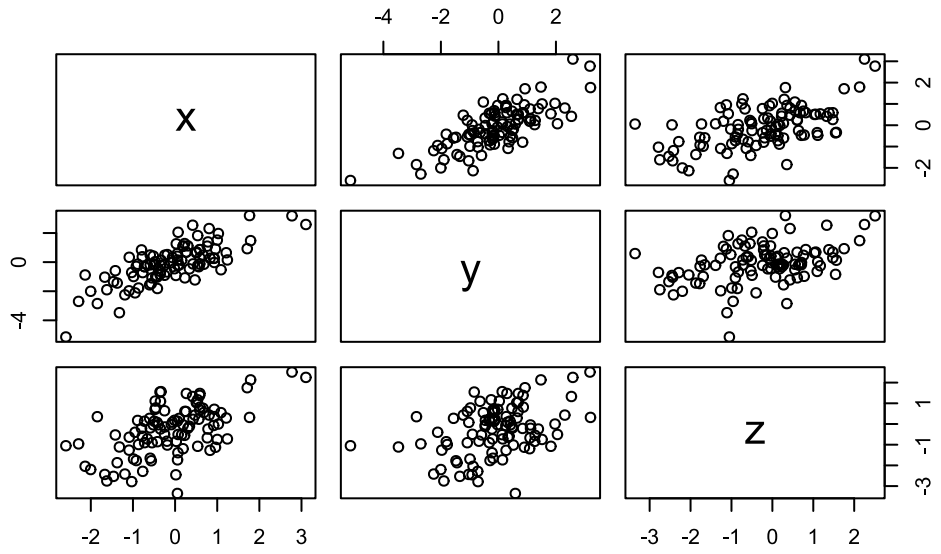
I think they are all equivalent?

Medium

M1

Simulate a random variable x that is positively correlated with z and y, this will create a spurious correlations between y and z. But after accounting for the affect of x on y, adding z doesn't.

```
n <- 100
# simulate x
x <- rnorm(n)
# simulate y so that it is positively correlated with x
y <- rnorm(n, x)
# simulate z so that it is positively coreelated with x
z <- rnorm(n, x)
# visualize the pairs
pairs(data.frame(x,y,z))
```




```
# look at the raw correlations
cor(data.frame(x,y,z))
```

```
          x         y         z
x 1.0000000 0.7591824 0.5798727
y 0.7591824 1.0000000 0.4108654
z 0.5798727 0.4108654 1.0000000
```

```
# least squares regression
X <- matrix(c(rep(1, length(y)),x,z), ncol = 3)
solve(t(X) %*% X) %*% (t(X) %*% y)
```

```
           [,1]
[1,] -0.0111515
[2,]  1.0629061
[3,] -0.0492667
```

```
lm(y ~ x + z)
```

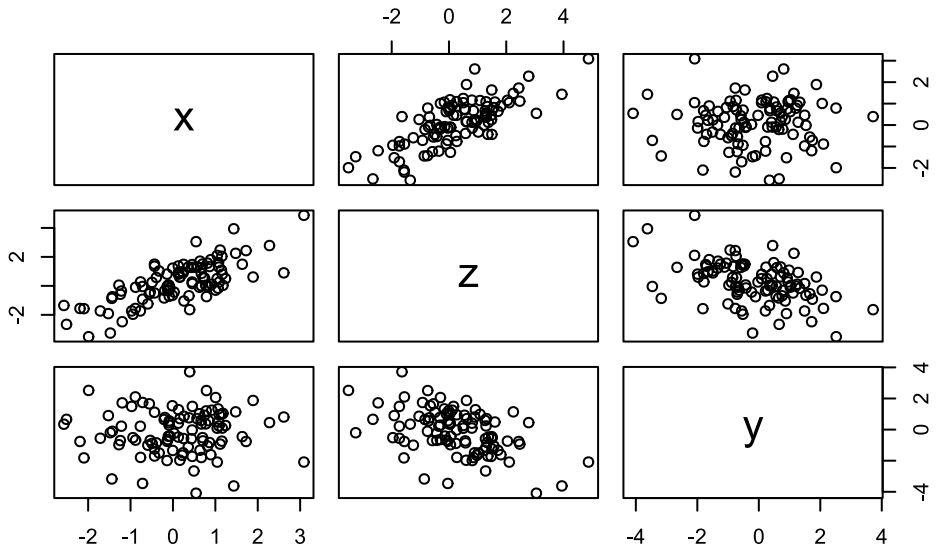
```


Call:
lm(formula = y ~ x + z)
```

```
Coefficients:
(Intercept)            x            z
   -0.01115      1.06291     -0.04927
```

M2

By simulating a random variable x and a random variable z that is correlated with x you get a positive correlation between x and z, then by simulating a random variable y that is positively correlated with x and negatively correlated with y. This makes no correlation between x and y and a reduced correlation between z and y. By adding them both into the multiple regression, the true values are recovered.

```
set.seed(120414)
# simulate x
x <- rnorm(n)
# simulate z so that it is positively correlated with x
z <- rnorm(n, x)
# simulate y so that it is positively correlated with x but negatively correlated
wity z
y <- rnorm(n, x - z)
# look at pairs plots to visualize
pairs(data.frame(x,z,y))
```



```
# look at the raw correlations
cor(data.frame(x,z,y))
```

```
           x          z           y
x 1.00000000  0.7426733  0.02266509
z 0.74267326  1.0000000 -0.47133835
y 0.02266509 -0.4713383  1.00000000
```

```
# least squares to recover the regression coefficients
X <- matrix(c(rep(1,length(y)), x, z), ncol = 3)
solve(t(X) %*% X) %*% t(X) %*% y
```

```
             [,1]
[1,]  0.004811758
[2,]  1.092155887
[3,] -1.075275811
```

M3

I guess you could try to predict marriage from divorce and age, presumably states with a younger median age at marriage would have a higher marriage rate and a lower divorce rate would lead to a higher marriage rate–I think

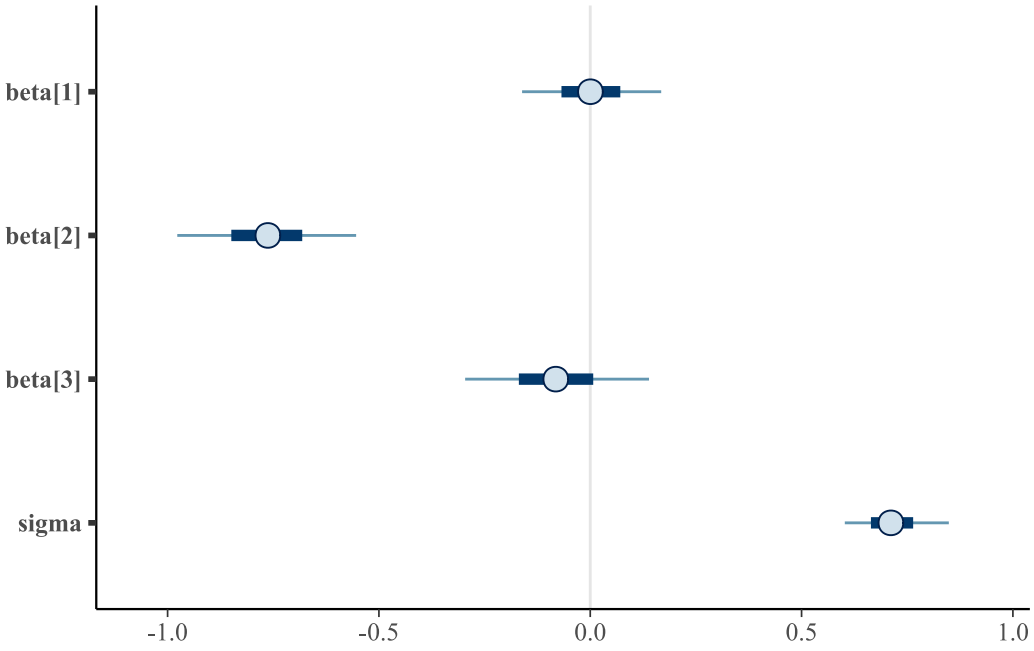
```
library(rethinking)
library(tidyverse)
library(cmdstanr)
library(bayesplot)

data("WaffleDivorce")
d <- WaffleDivorce

# function to standardize variables
stn <- function(x) (x - mean(x))/sd(x)

X <- matrix(c(rep(1, nrow(d)), stn(d$MedianAgeMarriage), stn(d$Divorce)),
            ncol = 3)
dat <- list(
  N = nrow(d),
  K = ncol(X),
  marriage = stn(d$Marriage),
  X = X
)

mod.3 <- cmdstan_model("stan_models/married_pred.stan")
```

```
Warning in readLines(stan_file): incomplete final line found on
'stan_models/married_pred.stan'
```

```
fit.3 <- mod.3$sample(
  data = dat,
  chains = 4,
  parallel_chains = 4,
  show_message = F
)

fit.3$diagnostic_summary()
```

```
$num_divergent
[1] 0 0 0 0

$num_max_treedepth
[1] 0 0 0 0

$ebfmi
[1] 0.9973762 1.0960696 0.9772913 1.0830302
```

```
mcmc_intervals(fit.3$draws(c("beta", "sigma")))
```



This model thinks that median marriage age is a better predictor of marriage rate than divorce rate.

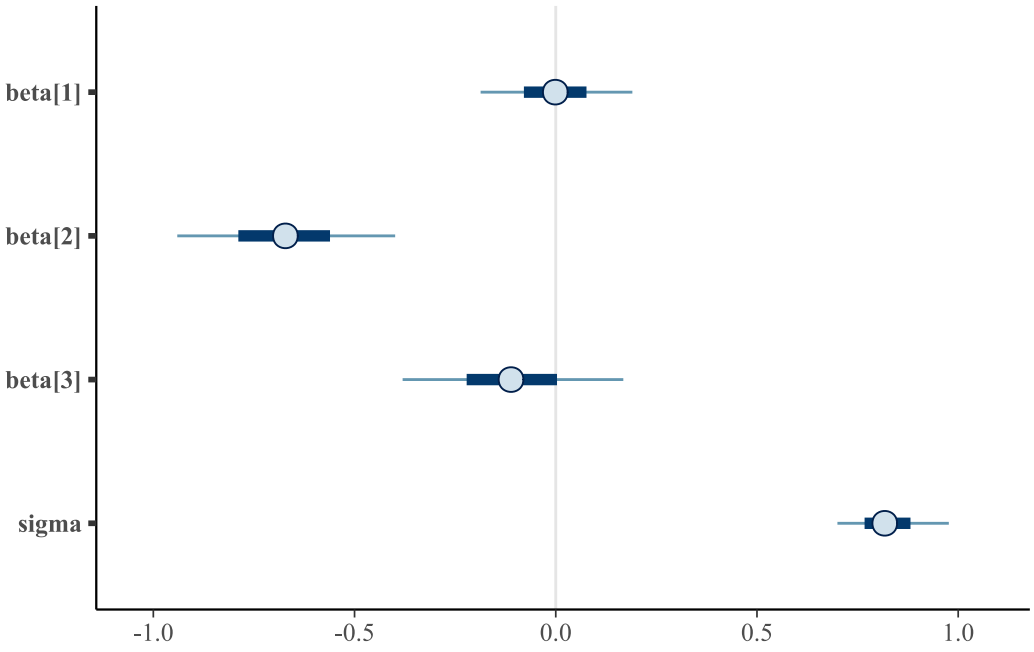
M4

```
# get the data into order
d <- WaffleDivorce
lds <- read.csv("lds_prop.csv")
lds <- lds %>%
  select(Location = "X.State", lds_prop)
d <- d %>%
  left_join(lds)

dat <- d %>%
  select(Divorce, age = MedianAgeMarriage, mar_rate = Marriage, lds = lds_prop)
%>%
  mutate(divorce = stn(Divorce),
         age = stn(age),
         mar_rate = stn(mar_rate),
         lds = stn(lds))

mod.4 <- cmdstan_model("stan_models/divorce_lds.stan")

# lets try it first without the lds data

# create a design matrix for the covariates, with a column of 1's for the
intercept
X = matrix(c(rep(1, nrow(dat)), dat$age, dat$mar_rate), ncol = 3)

stan_dat <- list(
  N = nrow(dat),
  K = ncol(X),
  X = X,
  divorce = dat$divorce
)

fit.4_nolds <- mod.4$sample(
  data = stan_dat,
  chains = 4,
  parallel_chains = 4,
  show_messages = F
)

fit.4_nolds$diagnostic_summary()
```

```
$num_divergent
[1] 0 0 0 0
```

```
$num_max_treedepth
[1] 0 0 0 0

$ebfmi
[1] 1.087619 1.091299 1.023643 1.086551
```

```
mcmc_intervals(fit.4_nolds$draws(c("beta", "sigma")))
```

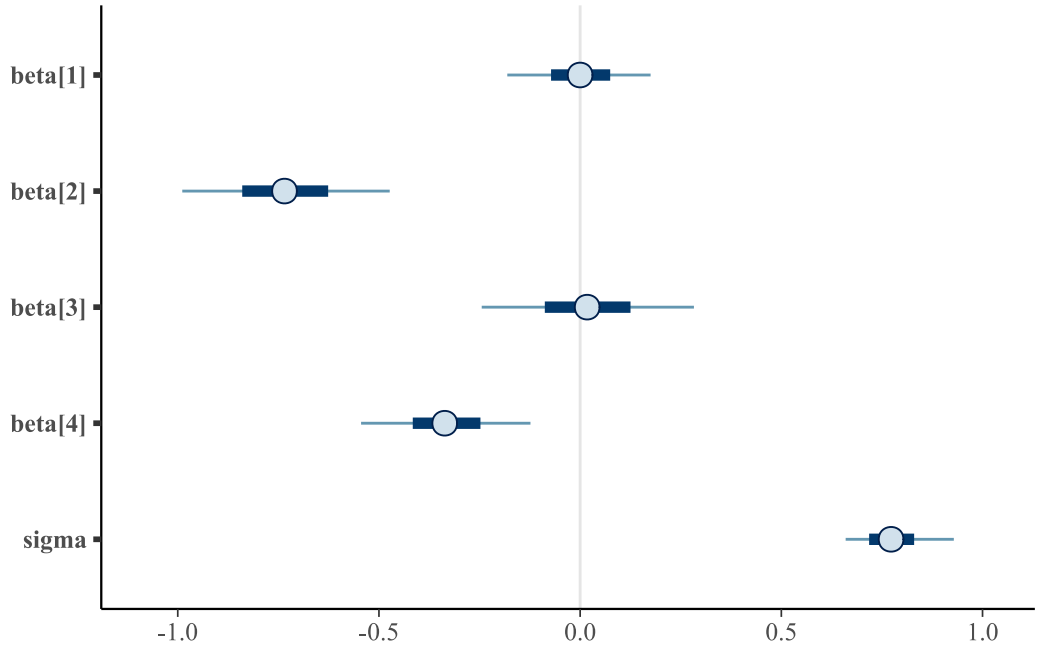



```
# now with the lds data


X = matrix(c(rep(1, nrow(dat)), dat$age, dat$mar_rate, dat$lds), ncol = 4)

stan_dat <- list(
  N = nrow(dat),
  K = ncol(X),
  X = X,
  divorce = dat$divorce
)



fit.4 <- mod.4$sample(
  data = stan_dat,
  chains = 4,
```

```
  parallel_chains = 4,
  show_messages = F
)

fit.4$diagnostic_summary()
```

```
$num_divergent
[1] 0 0 0 0

$num_max_treedepth
[1] 0 0 0 0

$ebfmi
[1] 0.9556615 1.0051774 1.0035906 0.9720306
```

```
mcmc_intervals(fit.4$draws(c("beta", "sigma")))
```



M5

$$obesity = \alpha + \beta_{gas} GasPrice + \beta_{eat} RestaurantVisits$$

$$obesity = \alpha + \beta_{gas} GasPrice + \beta_{exercise} ExerciseTime$$