

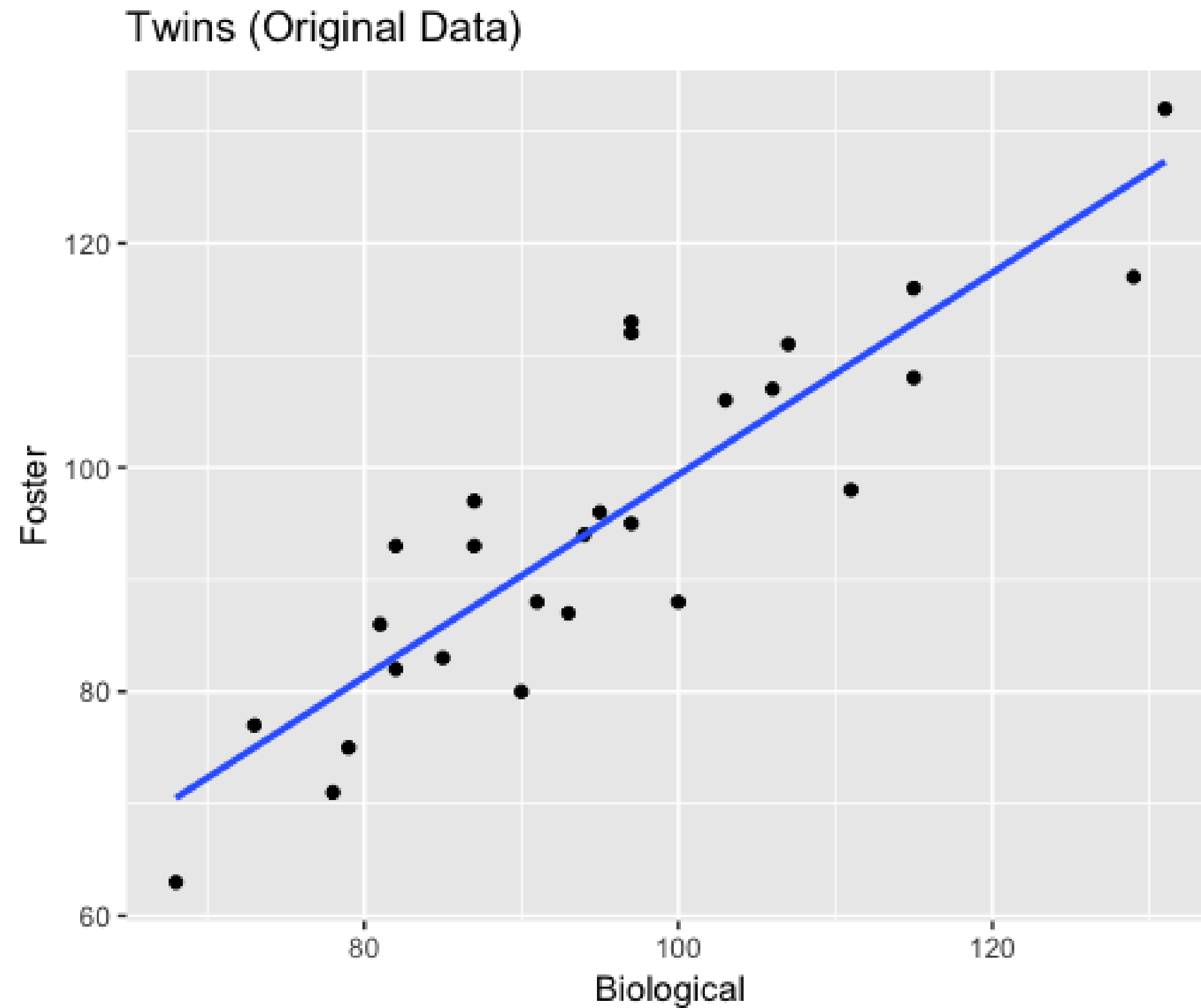


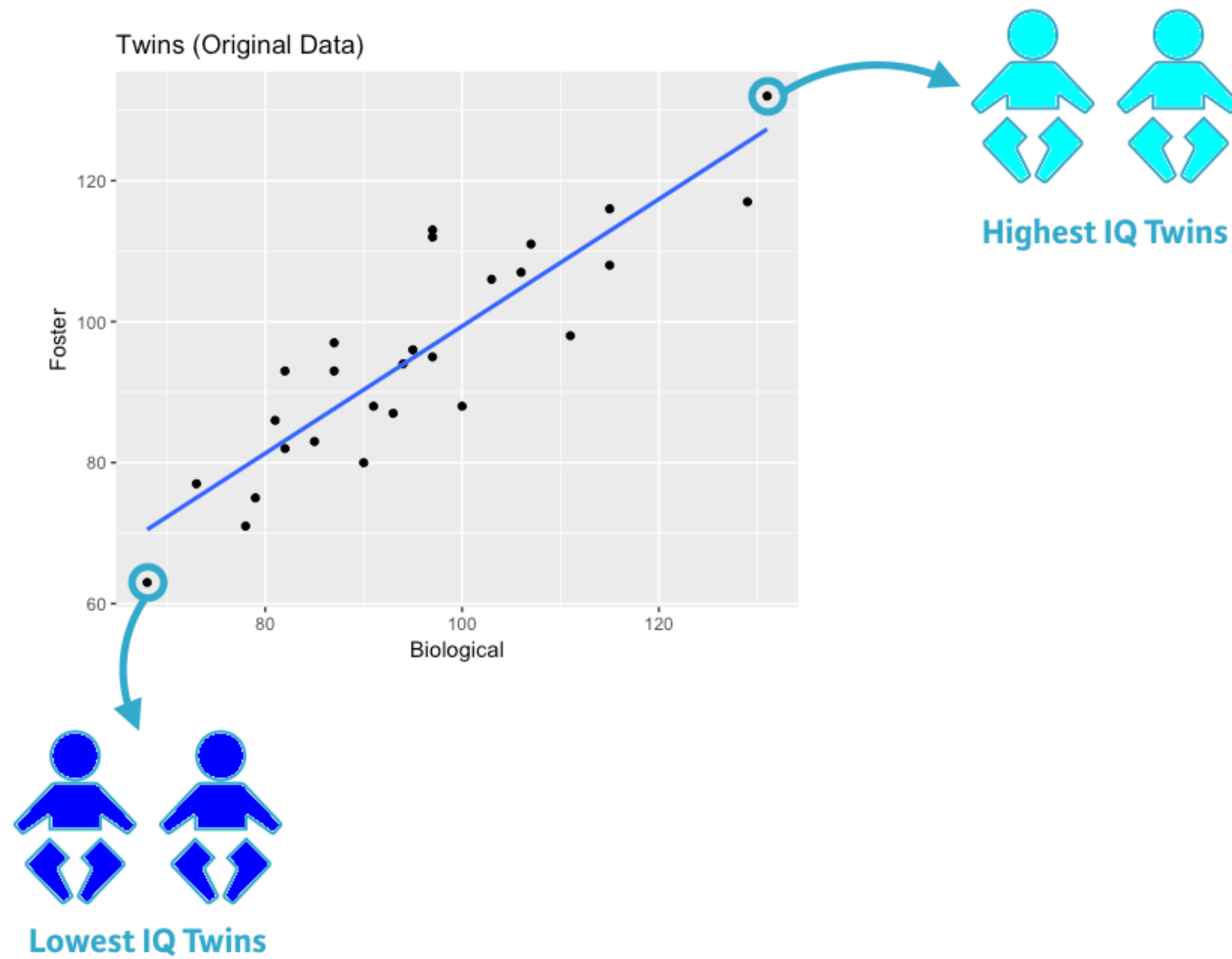
INFERENCE FOR LINEAR REGRESSION

Simulation-based Inference

Jo Hardin









Professor, Pomona College















Twin data

Foster		Biological	
	80		90
	108		115
	116		115
	93		83



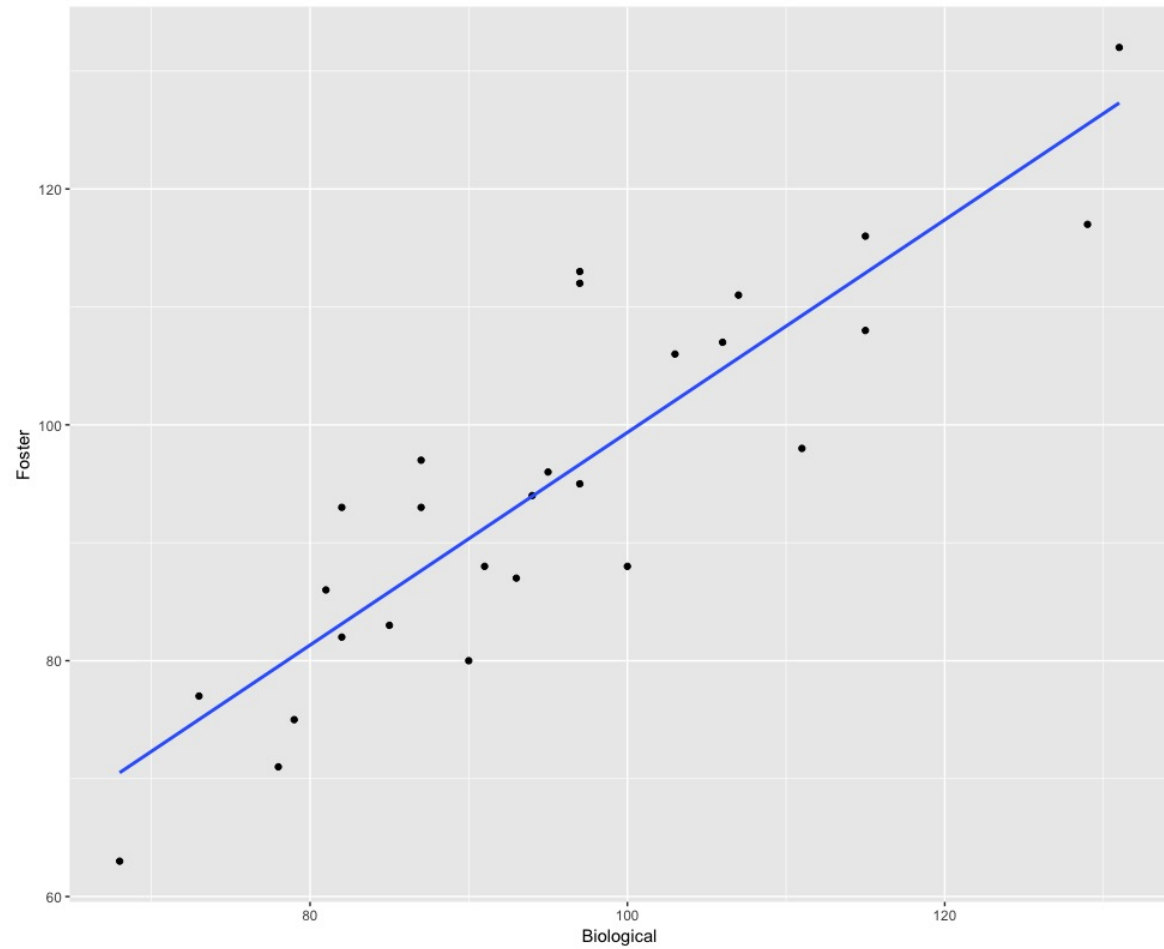
Permuted twin data

Foster		Biological	
	108		90
	93		115
	116		115
	80		83

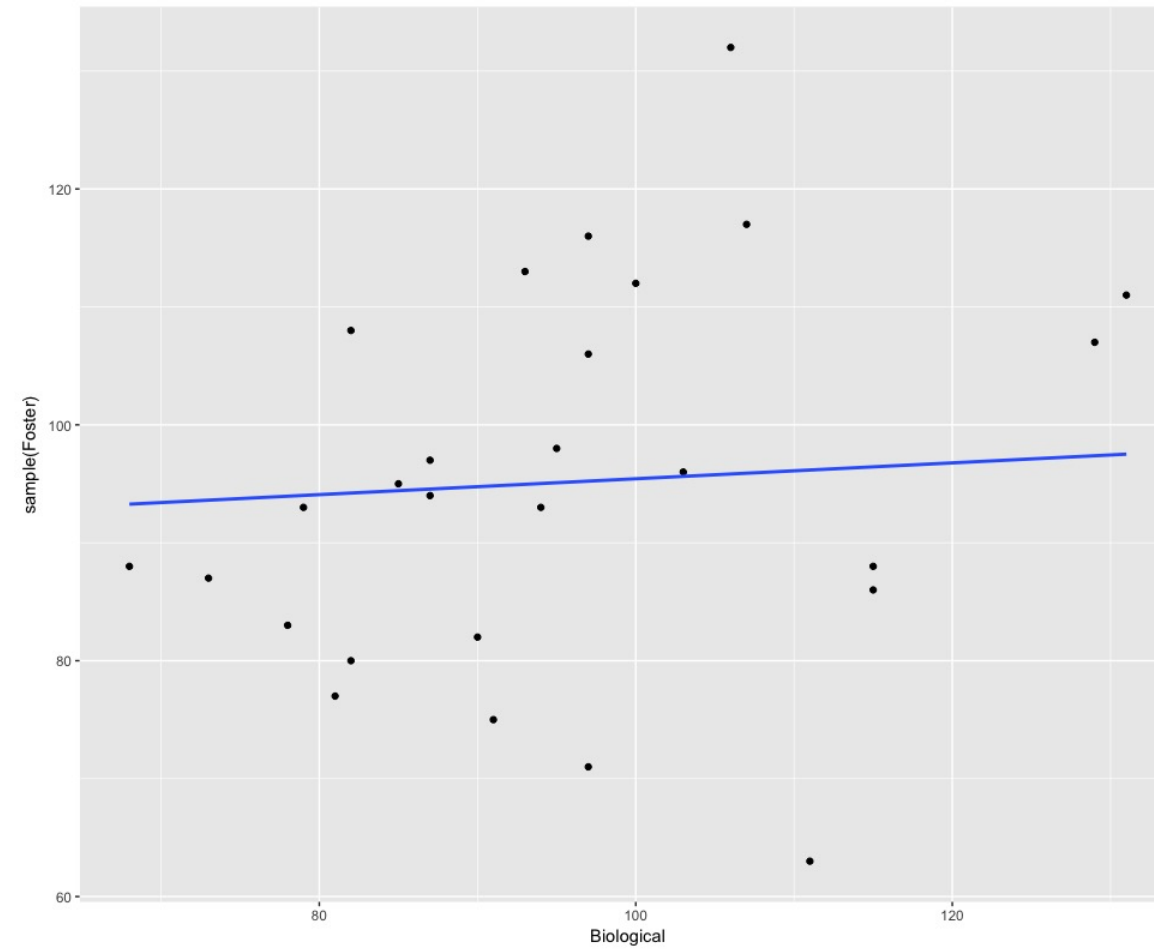


Permuted data (1) plotted

Original data



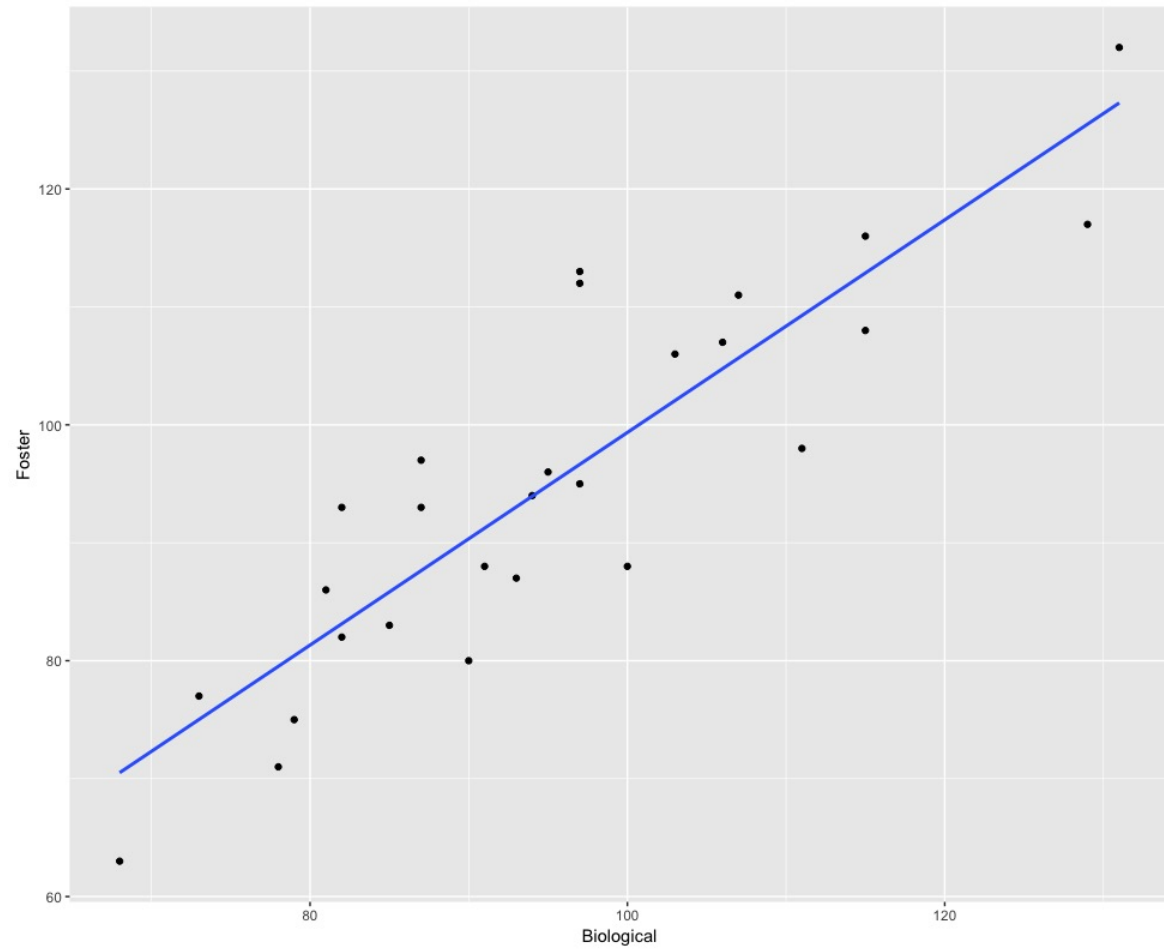
Permuted data (1)



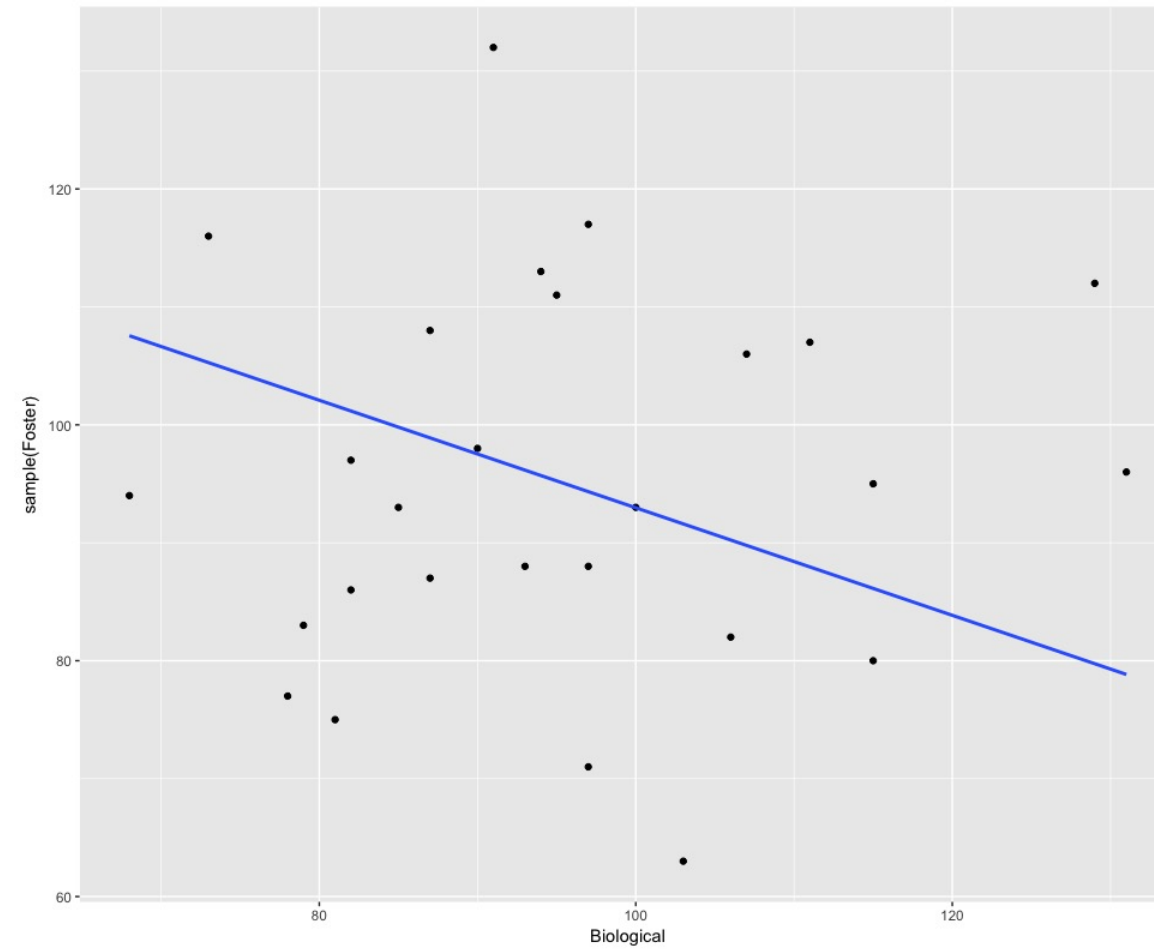


Permuted data (2) plotted

Original data



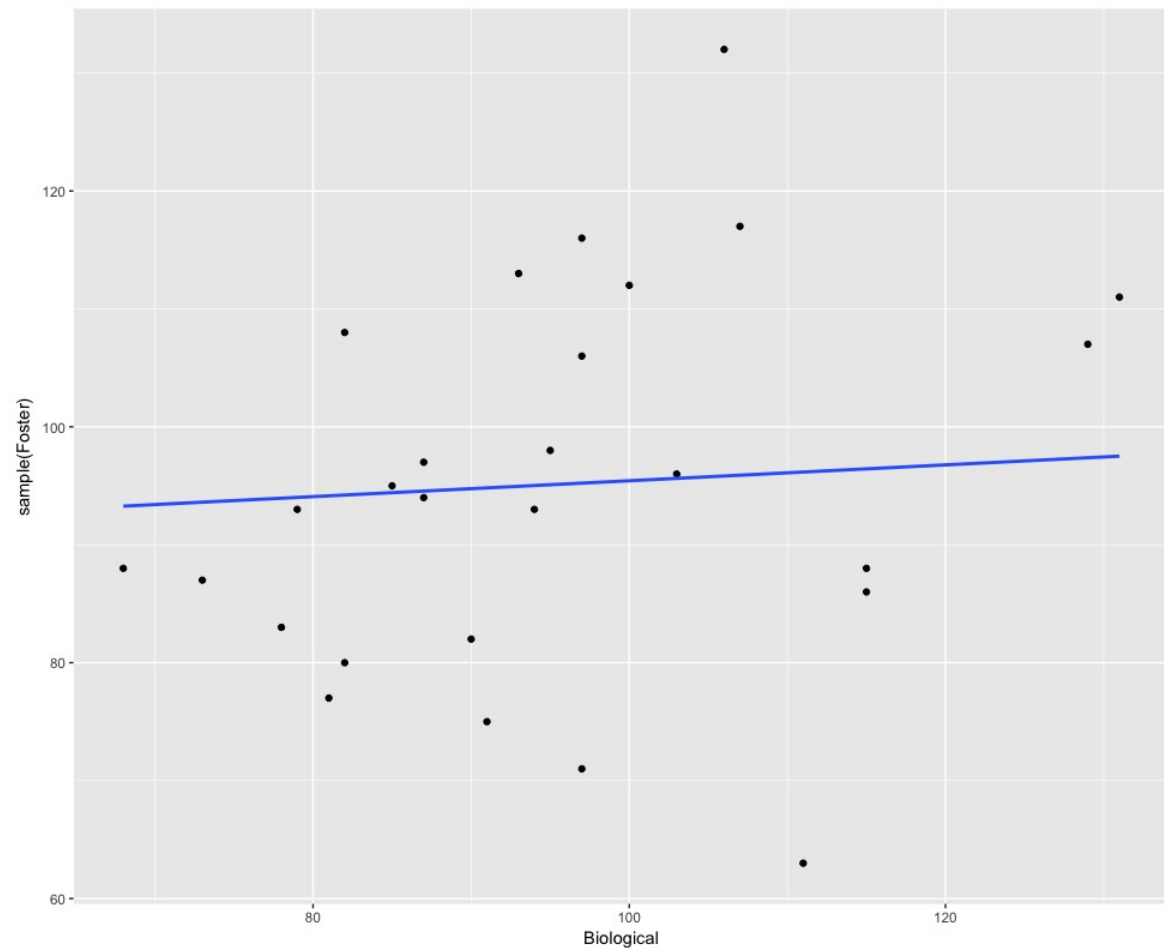
Permuted data (2)



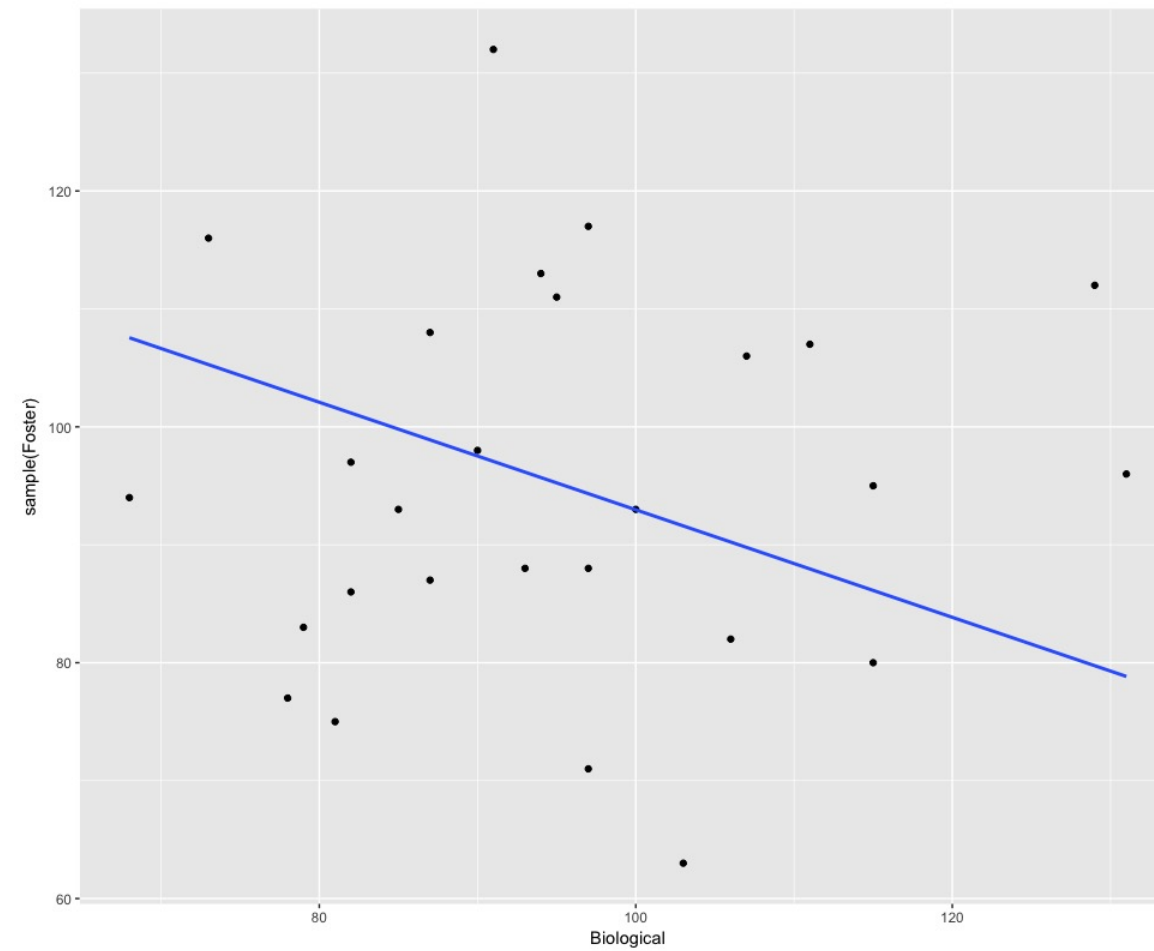


Permuted data (1) and (2)

Permuted data (1)



Permuted data (2)



Linear model on permuted data

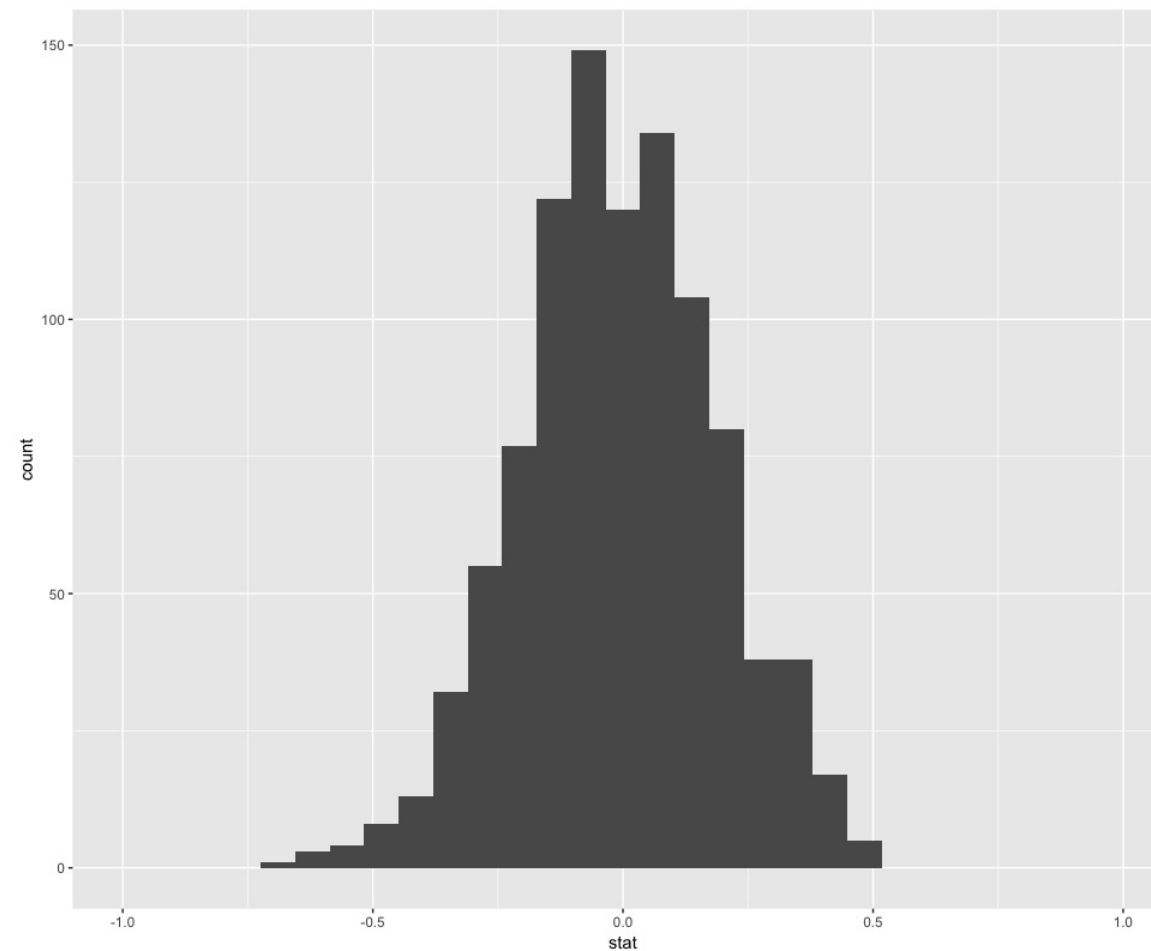
```
twins %>%
  specify(Foster ~ Biological) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 10, type = "permute") %>%
  calculate(stat = "slope")
```

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

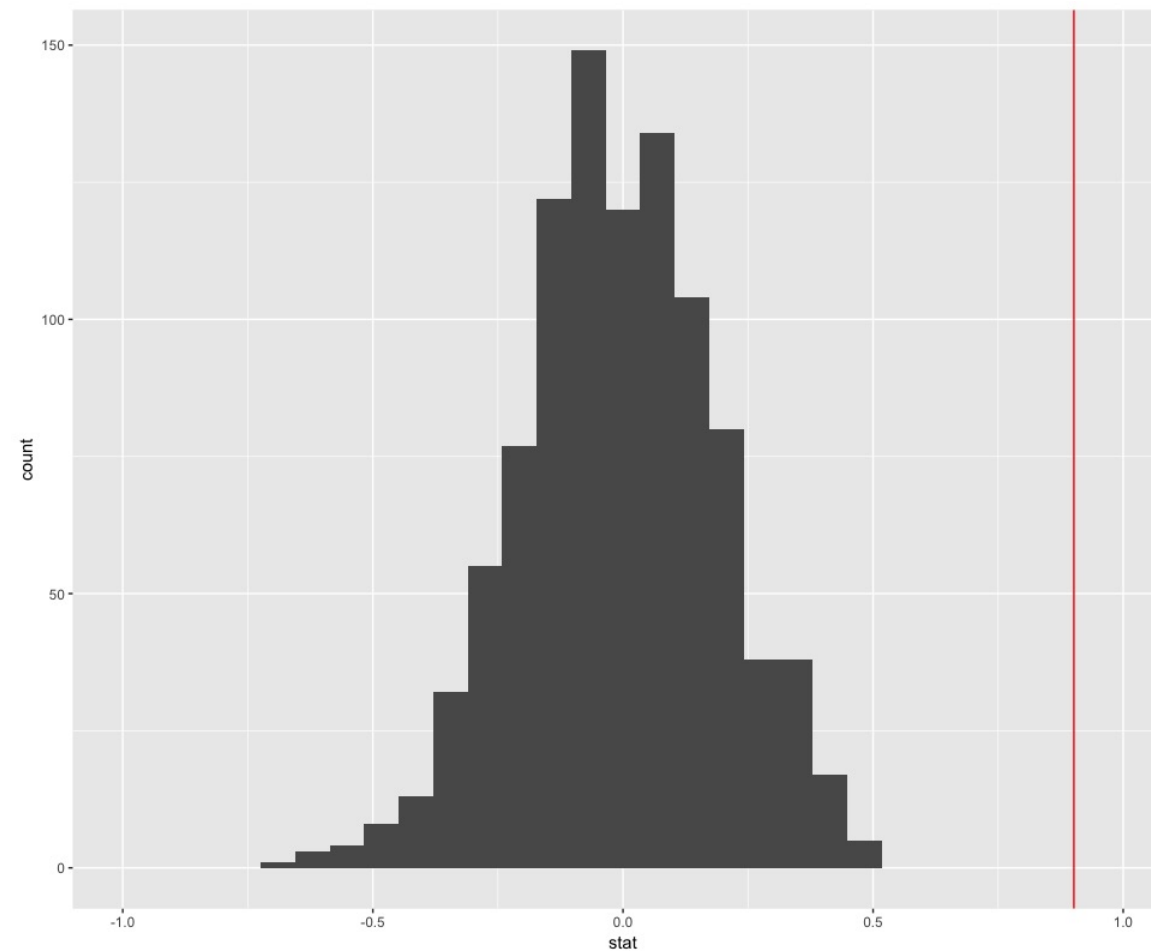
Many permuted slopes

```
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!











INFERENCE FOR LINEAR REGRESSION

Simulation-based CI for slope









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**Original Sample**

Foster		Biological	
	80		90
	108		115
	116		115
	93		83

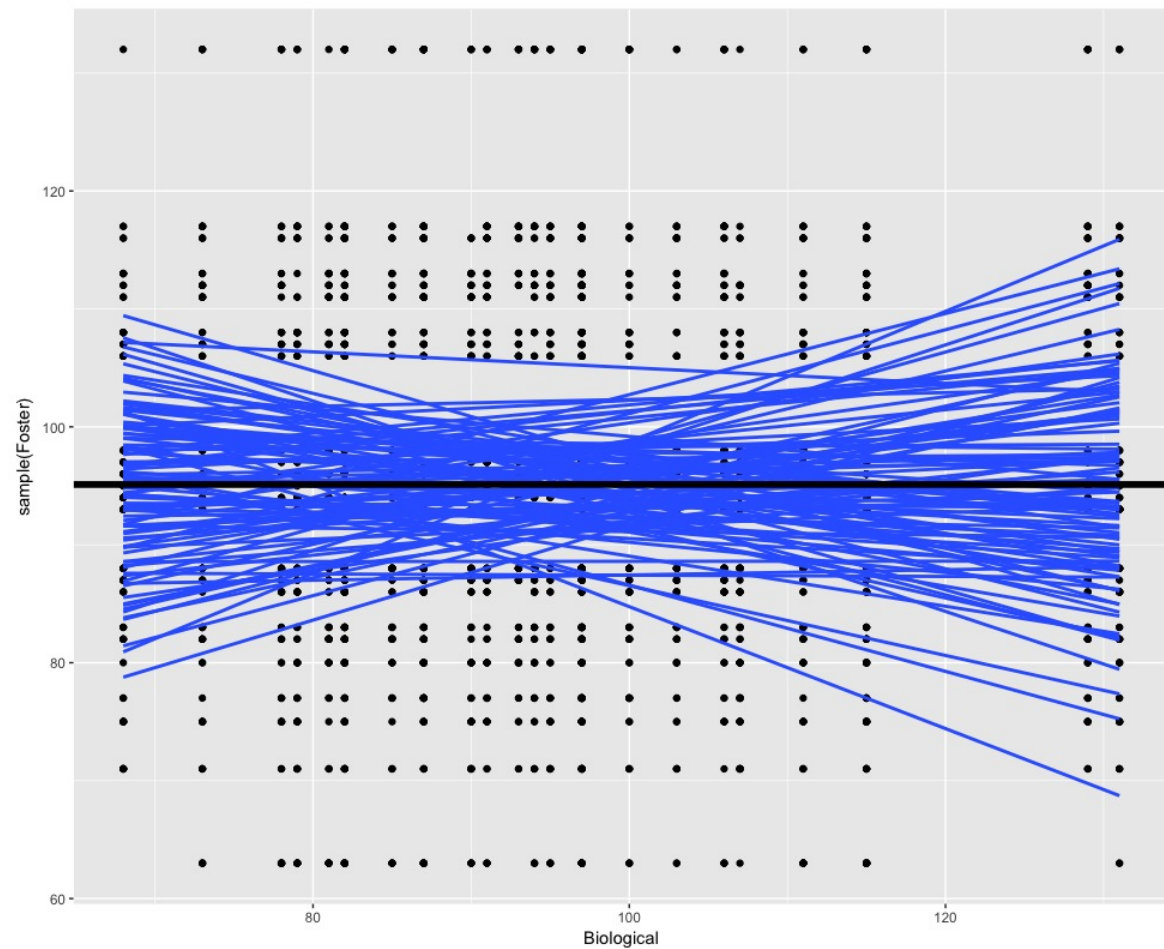
Bootstrapped Sample

Foster		Biological	
	93		83
	108		115
	108		115
	93		83

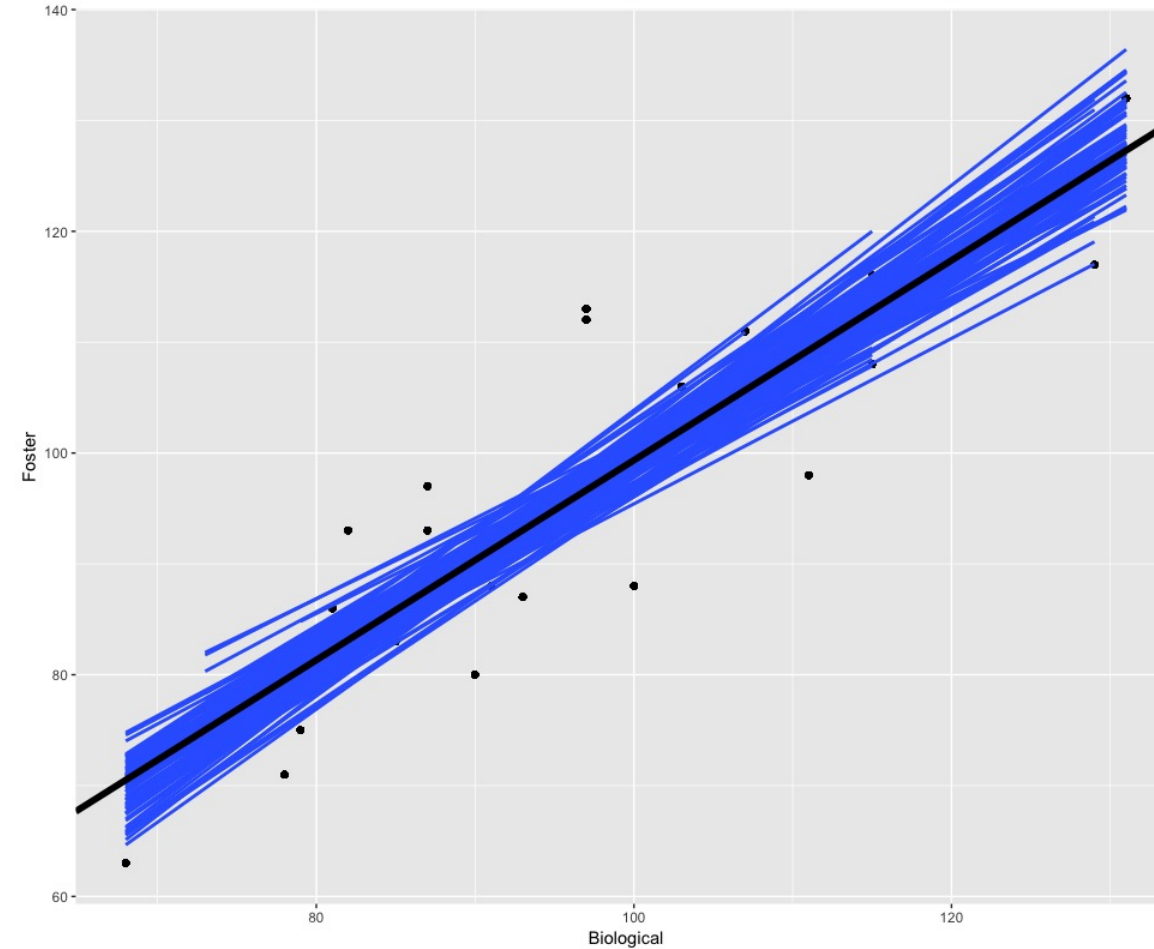


Permutation vs. bootstrap variability

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")
```

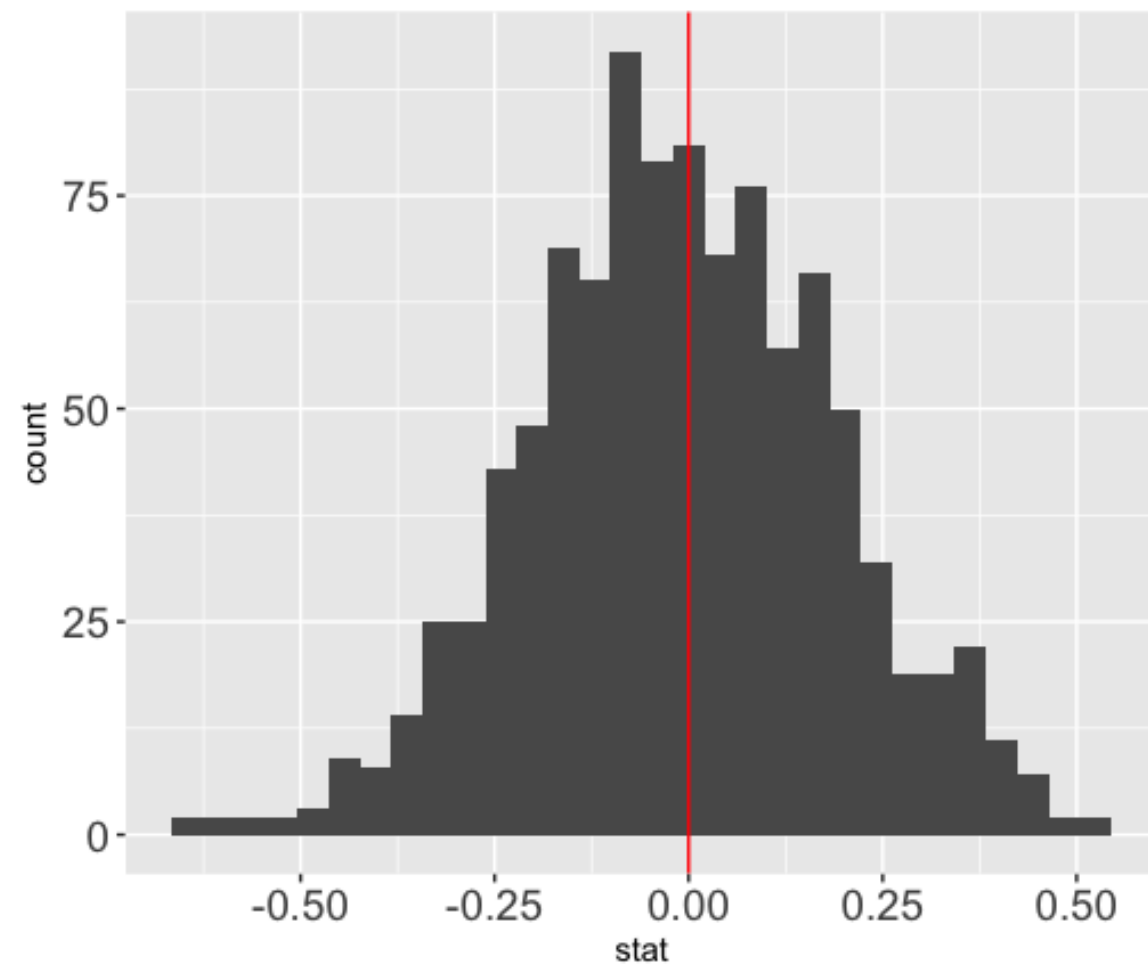
Bootstrap:

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

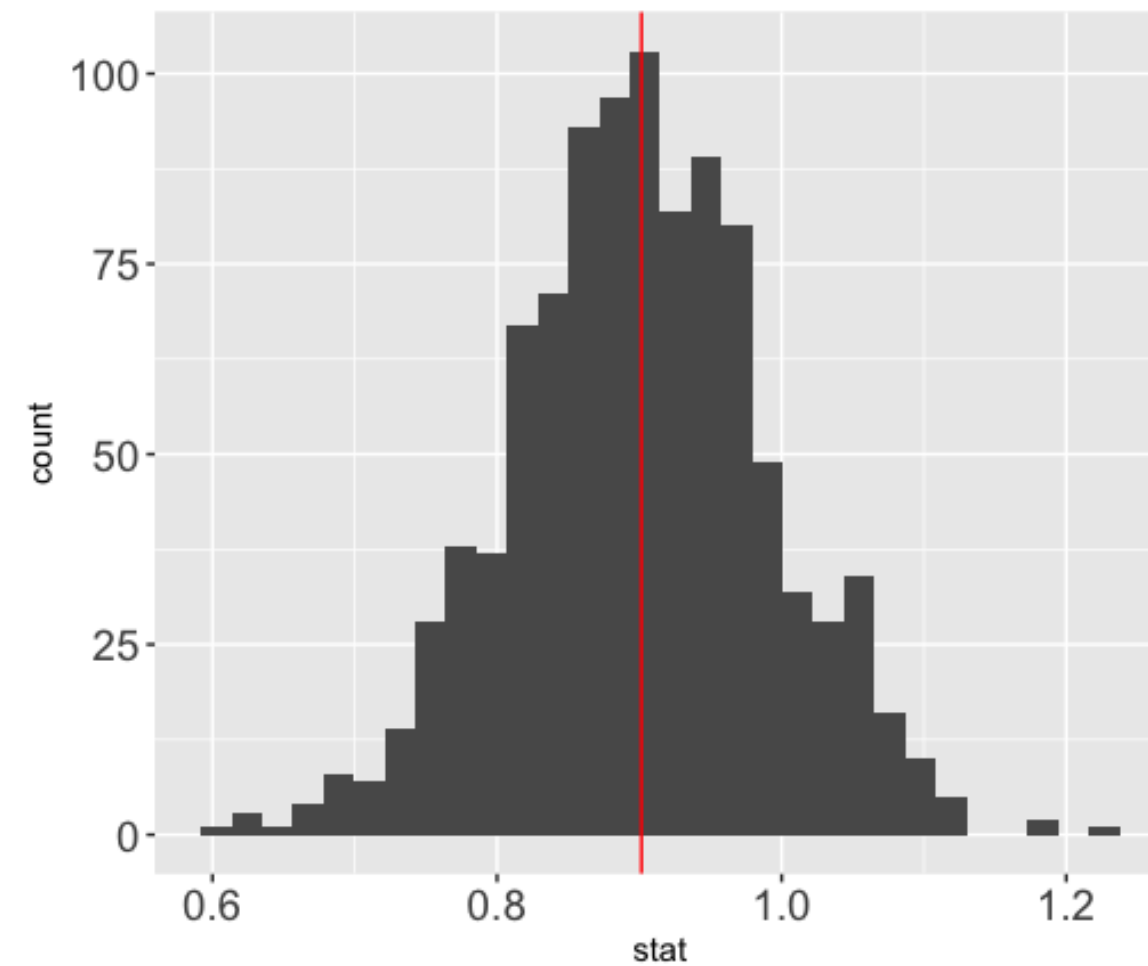



Sampling distribution: randomization vs. bootstrap

Slopes from permuted data



Slopes from bootstrapped data





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Let's practice!