Day 4

Everything Else

Austin Cutler
FSU

Agenda

- Final homework check
- Optimization
- Graphing regression results
- Parallelization with `map`
- Advanced Applications of Course Content

Final Homework check in

Let’s get optimal

Optimization

- There will be times where you may need to optimize a function in R
- When we say optimize, we're referring to finding the solution to a described problem
  - Most often this involves finding a local or global minimum or maximum (i.e., finding the point where our function's derivative equals 0)
- To do this, we can use the `optim()` function in R

`optim()`

- To use `optim()`, we first need to supply it with a function to optimize (Note: this is another use case for being comfortable with user created functions)
- You need to supply `optim()` with the starting value for the parameters to be optimized over
- You also need to define the method being used (we'll most often use 'L-BFGS-B')

optim()

- Below is an example:

```r
# first I need to define the function I want to optimize
function_1 <- function(x) {
# this function calculates the square of its input and adds 1
x^2 + 1
}
# second, I supply this function to optim()
optim(par = 5, function_1, method = "L-BFGS-B")
```

```
$par
[1] 4.984086e-25

$value
[1] 1

$counts
function gradient
       4        4

$convergence
[1] 0
```

```
$message
[1] "CONVERGENCE: NORM OF PROJECTED GRADIENT <= PGTOL"
```

`optim()`

- The output of `optim()` is as follows:
  - `convergence` will indicate if the algorithm converged (i.e., if a minimum can be found), will be 0 if it did
  - `par` is the value where the given function is minimized
  - `value` is the *global* minimum of the function

Maximization

- By default, `optim()` will estimate the minimum, however, we can change this to be the maximum if we add `control = list('fnscale' = -1)` to our original code

```
1 function_2 <- function(x) {
2   exp(x)
3 }
4
5 optim(par = 5, function_2, method = "L-BFGS-B",control = list('fnscale' = -
```

```
Error in optim(par = 5, function_2, method = "L-BFGS-B", control =
list(fnscale = -1)): L-BFGS-B needs finite values of 'fn'
```

Bounded Optimization

- In `optim()`, we can specify lower and upper bounds of the range we want to consider a function, which at times may fix this issue

```
1 optim(par = 5, function_2, method = "L-BFGS-B",control = list('fnscale' = -
```

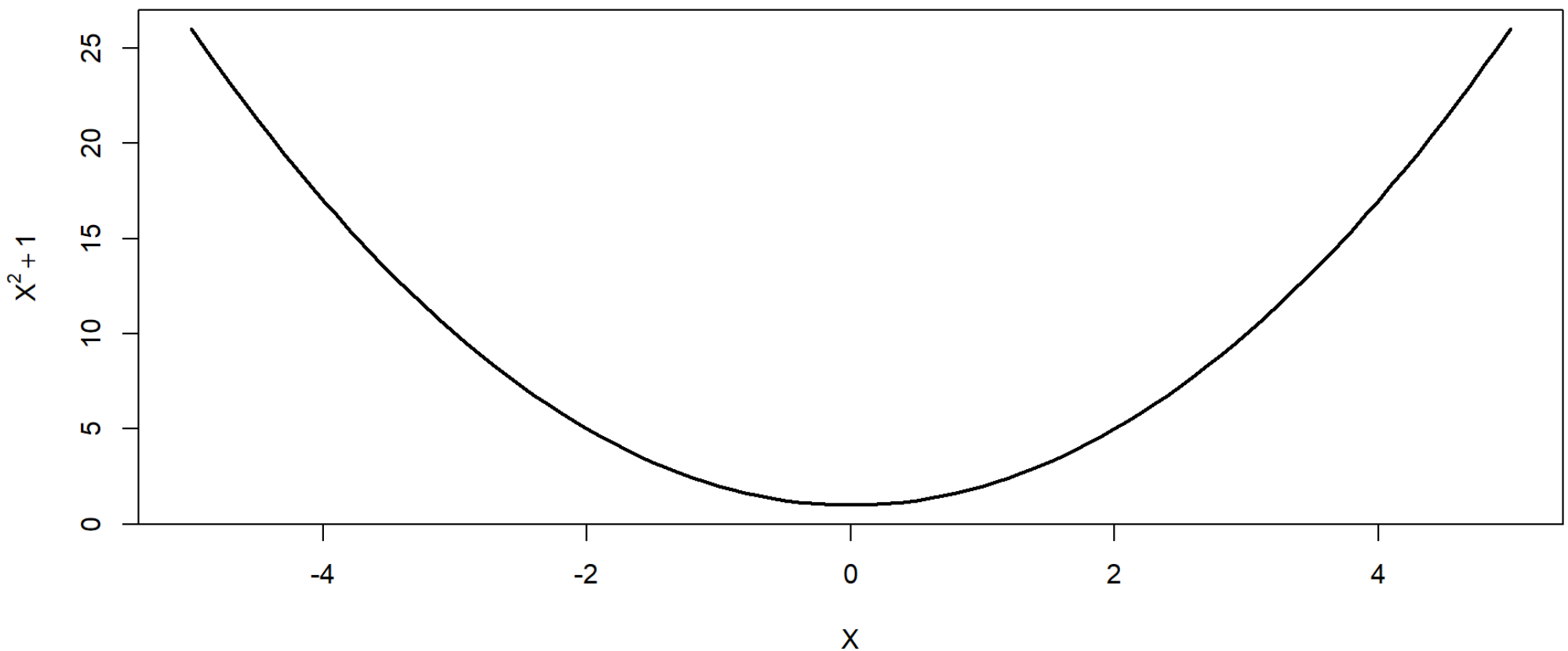
```
$par
[1] 100

$value
[1] 2.688117e+43

$counts
function gradient
       2        2

$convergence
[1] 0

$message
[1] "CONVERGENCE: NORM OF PROJECTED GRADIENT <= PGTOL"
```

Graphing Functions

- Sometimes it is useful to graph functions to better understand how they work
  - Or, if you wind up teaching methods, it can be very helpful
- To do this with base R, we can use the `curve()` function
- For ggplot, we use the `stat_function()` function
- In both cases, we will need to specify the range of values we want our function graphed over

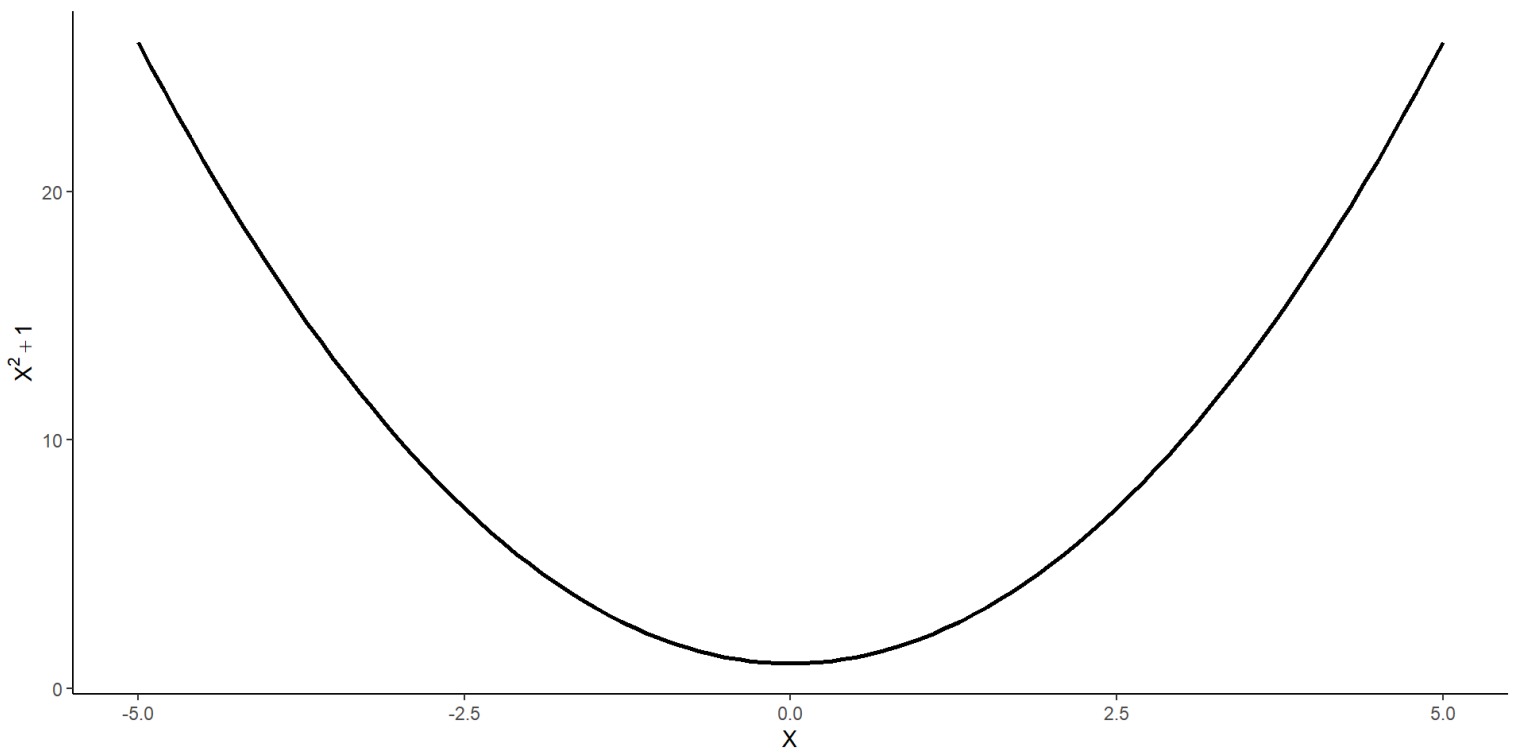
curve()

```
curve(function_1, from = -5, to = 5,
      xlab = 'X', ylab = expression(X^2+1), lwd = 2)
```



stat_function()

```
1  library(tidyverse)
2
3  tibble(x = seq(-5,5,by =  .1)) %>%
4    ggplot(aes(x = x))+
5    stat_function(fun = function_1, linewidth = 1)+
6    labs(x = 'X', y = expression(X^2+1))+
7    theme_classic()
```



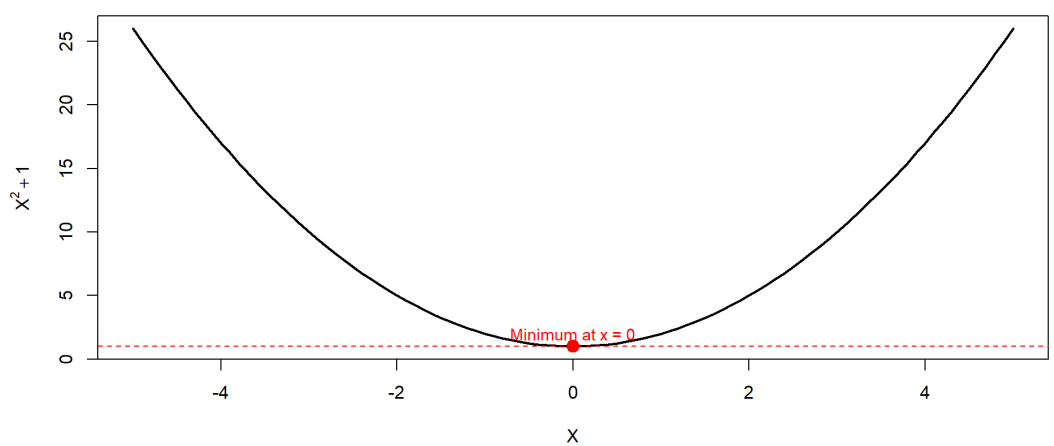
More on Graphing Functions

- We can also use `optim()` to add additional information about the function to our figure
- First we need to save the data, then add it to the figures

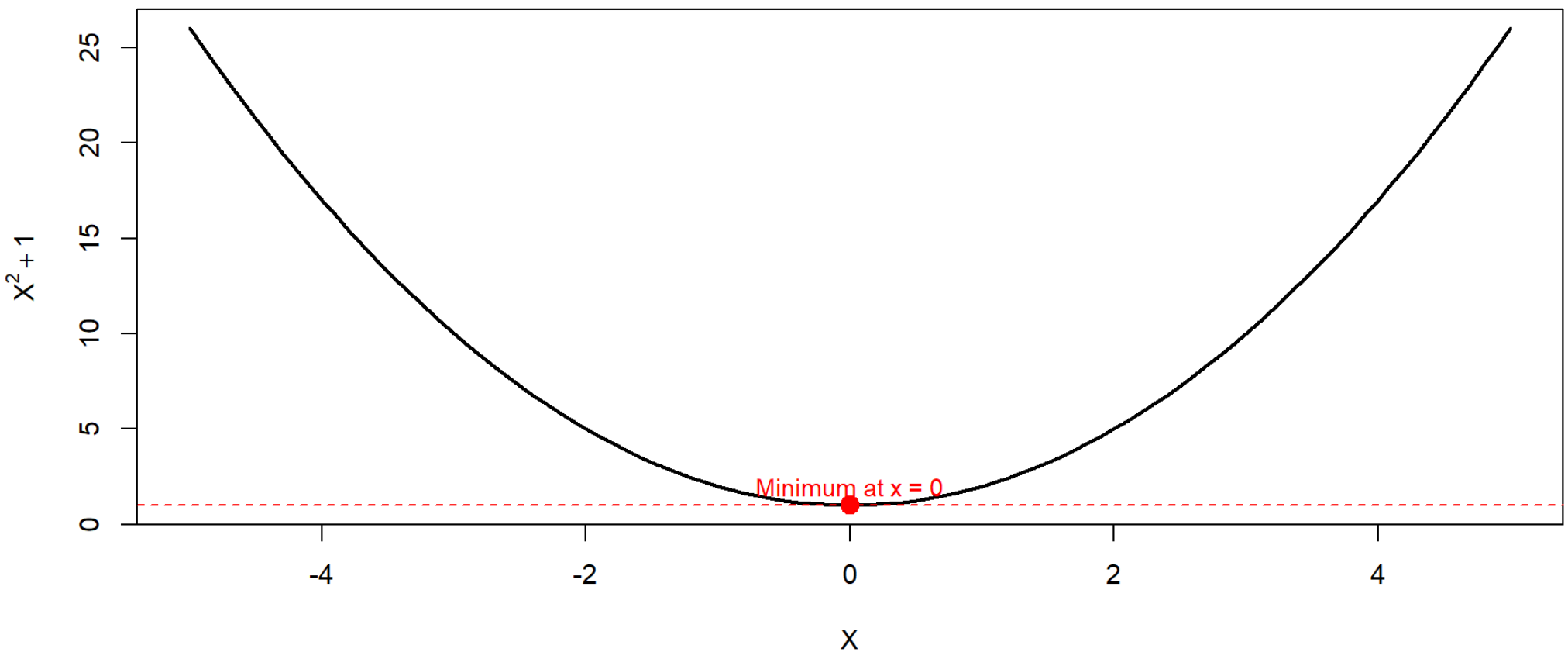
```
opt_result <- optim(par = 5, function_1, method = "L-BFGS-B")
# Extract the minimum point
x_min <- opt_result$par
y_min <- opt_result$value
```

curve()

```r
curve(function_1, from = -5, to = 5,
      xlab = 'X', ylab = expression(X^2 + 1), lwd = 2)

# Add red point from optim()
points(x_min, y_min, col = "red", pch = 19, cex = 1.5)

# tangent line
abline(h = y_min, col = "red", lty = 2)

# label
text(x_min, y_min + 1, labels = paste0("Minimum at x = ", round(x_min, 2)),
```

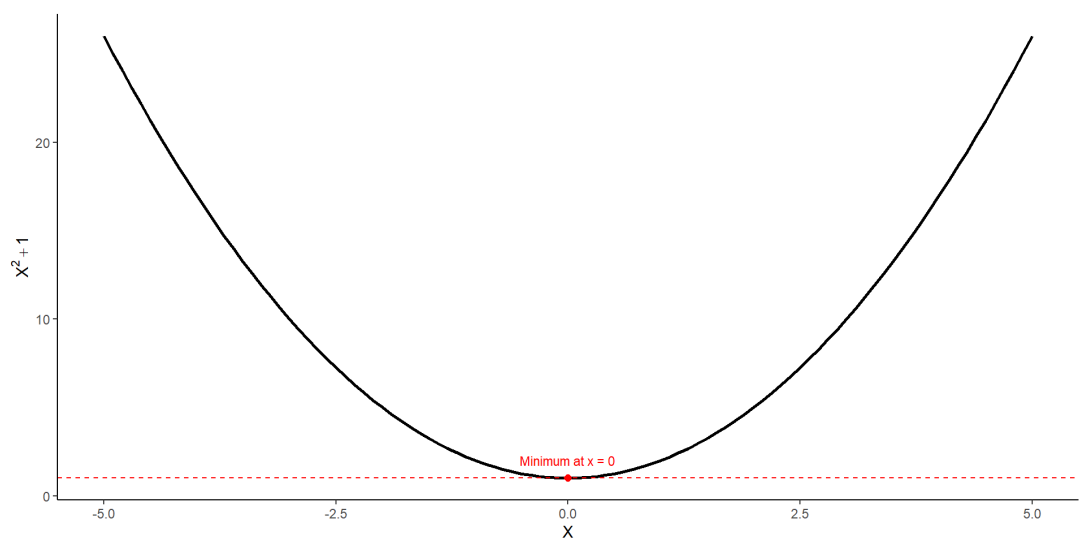


curve()

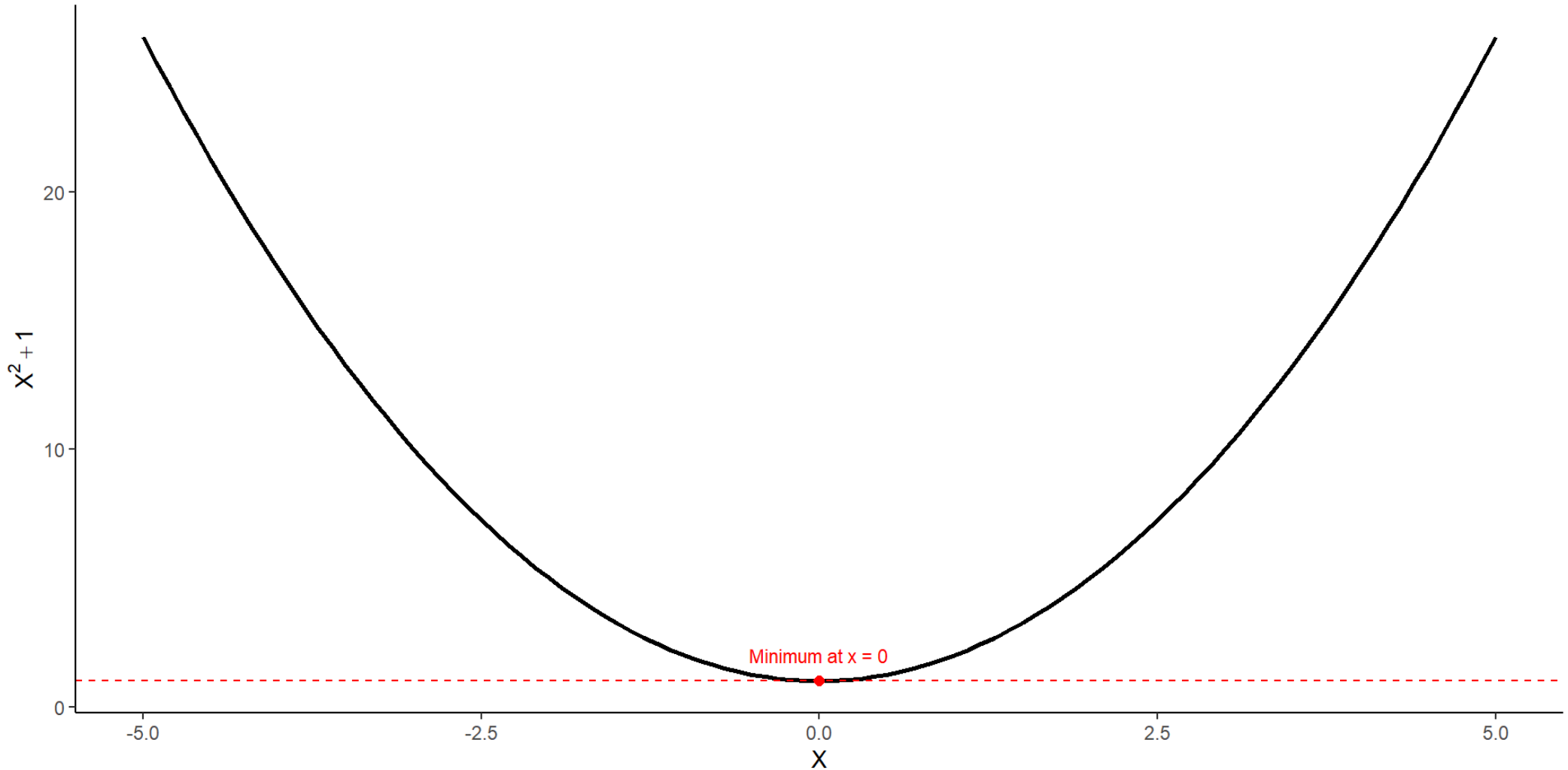


stat_function()

```r
tibble(x = seq(-5, 5, by = 0.1)) %>%
  ggplot(aes(x = x)) +
  stat_function(fun = function_1, linewidth = 1) +
  geom_point(data = tibble(x_min,y_min),
             aes(x = x_min, y = y_min), color = "red", size = 2) +
  geom_hline(yintercept = y_min, linetype = 2, color = "red") +
  annotate("text", x = x_min, y = y_min + 1,
           label = paste0("Minimum at x = ", round(x_min, 2)),
           color = "red", size = 3) +
  labs(x = expression(X), y = expression(X^2 + 1)) +
  theme_classic()
```



stat_function()



Practice

Complete the following problems:

- Create a function in R that is a negative quadratic ($-x^2 + 10$). Find the local maximum by hand, and find the maximum using `optim()`, compare your answers.
- Create a function that has a minimum *that is not a quadradic*. Plot the function, then calculate the value of the function that produces the minimum and maximum using `optim()`.
- Create a function that contains both a maximum and a minimum and plot the function. Calculate the value of the function that produces the minimum, the maximum, as well as the values of the minimum and maximum.

Presenting Regression Results

- One of the most important skills for being a political scientist is knowing how to present the results of our research
- The most important question to ask yourself when presenting results is to ask yourself “what is my quantity of interest?”
- The quantity of interest is whatever quantity is being used for the hypothesis test
  - The slope of a line
  - A difference in means
  - The difference between two slopes
  - Predicted probabilities across the range of a variable

Coefficient Plots

- The most effective way of showing regression results is using a coefficient plot
- With the skills you've already developed, you can create coefficient plots by hand easily
  - This is how I typically will get my results
- There are also several packages out there that produce very nice coefficient plots

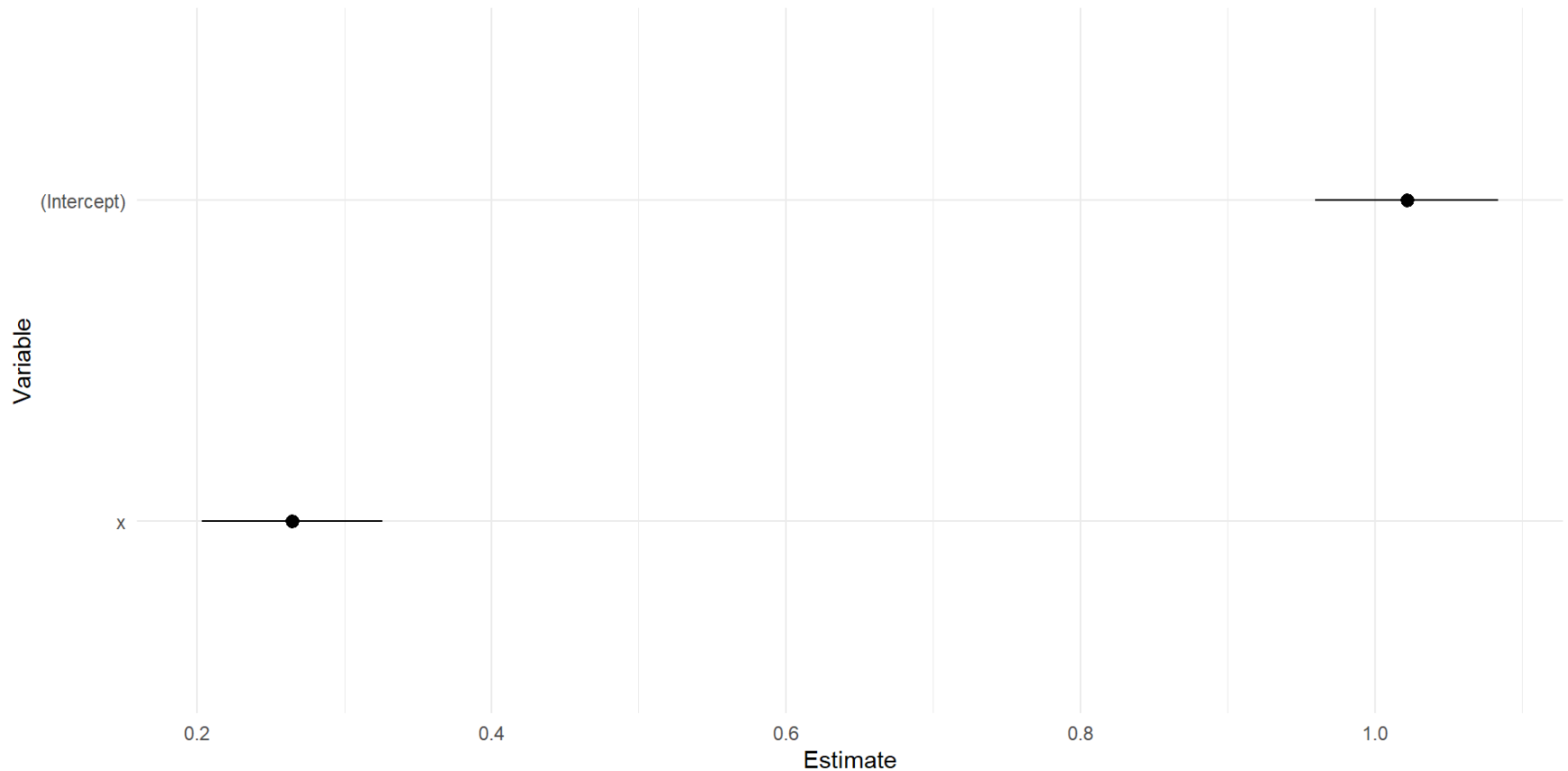
By Hand

- To make a coefficient plot by hand, all you need is your coefficient names, the coefficient value, and the standard error

```r
x  <- rnorm(1000)
y <- 1+.25*x+rnorm(1000)

fit <- lm(y~x)

##extracting standard error
se <-  summary(fit)$coefficients[, "Std. Error"]

#in this case I'm typing the variable names by hand, you can get this out i
tibble(var  = c('(Intercept)','x'),
       coef = coef(fit),
       se   = se) %>%
  mutate(lower = coef - 1.96*se,
         upper = coef + 1.96*se) -> coef_dat
```

By Hand

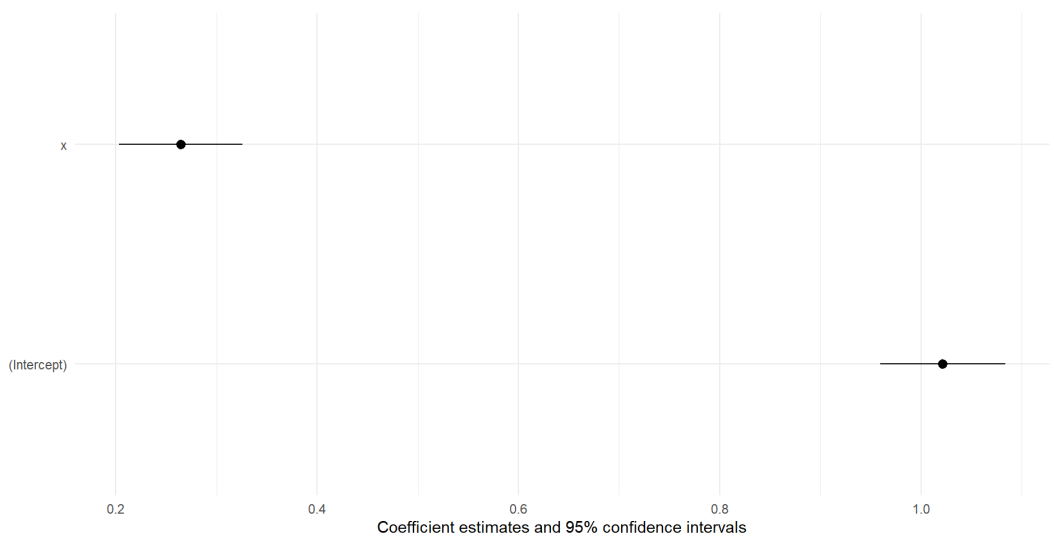
```
coef_dat %>%
  ggplot(aes(x = coef, y = fct_rev(var)))+
  geom_pointrange(aes(xmin = lower, xmax = upper))+
  labs(x = 'Estimate', y = 'Variable')+
  theme_minimal()
```



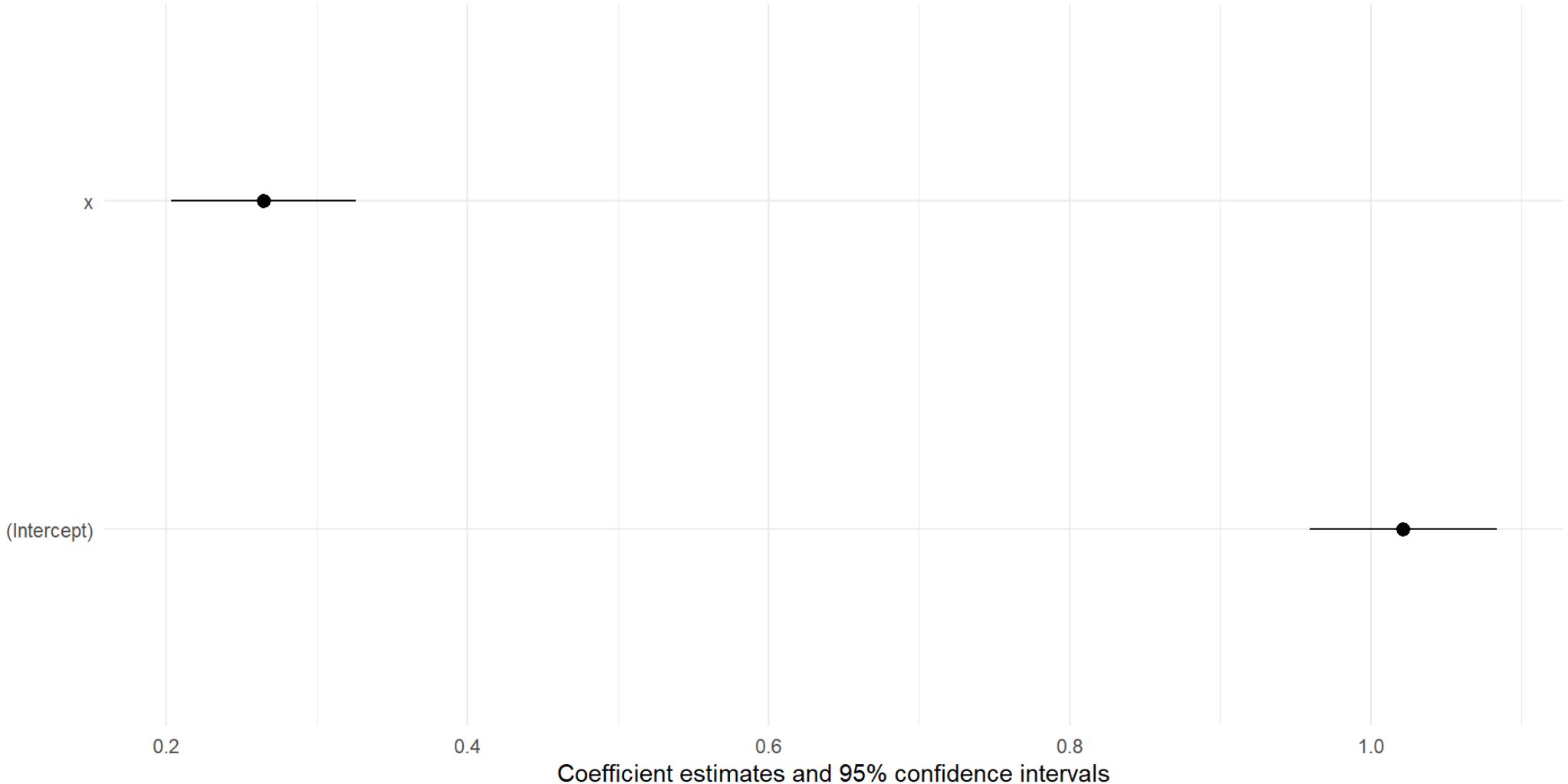
arm, broom, and modelsummary

- Broom, arm, and modelsummary are all packages offer caned alternatives to creating the figure by hand
- the `modelplot()` function is from the model summary package

```
1  library(broom)
2  library(modelsummary)
3  library(arm)
4
5  modelplot(fit)
```



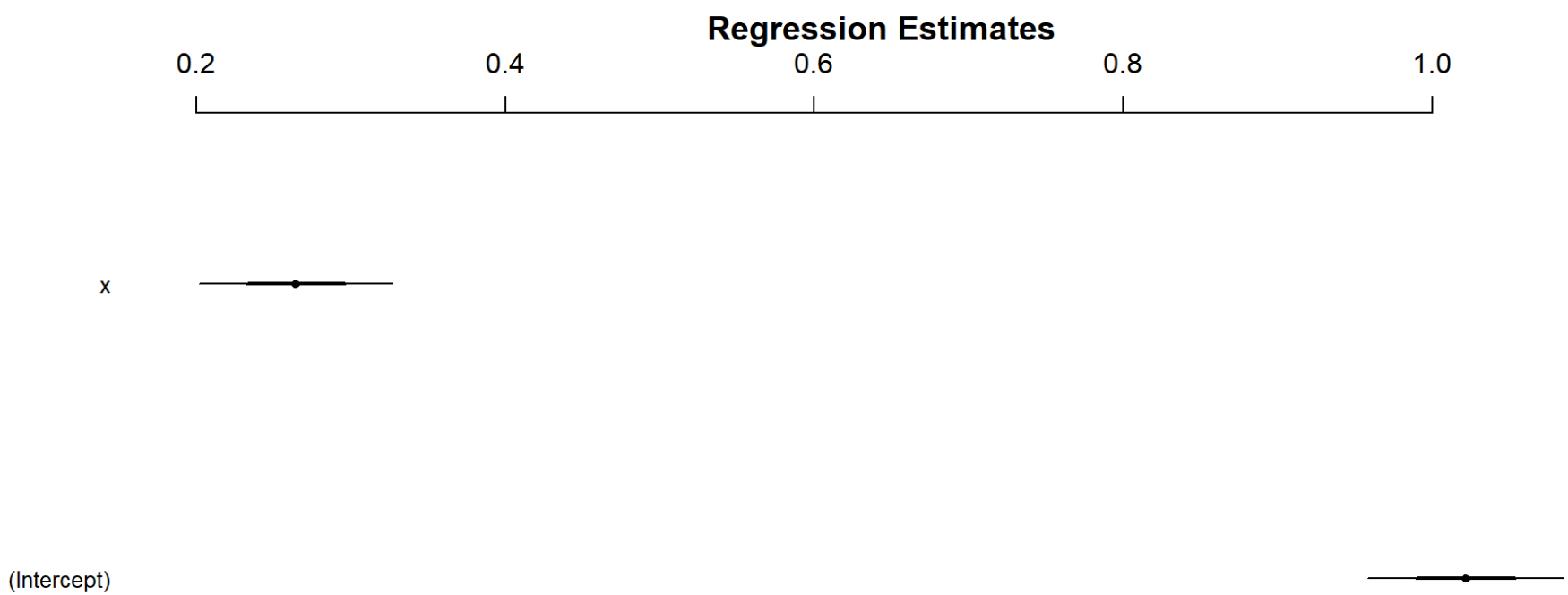
modelsummary



arm

- `coefplot()` is from the arm package

```
1  coefplot(fit, intercept = TRUE)
```



broom

- While broom doesn't have a built in plot function, it is a great way to clean data from a regression model
- `tidy()` is from the broom package and put the regression output into a tibble

```
1 tidy(fit)
```

```
# A tibble: 2 × 5
  term        estimate std.error statistic   p.value
  <chr>          <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept)    1.02     0.0317     32.3  4.60e-157
2 x              0.264    0.0313      8.45 9.82e- 17
```

Multiple models

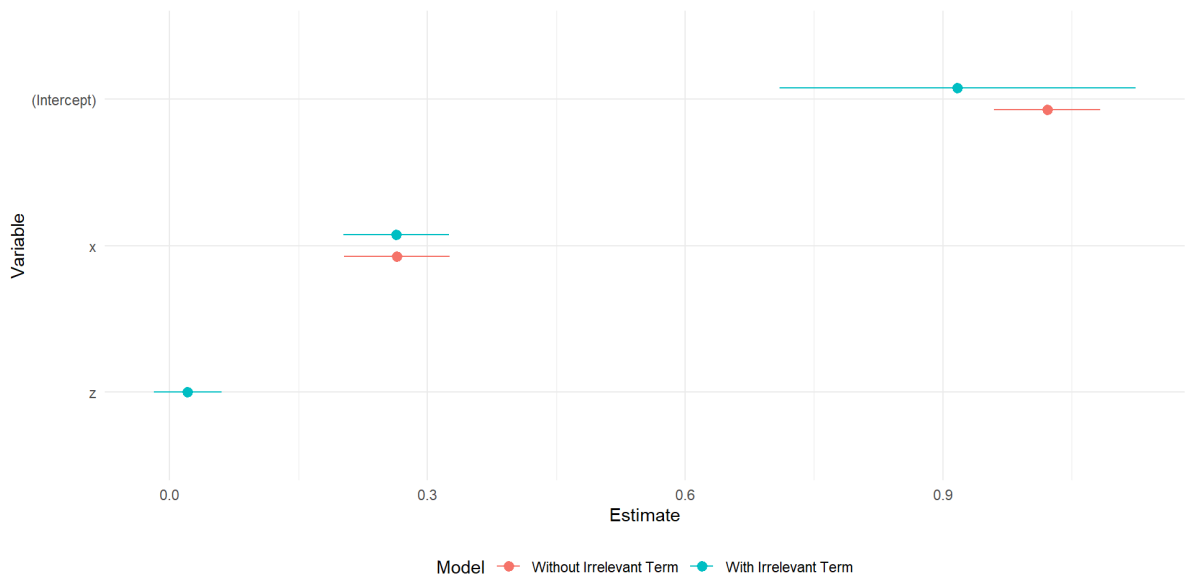
- It can also be useful to put multiple models on the same plot
- Some situations where this may be useful include:
  - Showing a model with and without interaction terms
  - Showing the effect of your main IV with and without controls
  - Showing the effect of your main IV on multiple DVs

Multiple models

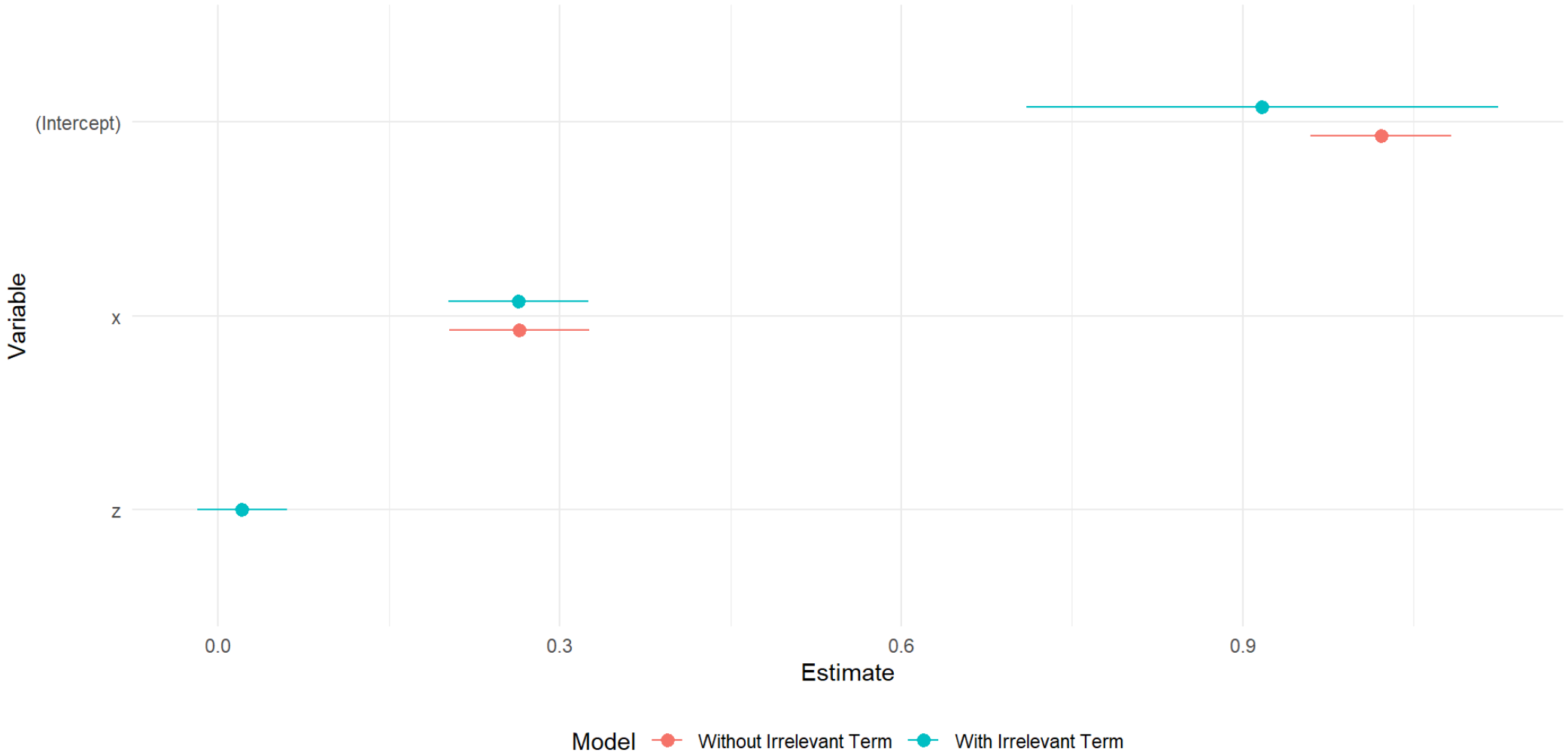
```r
z <- rgamma(1000, 10, 2)
fit1 <- lm(y~x+z)

tidy(fit1) %>%
  rename(coef = estimate,
         var  = term) %>%
  mutate(lower = coef - 1.96*std.error,
         upper = coef + 1.96*std.error,
         model = 'With Irrelevant Term') -> coef_dat1

coef_dat %>%
  mutate(model = 'Without Irrelevant Term') -> coef_dat

coef_dat %>%
  bind_rows(coef_dat1) -> both_mods
```

Multiple models

```
both_mods %>%
  mutate(model = factor(model,
                        levels = c('Without Irrelevant Term',
                                   'With Irrelevant Term'))) %>%
  ggplot(aes(x = coef, y = fct_rev(var), color = model))+
  geom_pointrange(aes(xmin = lower, xmax = upper),
                  position = position_dodge(.3))+
  labs(x = 'Estimate', y = 'Variable', color = 'Model')+
  theme_minimal()+
  theme(legend.position = 'bottom')
```

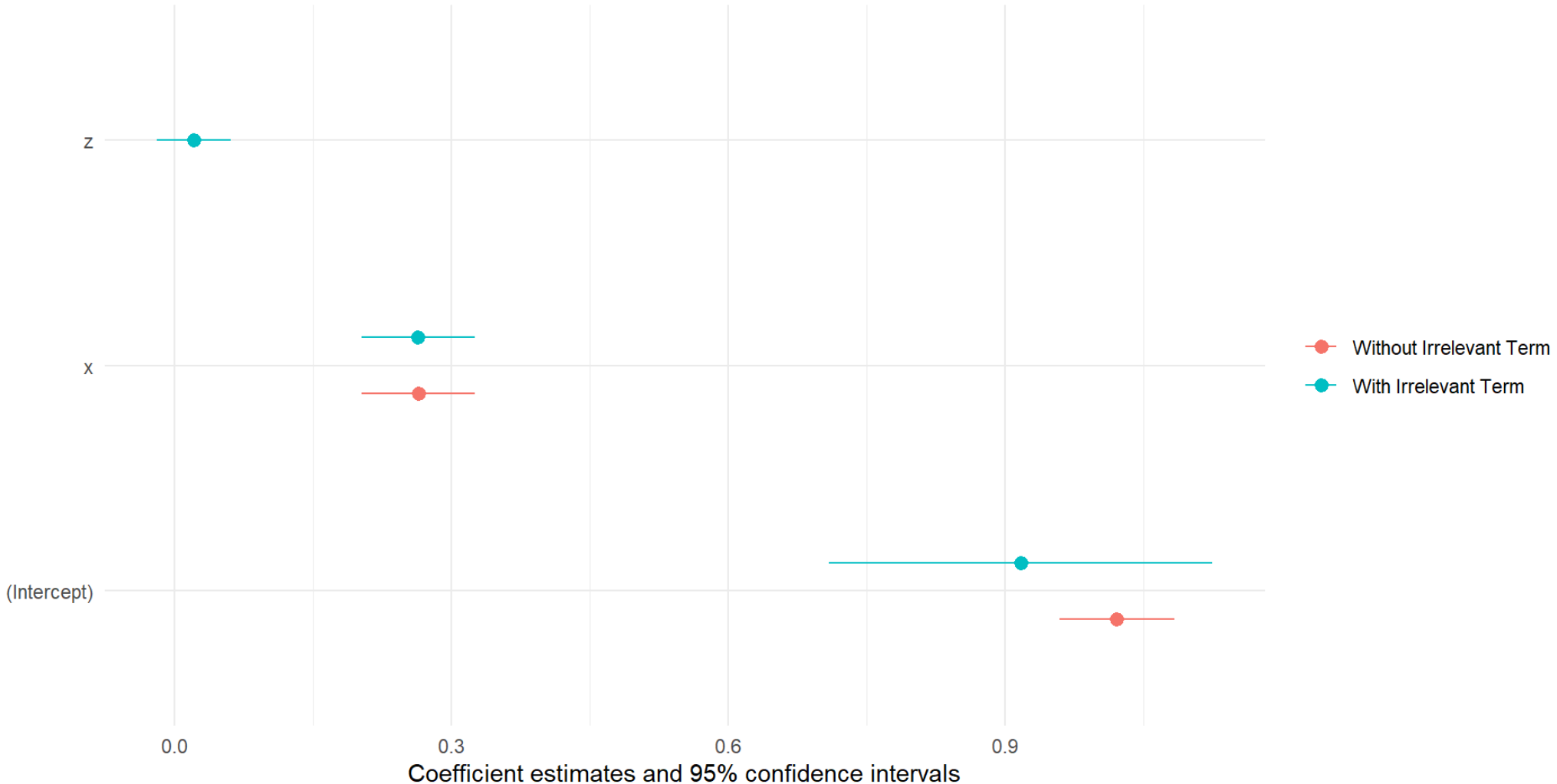


Multiple models



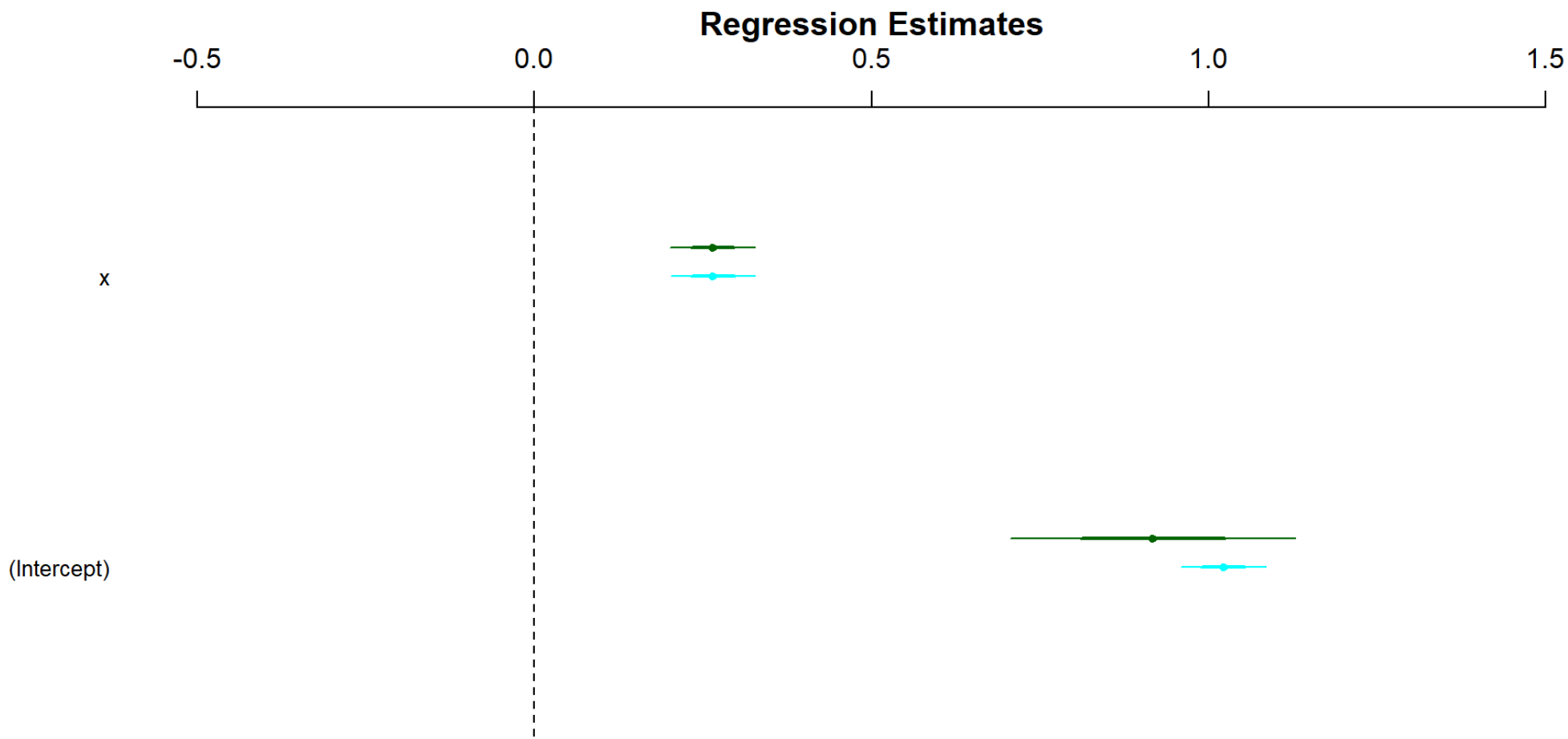
Multiple models with modelsummary

```
1  modelplot(list('Without Irrelevant Term'=fit,'With Irrelevant Term'=fit1))
```



Multiple models with arm

```
1 coefplot(fit, intercept = TRUE,xlim = c(-.5,1.5),col.pts = "cyan")
2 coefplot(fit1, intercept = TRUE, add = TRUE, col.pts = "darkgreen")
```



Fixed and Random Effects

- I'm going to handwave over the math for this part, but fixed effects and random effects/intercepts are ways in which we can account for higher level data in our models
- Fixed effects are included in our model the same exact way we include any other covariates
- For including random intercepts, we have a couple options: `lme4`, `lmertest`, and `brm`
  - lme4 and lmertest are packages to fit frequintist models with random intercepts
  - brm is a package that makes fitting Bayesian regression models a lot easier

lme4 and lmertest

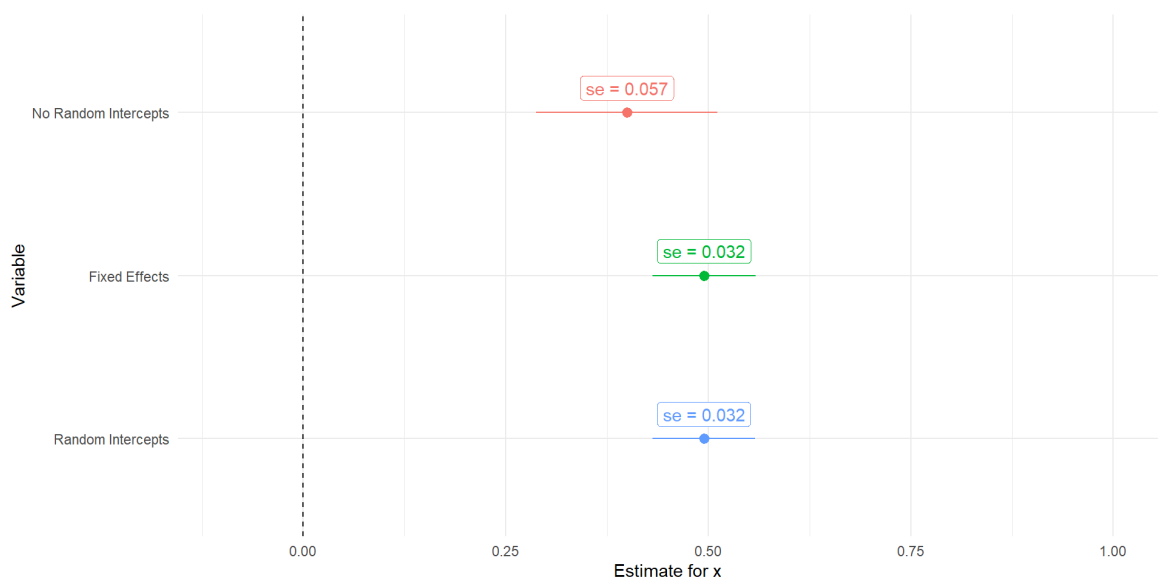
- For both packages, the function is `lmer()`
- The function from lme4 does not privde p-values for your fixed effect terms, while the one from lmertest does, if you're into that sort of thing
- For actually using random intercepts, we write the formula the exact same way, and add the random intercepts with `(1|var)`

Random Intercepts

```r
library(lmerTest)

#setting up our problem
##redrawing x
x <- rnorm(1000)

#setting up our grouping variable
groups <- c('g1','g2','g3','g4')
group <- sample(groups, size = 1000, replace = TRUE)

# Create group-specific intercepts (random intercepts)
group_intercepts <- rnorm(length(groups), mean = 0, sd = 2)
names(group_intercepts) <- groups

tibble(x     = x,
       group = group) %>%
  group_by(group) %>%
  mutate(group_int = group_intercepts[group],
```

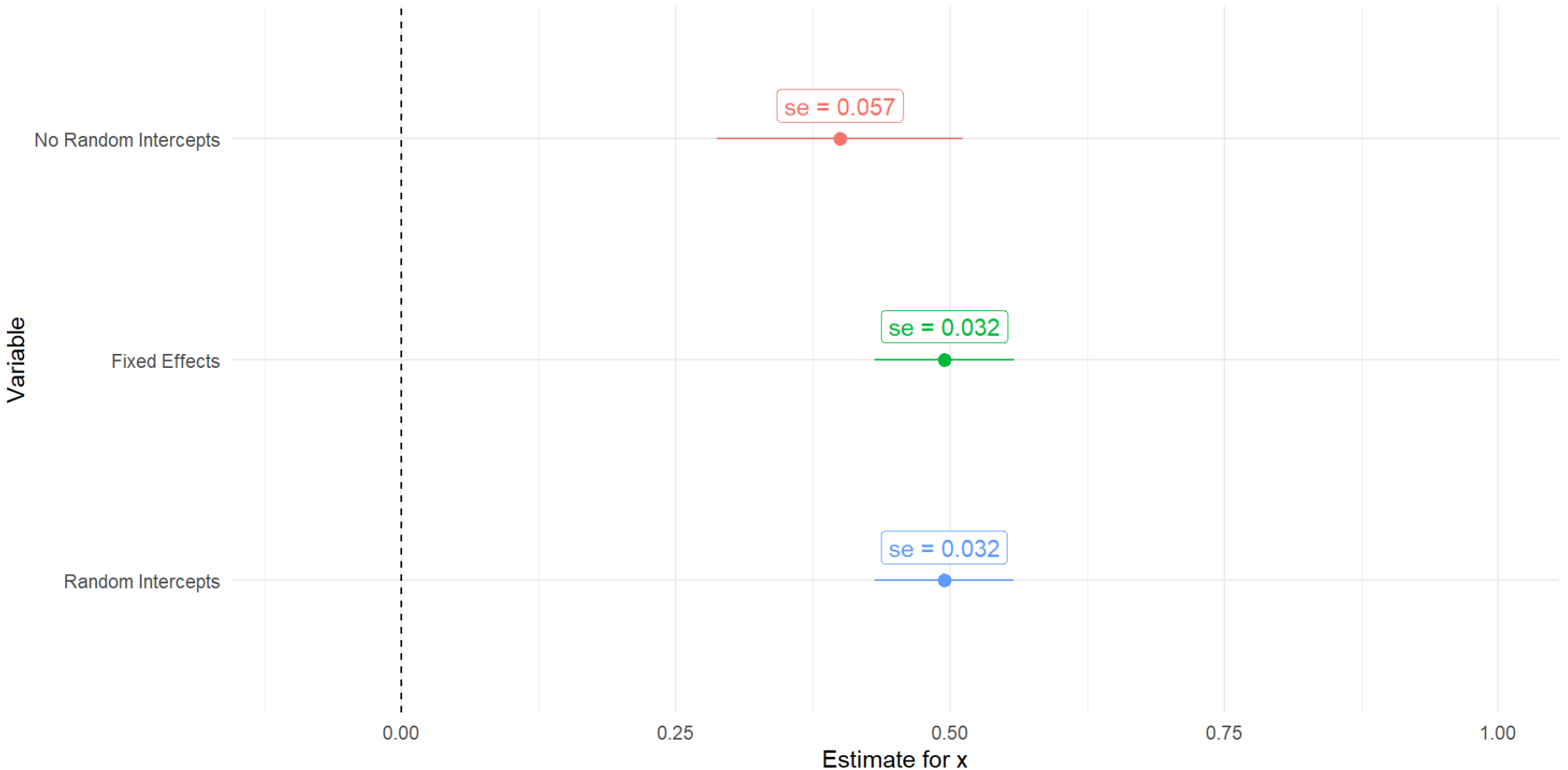
Random Intercepts

- Note that the underlying data generating process has a different intercept based on our grouping variable
- When we don't account for this, the uncertainty in our regression coefficients increases dramatically
- Depending on the severity of the problem, this can also result in bias being introduced in our regression coefficient



Random Intercepts

- Code



With more variation in the intercepts

- The more different our intercepts are, the worse our uncertainty will get without the random intercepts

▶ Code