Simulation-based Inference

INFERENCE FOR LINEAR REGRESSION IN R

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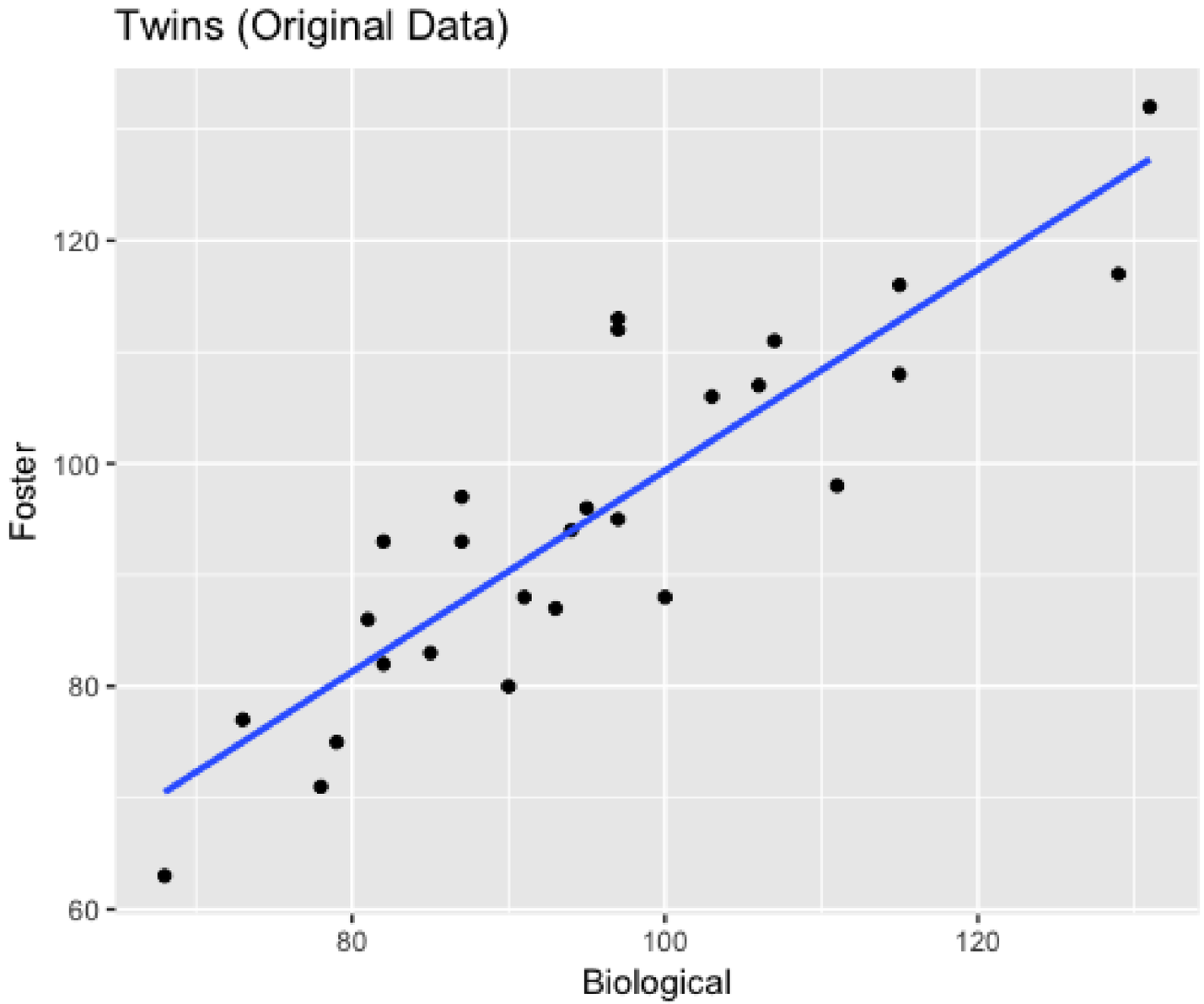
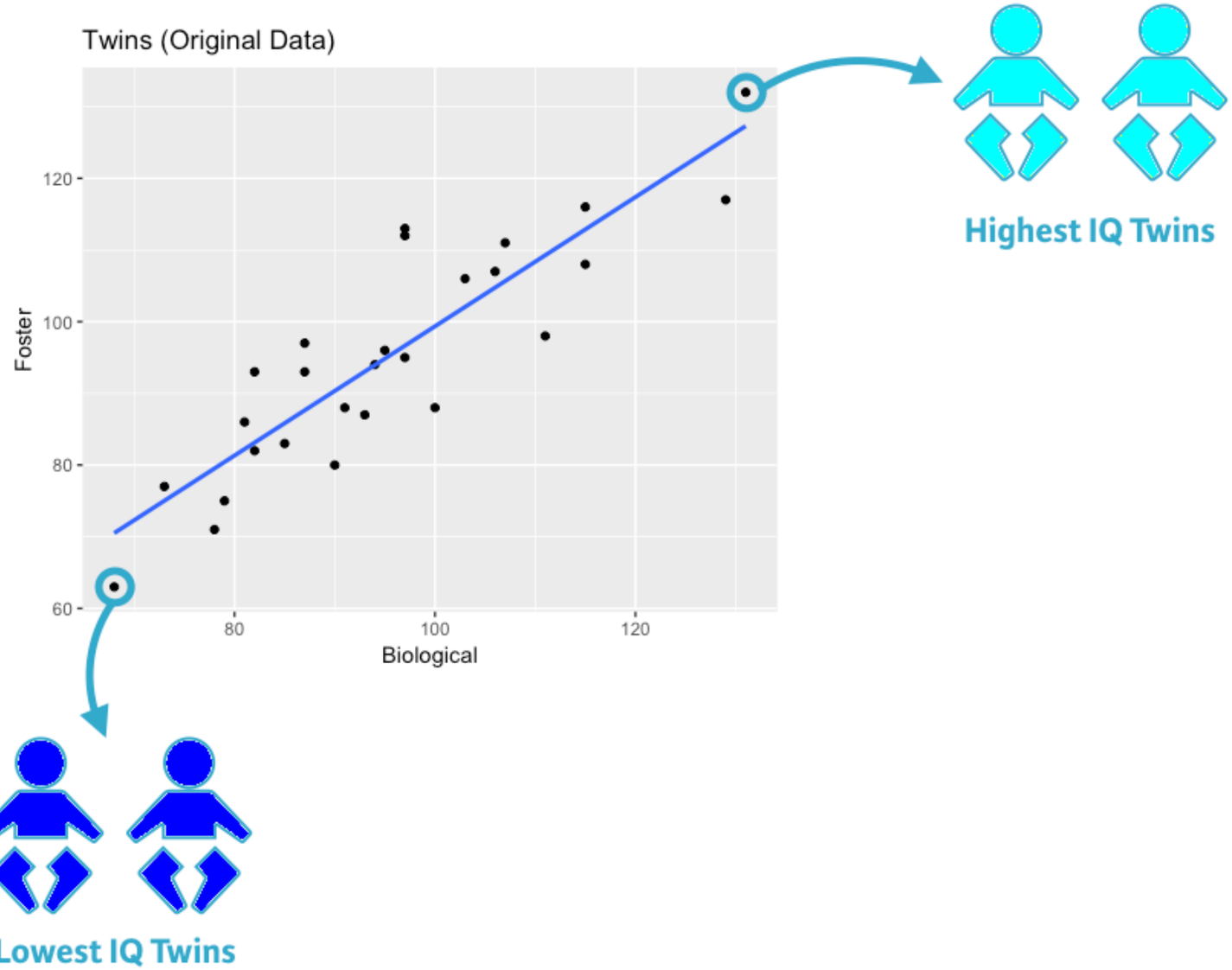

Twins (Original Data)
Foster
120
100
80
60
80
100
120
Biological


Twins (Original Data)
Foster
Biological
120
100
80
60
80
100
120
Highest IQ Twins
Lowest IQ Twins

Twin data

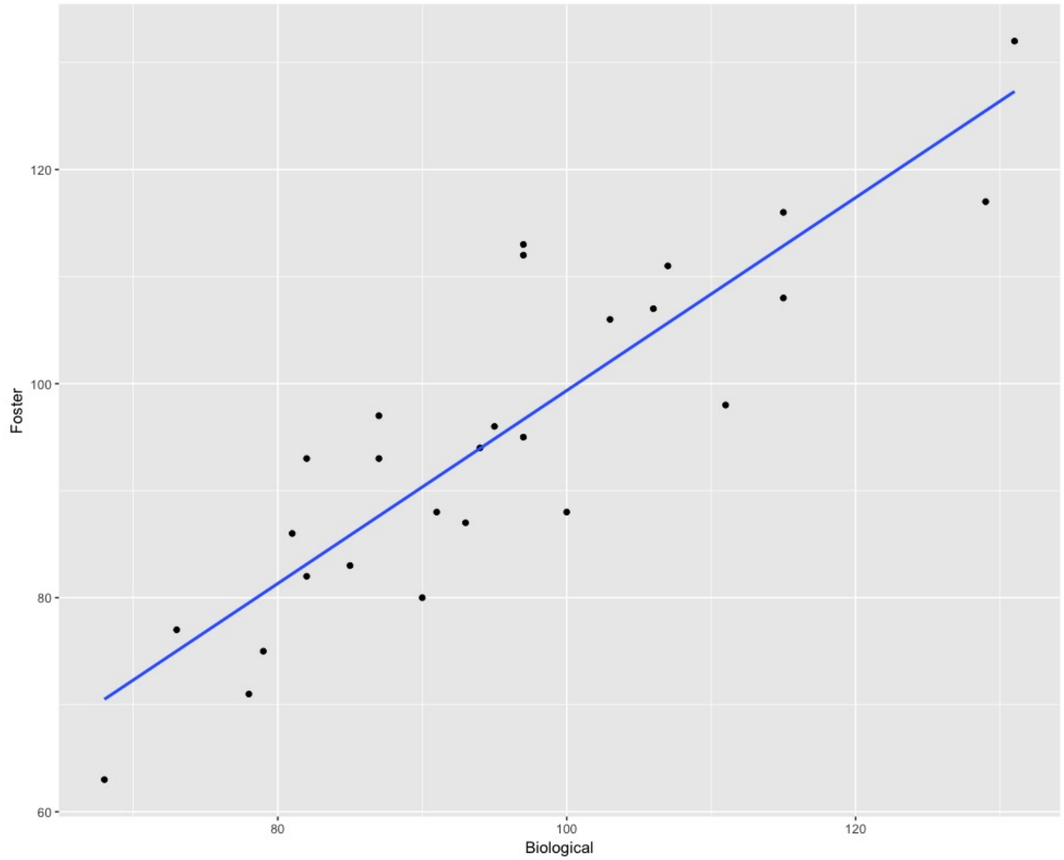
Foster	Biological
 80	 90
 108	 115
 116	 115
 93	 83

Permuted twin data

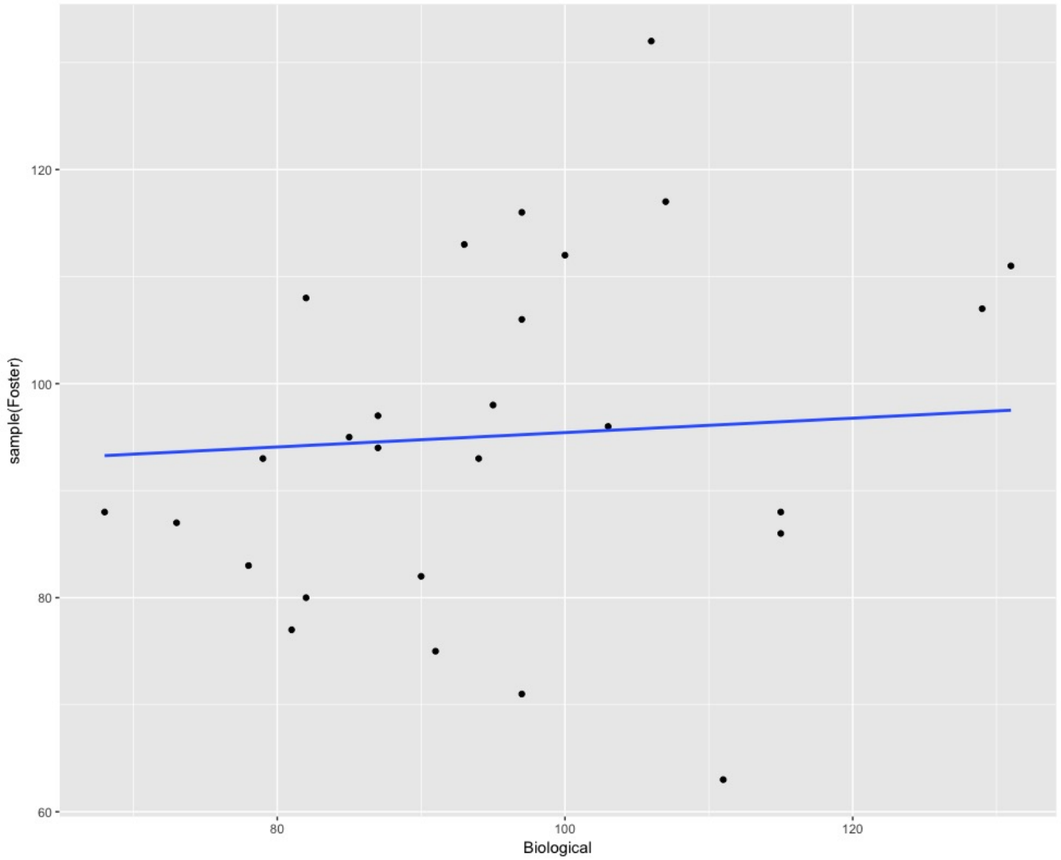
Foster	Biological
 108	 90
 93	 115
 116	 115
 80	 83

Permuted data (1) plotted

Original data

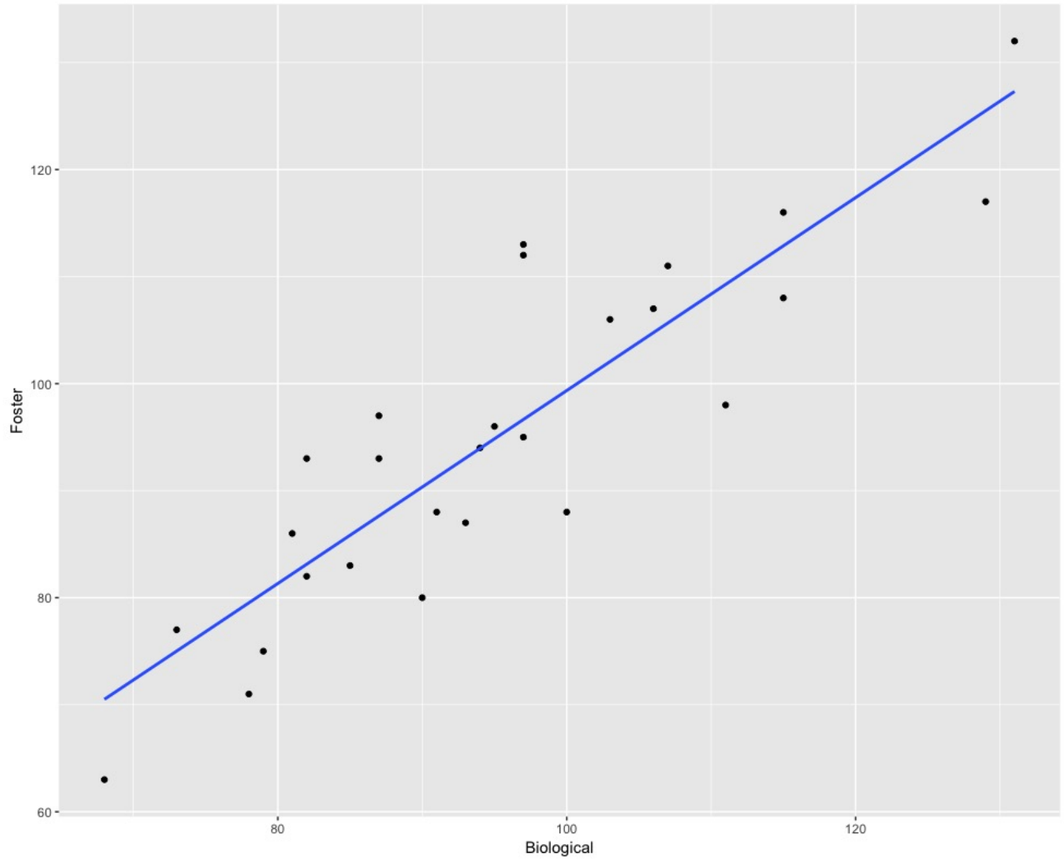


Permuted data (1)

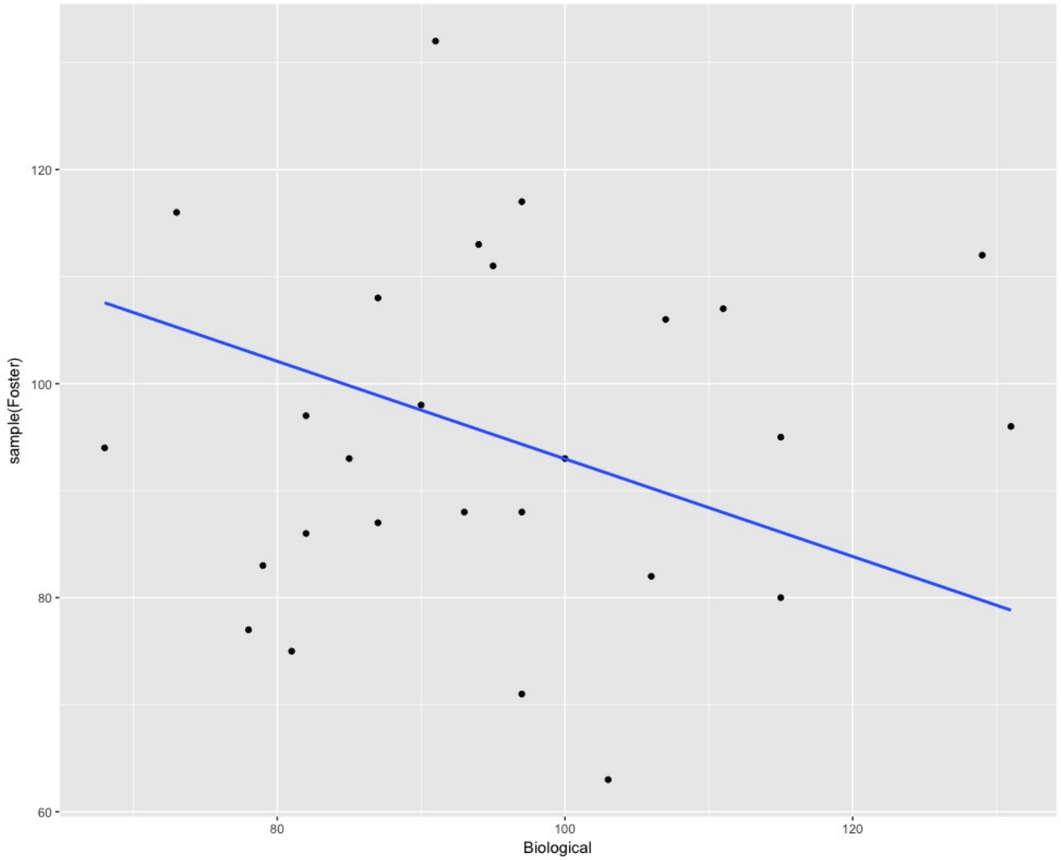


Permuted data (2) plotted

Original data

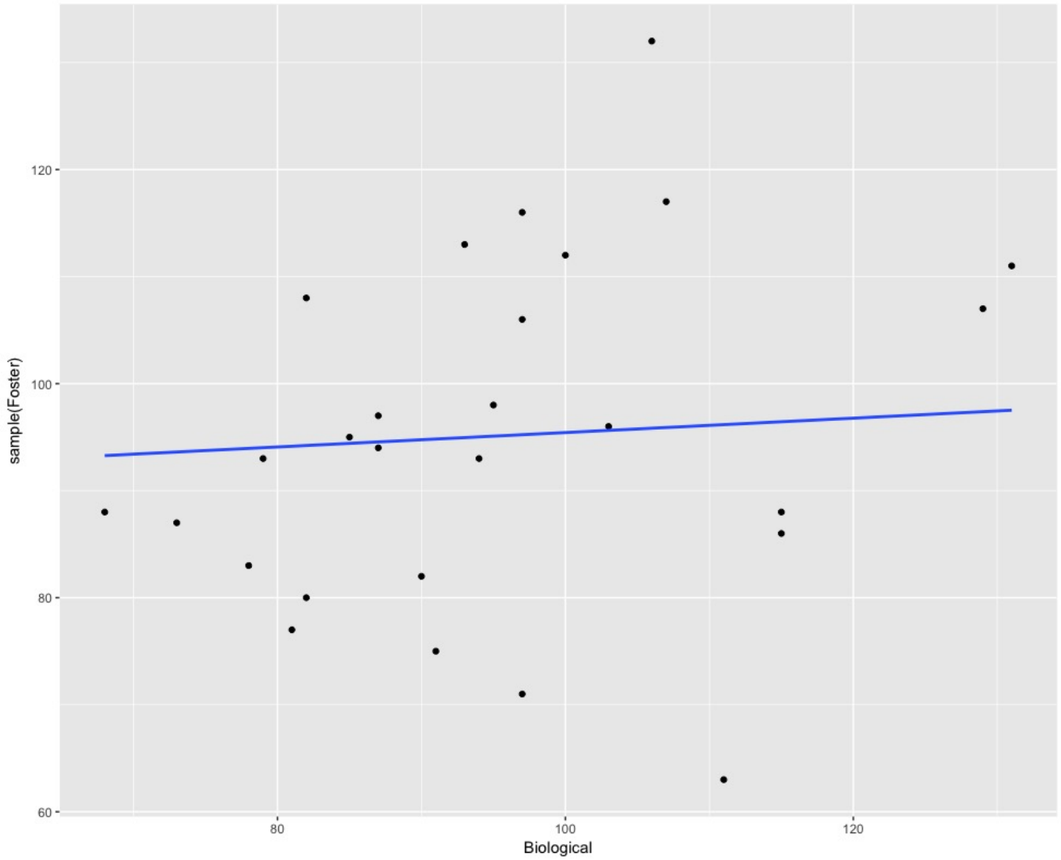


Permuted data (2)

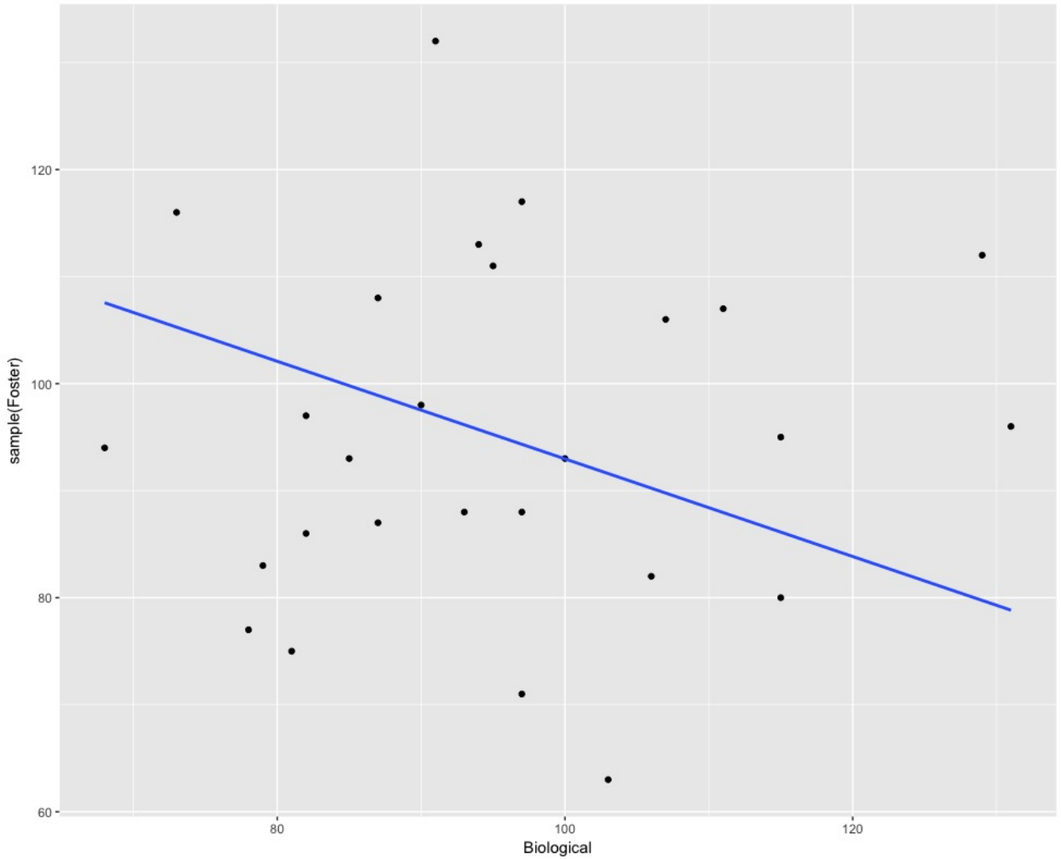


Permuted data (1) and (2)

Permuted data (1)



Permuted data (2)



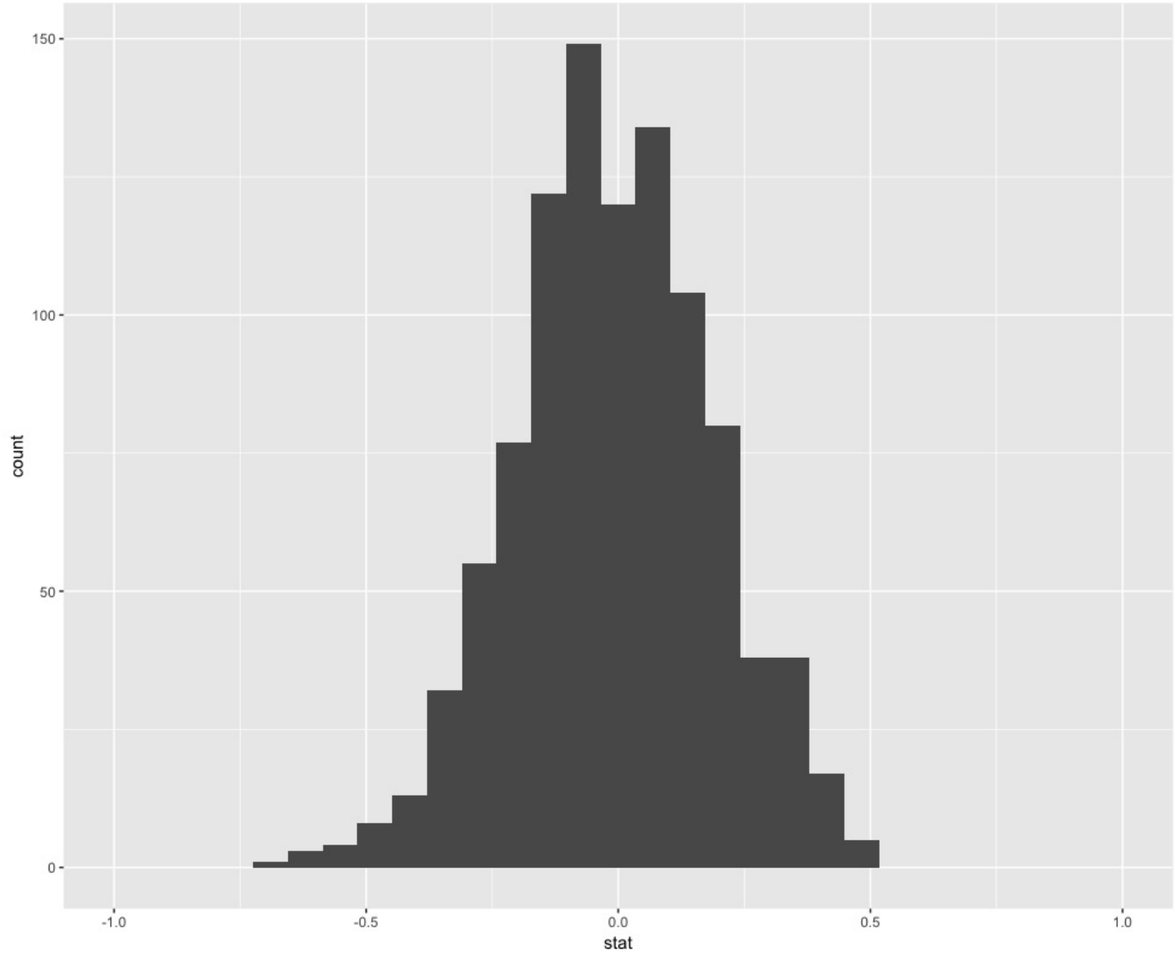
```
twins %>%
   specify(Foster ~ Biological) %>%
   hypothesize(null = "independence") %>%
   generate(reps = 10, type = "permute") %>%
   calculate(stat = "slope")
```

```
A tibble: 10 x 2
   replicate          stat
       <int>         <dbl>
 1         1  0.0007709302
 2         2 -0.0353592305
 3         3 -0.0278627974
 4         4 -0.0072547982
 5         5 -0.1252761541
 6         6 -0.1669869287
 7         7 -0.2610519170
 8         8 -0.0157695494
 9         9  0.0581361900
10        10  0.1598471947
```

Many permuted slopes

```
perm_slope <- twins %>%
   specify(Foster ~ Biological) %>%
   hypothesize(
     null = "independence"
     ) %>%
   generate(reps = 1000,
            type = "permute") %>%
   calculate(stat = "slope")

ggplot(data = perm_slope, aes(x = stat)) +
   geom_histogram() +
   xlim(-1,1)
```

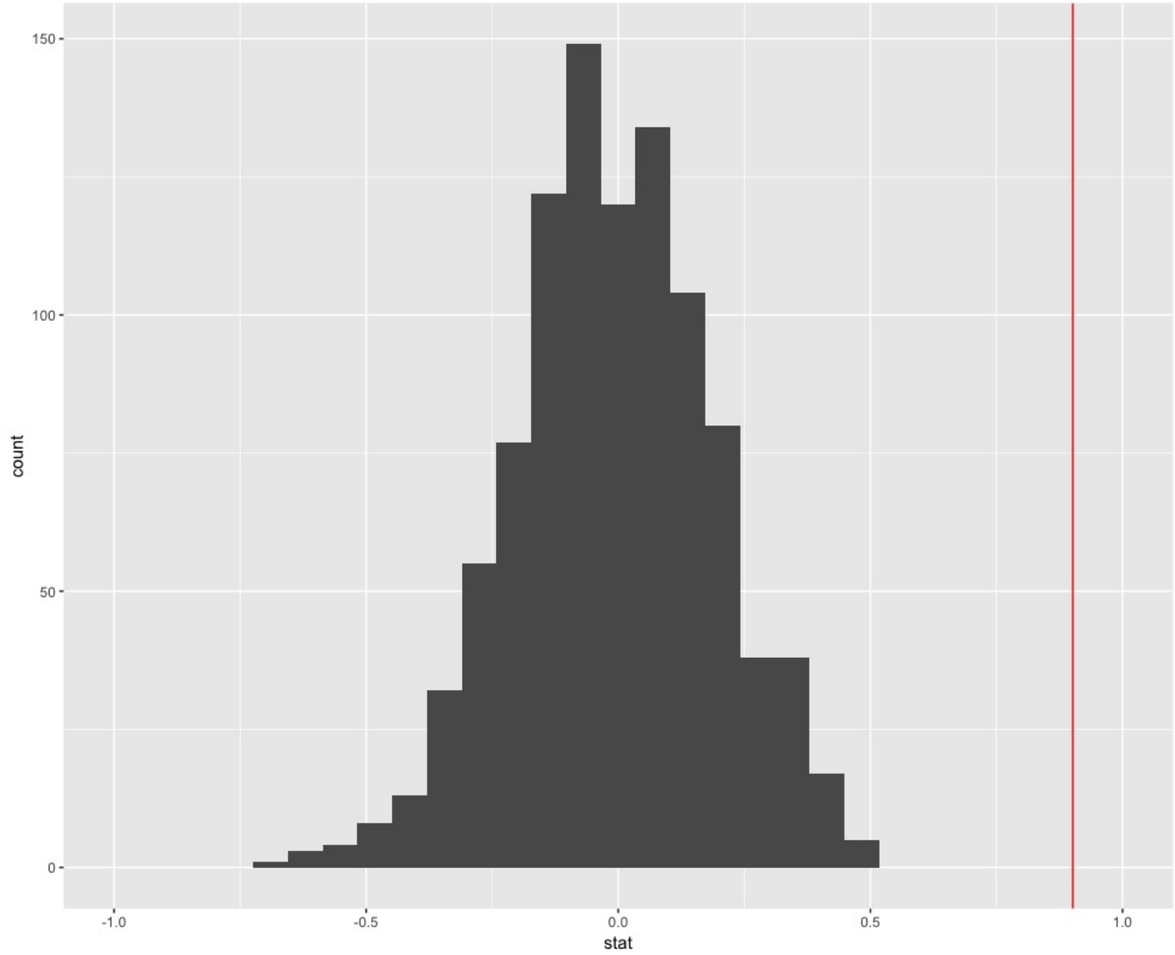


Permuted slopes with observed slope in red

```
obs_slope <- lm(Foster ~ Biological,
                data = twins) %>%
   tidy() %>%
   filter(term == "Biological") %>%
   select(estimate) %>%
   pull()
obs_slope
```

```
0.901436
```

```
ggplot(data = perm_slope, aes(x = stat)) +
   geom_histogram() +
   geom_vline(xintercept = obs_slope, color = "red")
   + xlim(-1,1)
```



Let's practice!

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Simulation-based CI for slope

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Original Sample

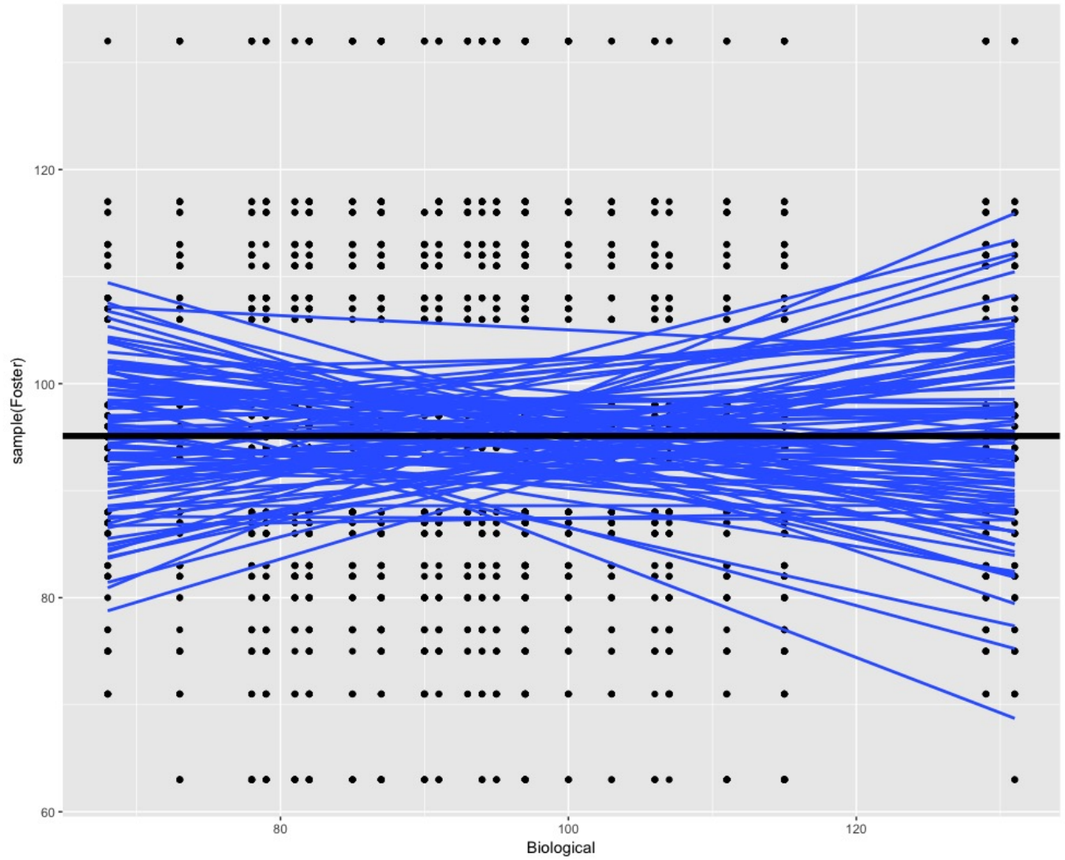
Foster	Biological
80	90
108	115
116	115
93	83

Bootstrapped Sample

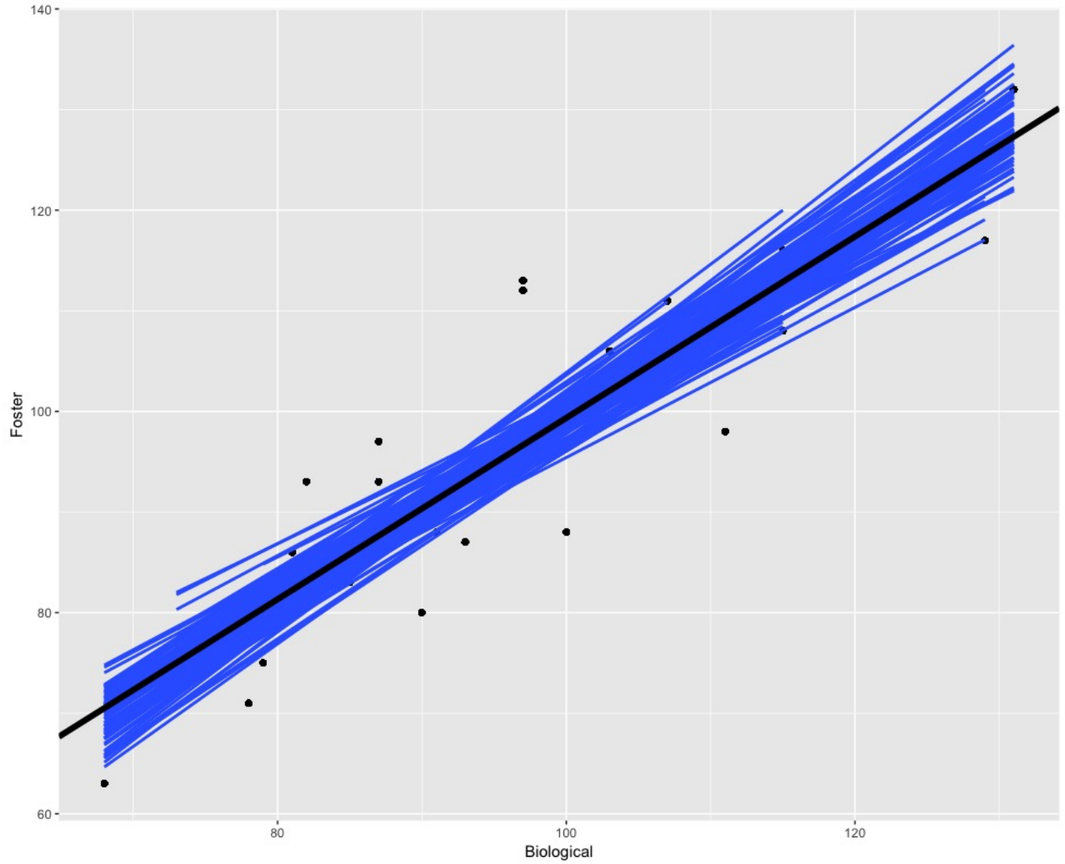
Foster	Biological
93	83
108	115
108	115
93	83

Permutation vs. bootstrap variability

Slopes from permuted data



Slopes from bootstrapped data



Permutation vs. bootstrap code

Permutation:

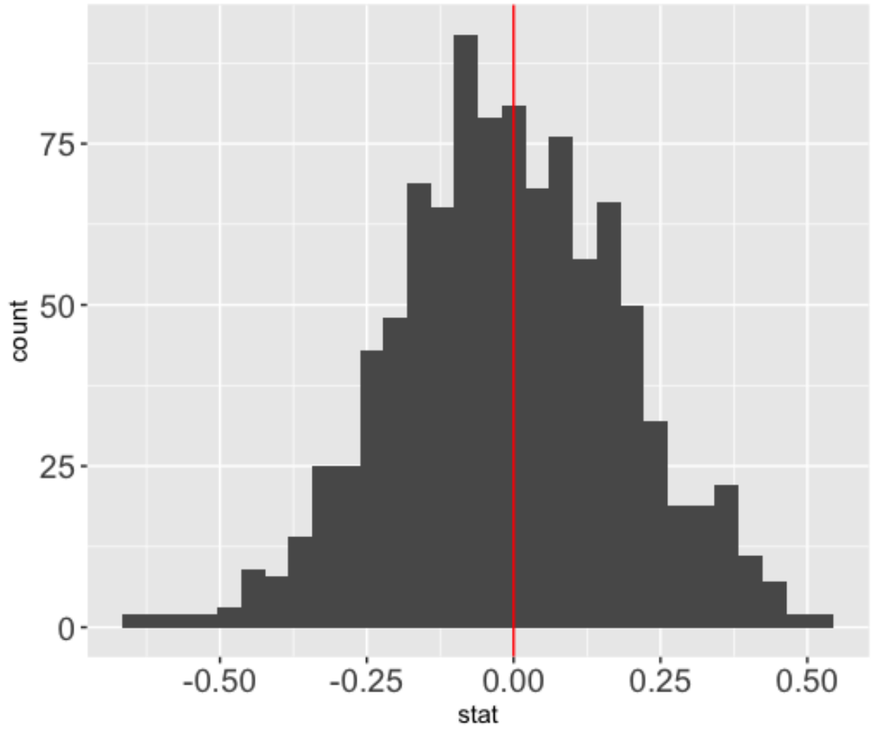
```
twins %>%
  specify(Foster ~ Biological) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 100, type = "permute") %>%
  calculate(stat = "slope")
```

Bootstrap:

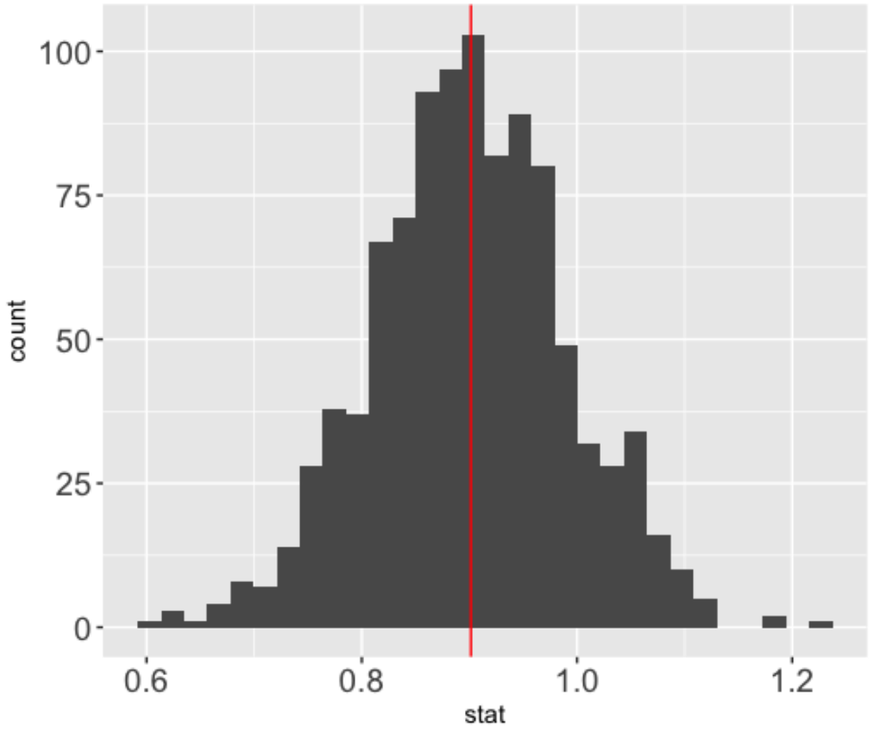
```
twins %>%
  specify(Foster ~ Biological) %>%
  generate(reps = 100, type = "bootstrap") %>%
  calculate(stat = "slope")
```

Sampling distribution: randomization vs. bootstrap

Slopes from permuted data



Slopes from bootstrapped data



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