INFERENCE FOR LINEAR REGRESSION

Simulation-based Inference

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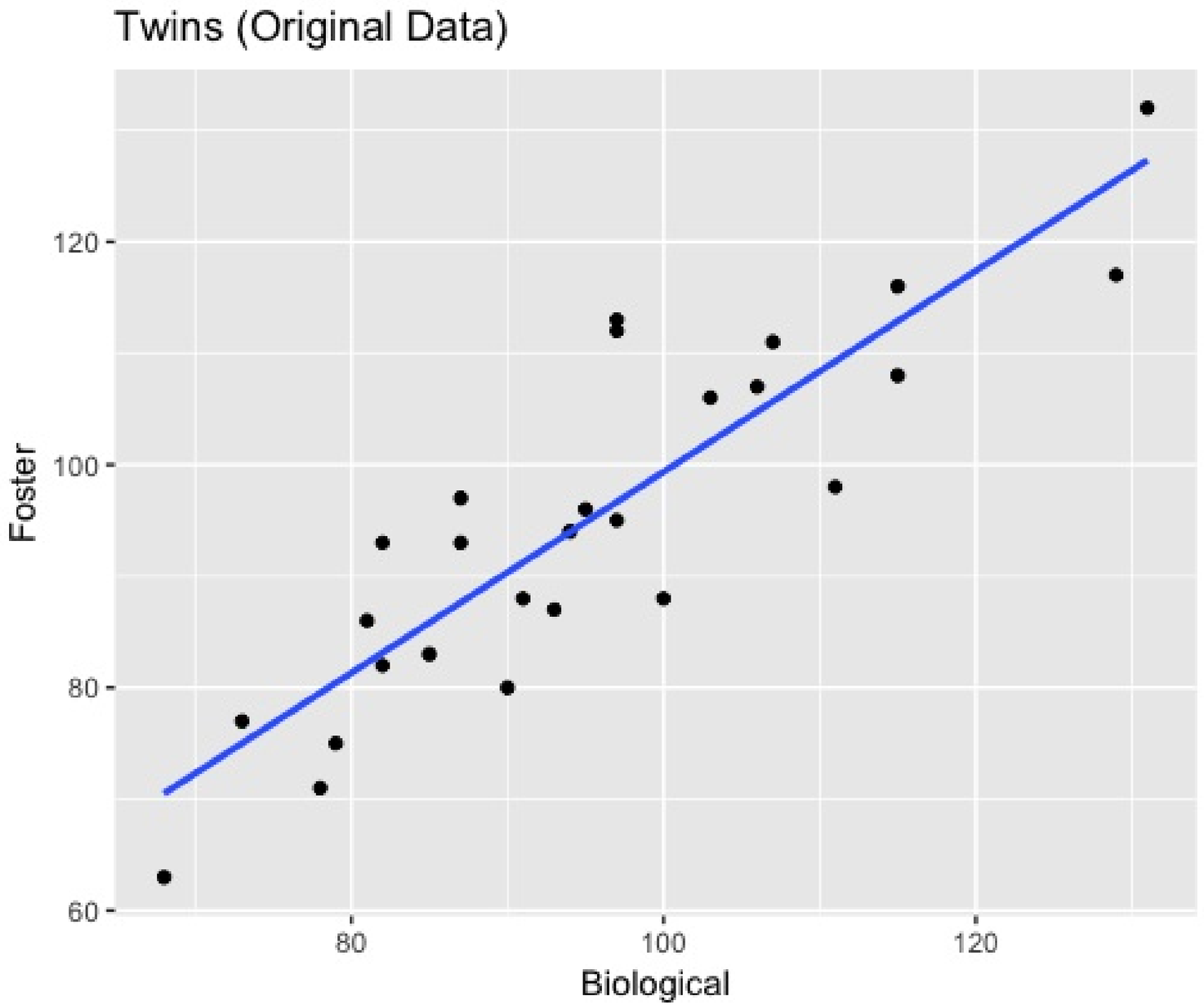
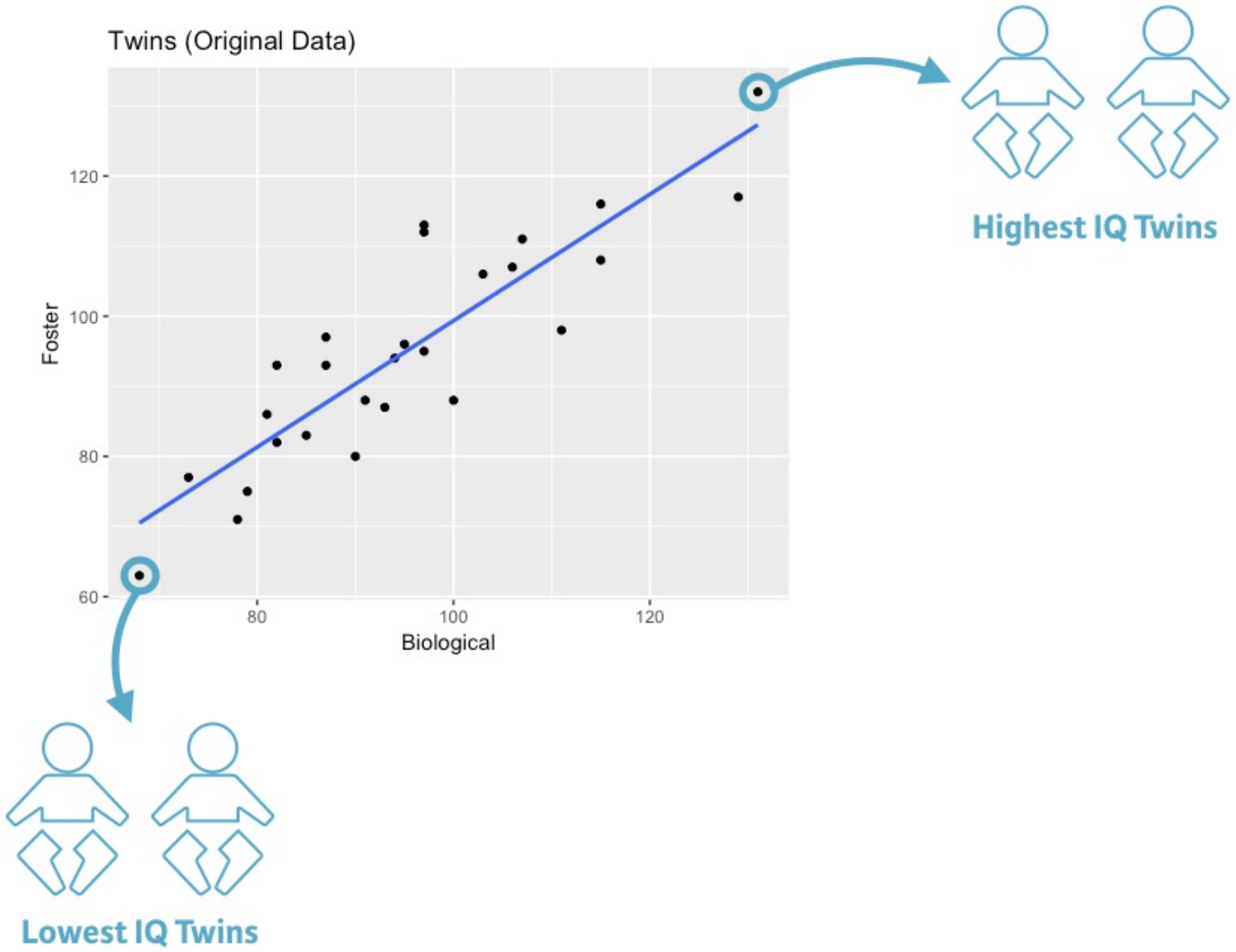

Twins (Original Data)
Foster
120
100
80
60
80
100
120
Biological


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

Twin data

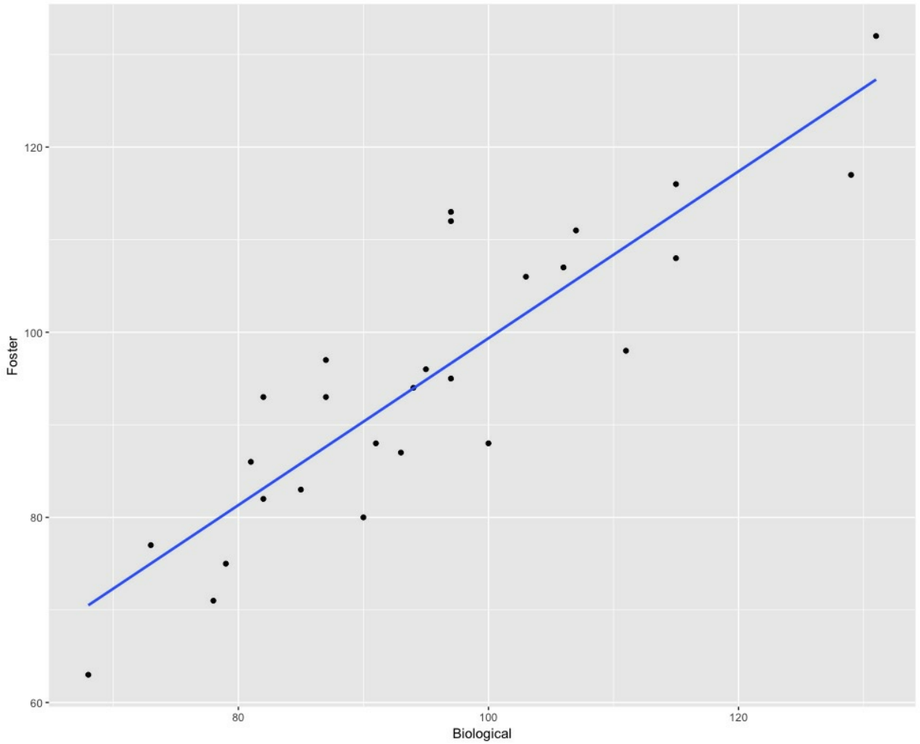
Foster	Biological
80	90
108	115
116	115
93	83

Permuted twin data

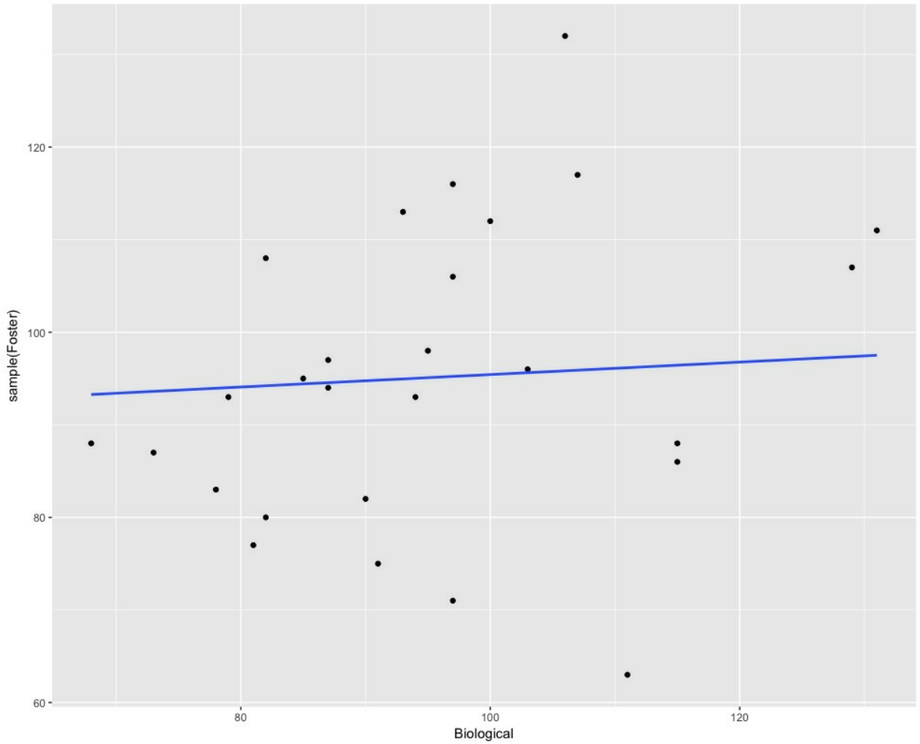
Foster	Biological
108	90
93	115
116	115
80	83

Permuted data (1) plotted

Original data

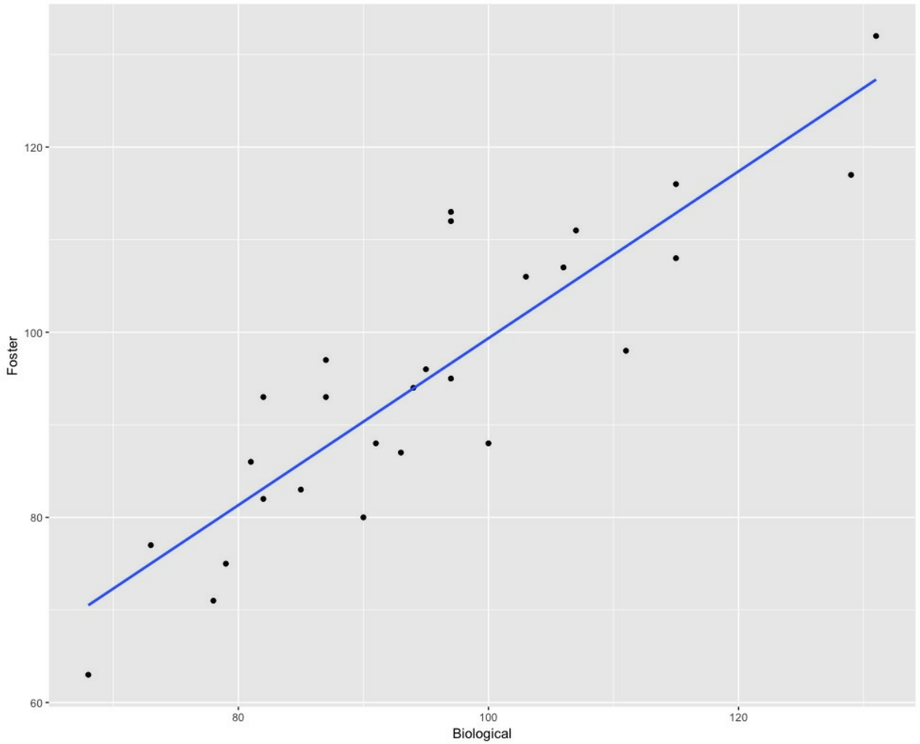


Permuted data (1)

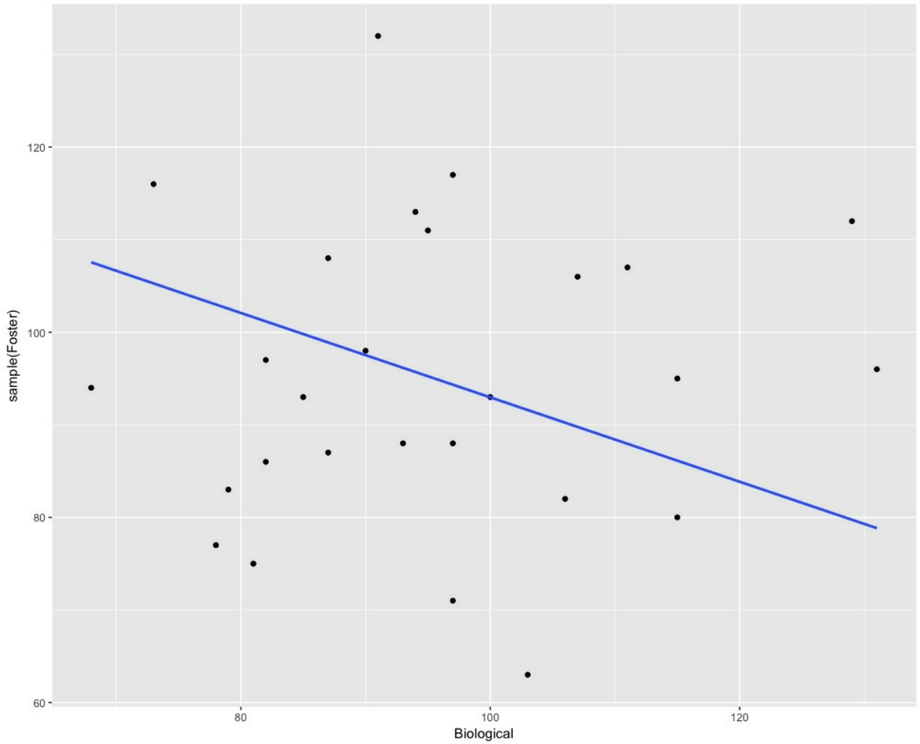


Permuted data (2) plotted

Original data

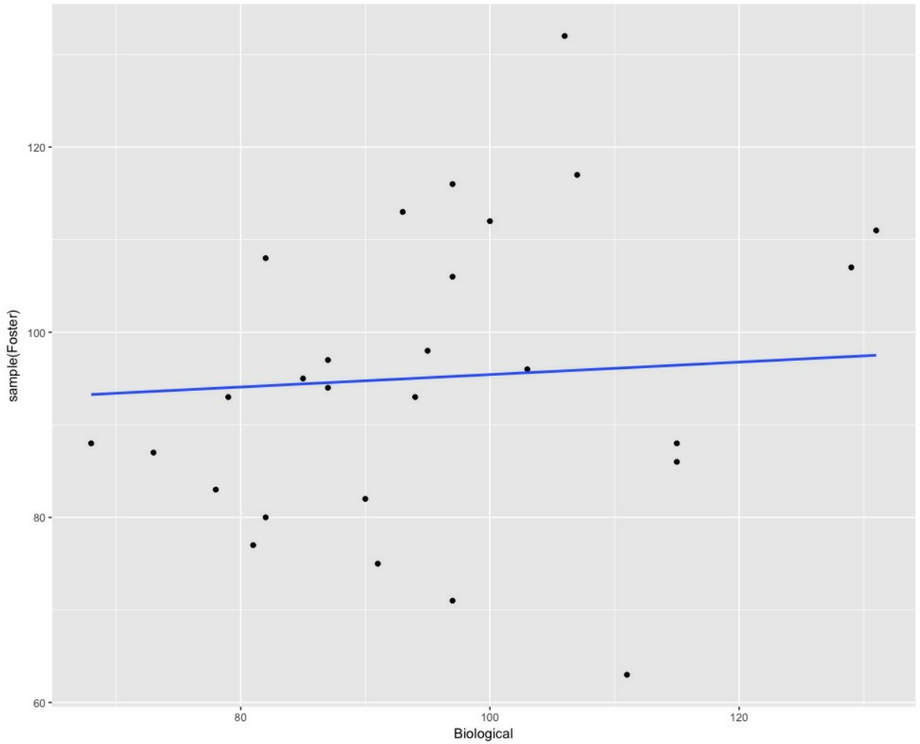


Permuted data (2)

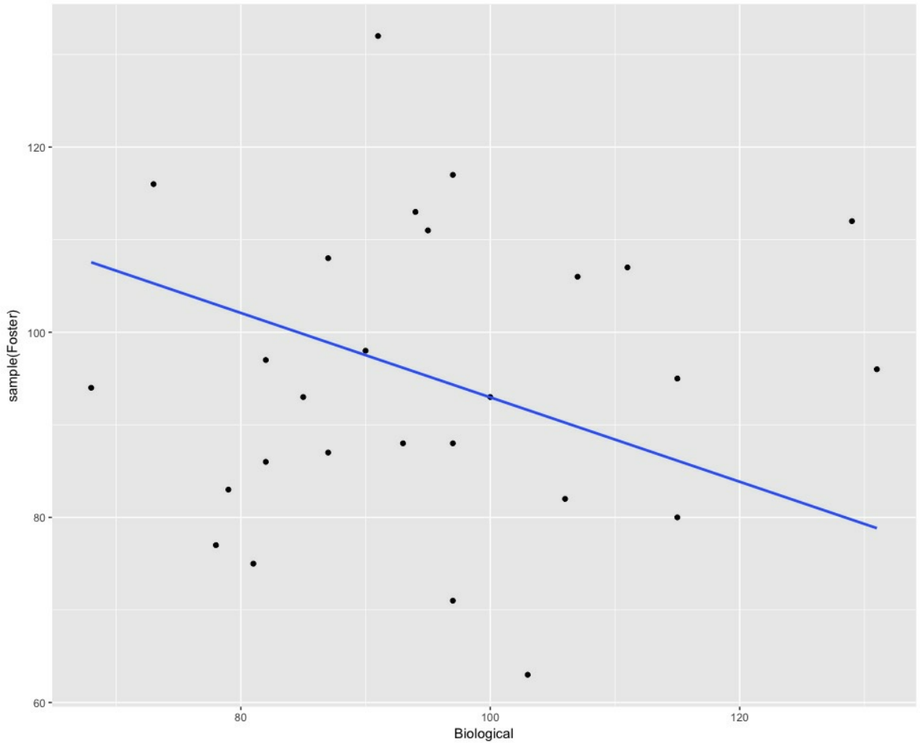


Permuted data (1) and (2)

Permuted data (1)



Permuted data (2)



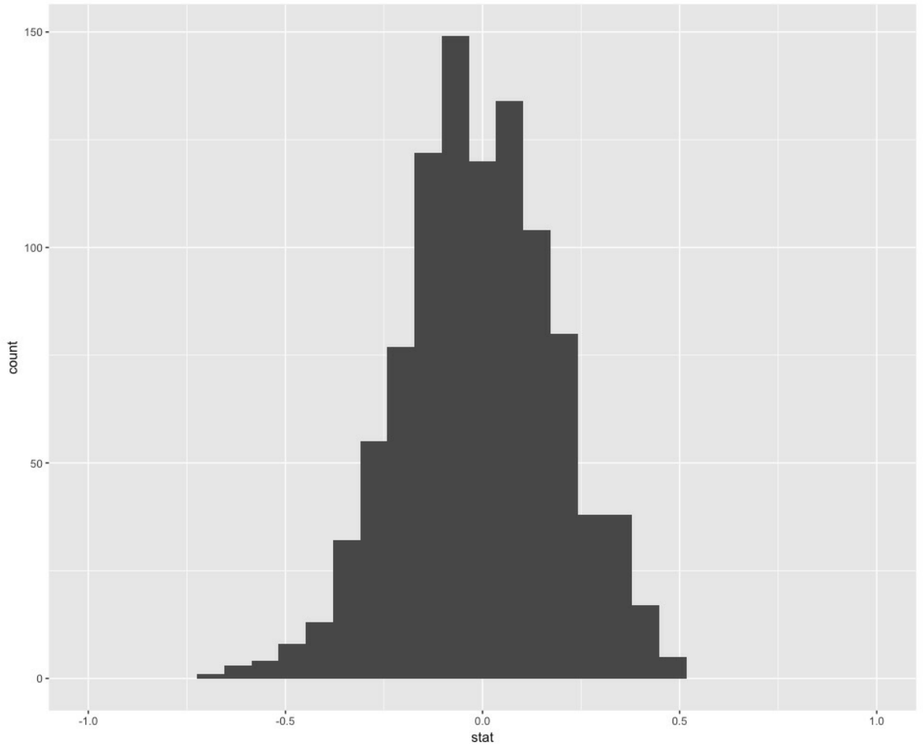
Linear model on permuted data

```
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)
```

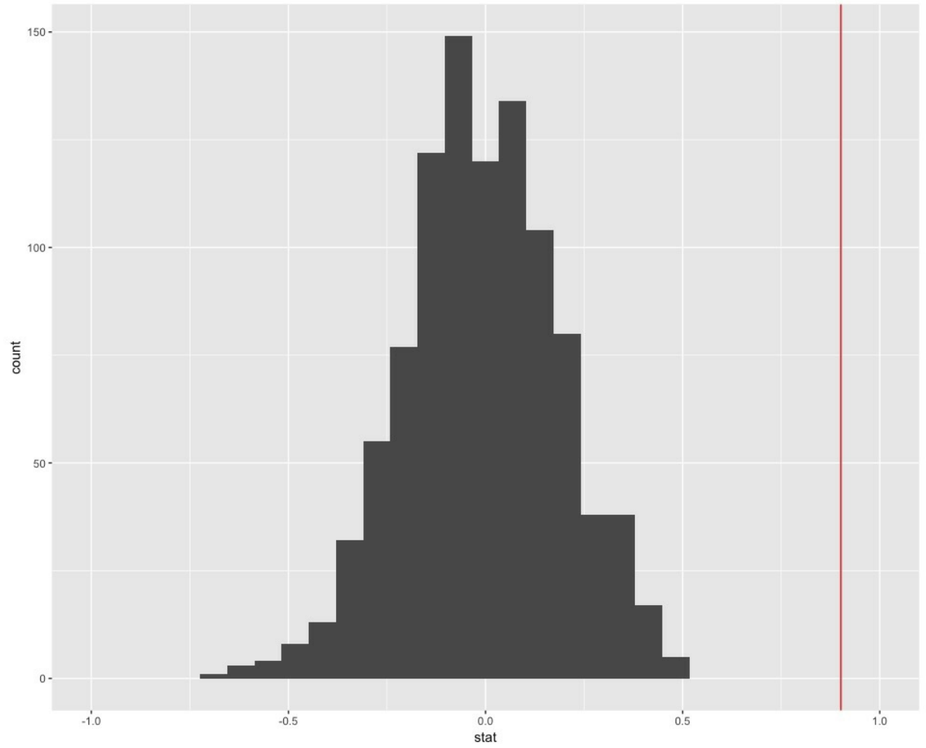


Permuted slopes with observed slope in red

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

obs_slope
# [1] 0.901436

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



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Let's practice!

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Simulation-based CI for slope

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Original Sample

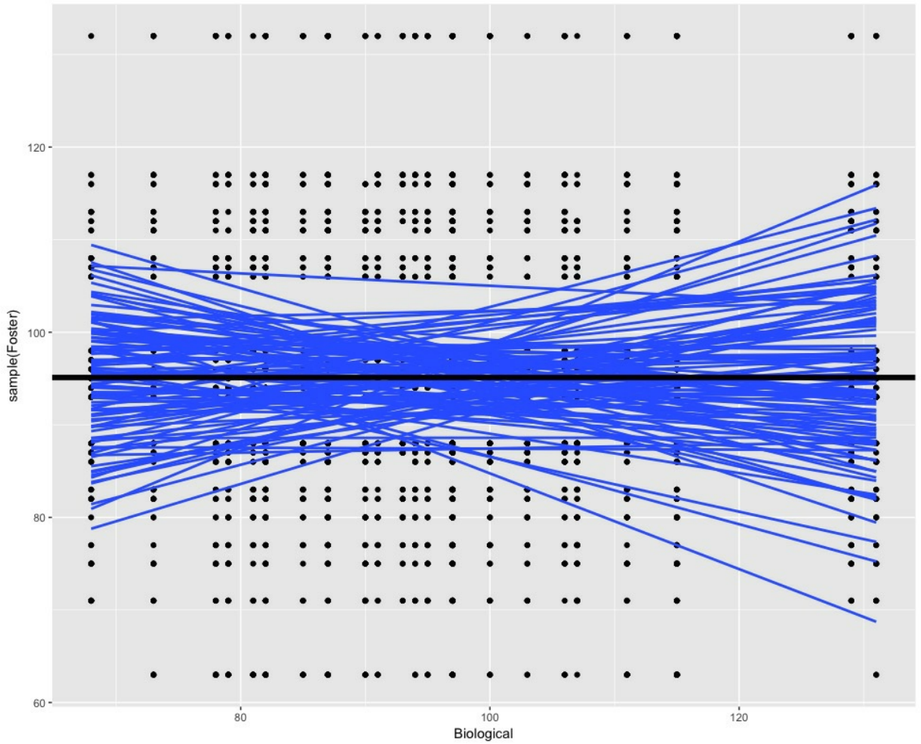
Foster	Biological
80	90
108	115
116	115
93	83

Bootstrapped Sample

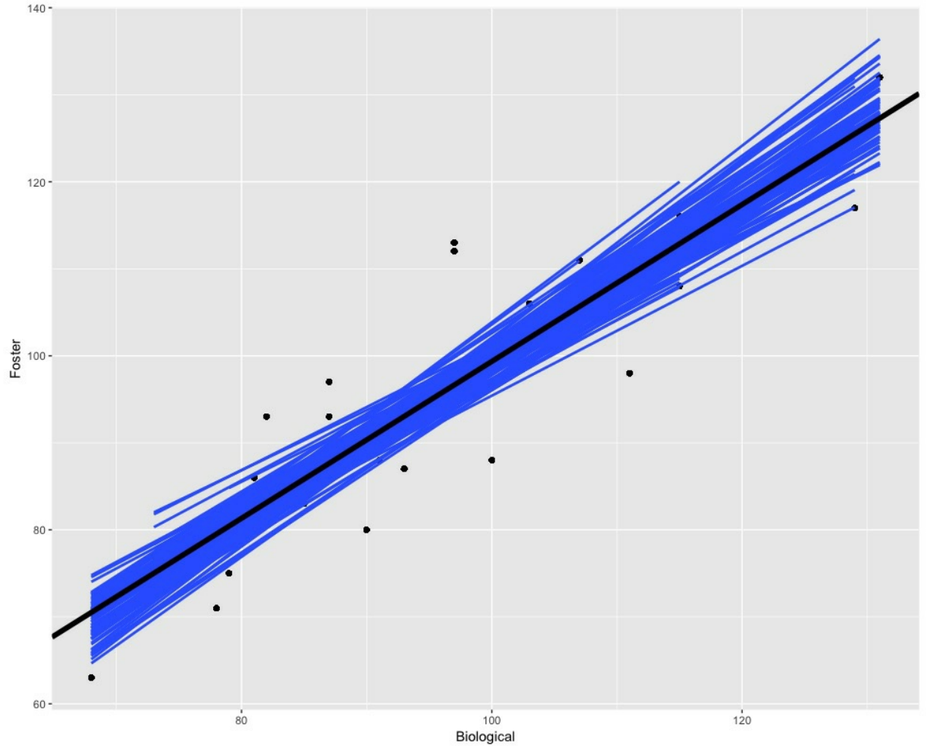
Foster	Biological
93	83
108	115
108	115
93	83

Permutation vs. bootstrap variability

Slopes from permuted data



Slopes from bootstrapped data



Permutation vs. boostrap code

Permutation:

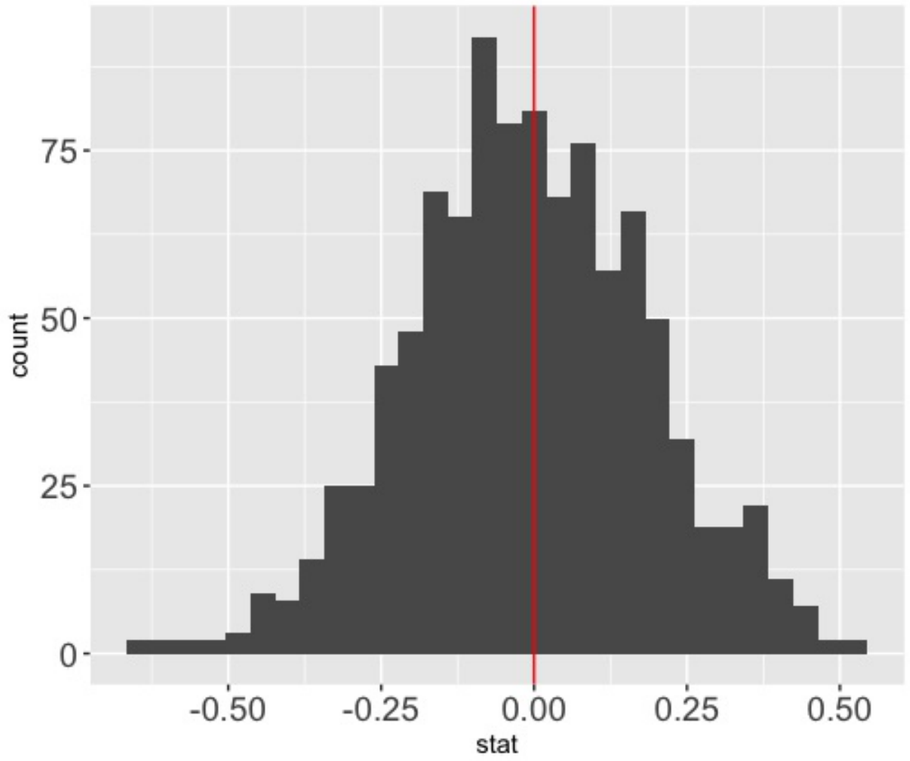
```
twins %>%
  specify(Foster ~ Biological) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 100, type = "permute") %>%
  calculate(stat = "slope")
```

Bootstrap:

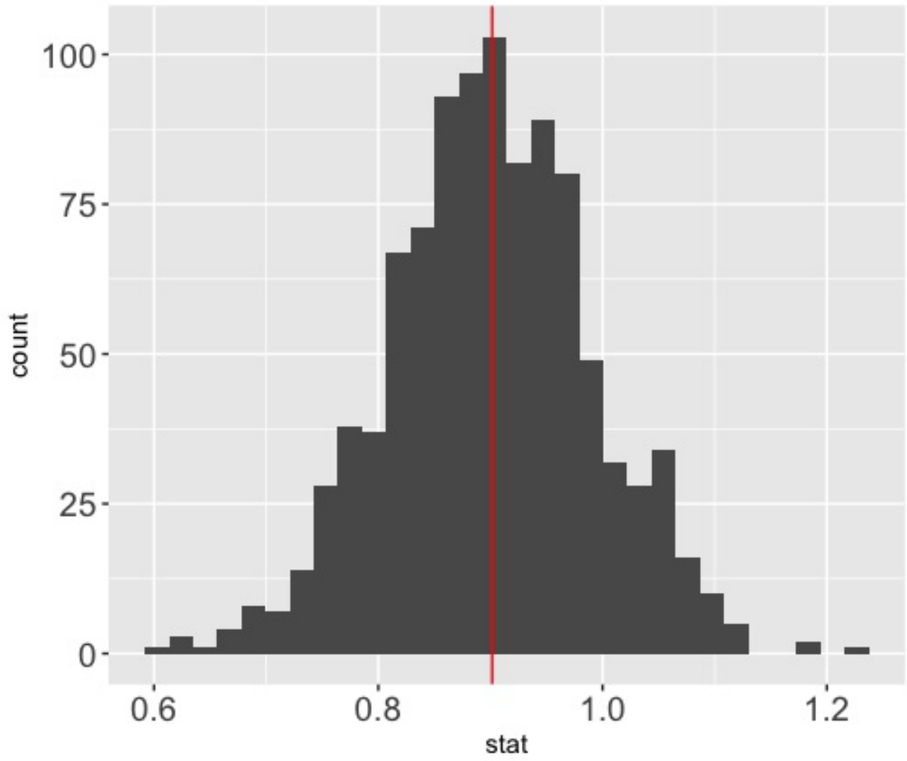
```
twins %>%
  specify(Foster ~ Biological) %>%
  generate(reps = 100, type = "bootstrap") %>%
  calculate(stat = "slope")
```

Sampling distribution: randomization vs. bootstrap

Slopes from permuted data



Slopes from bootstrapped data



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Let's practice!