CCFRP Central California Fork Length and Total Length Comparison

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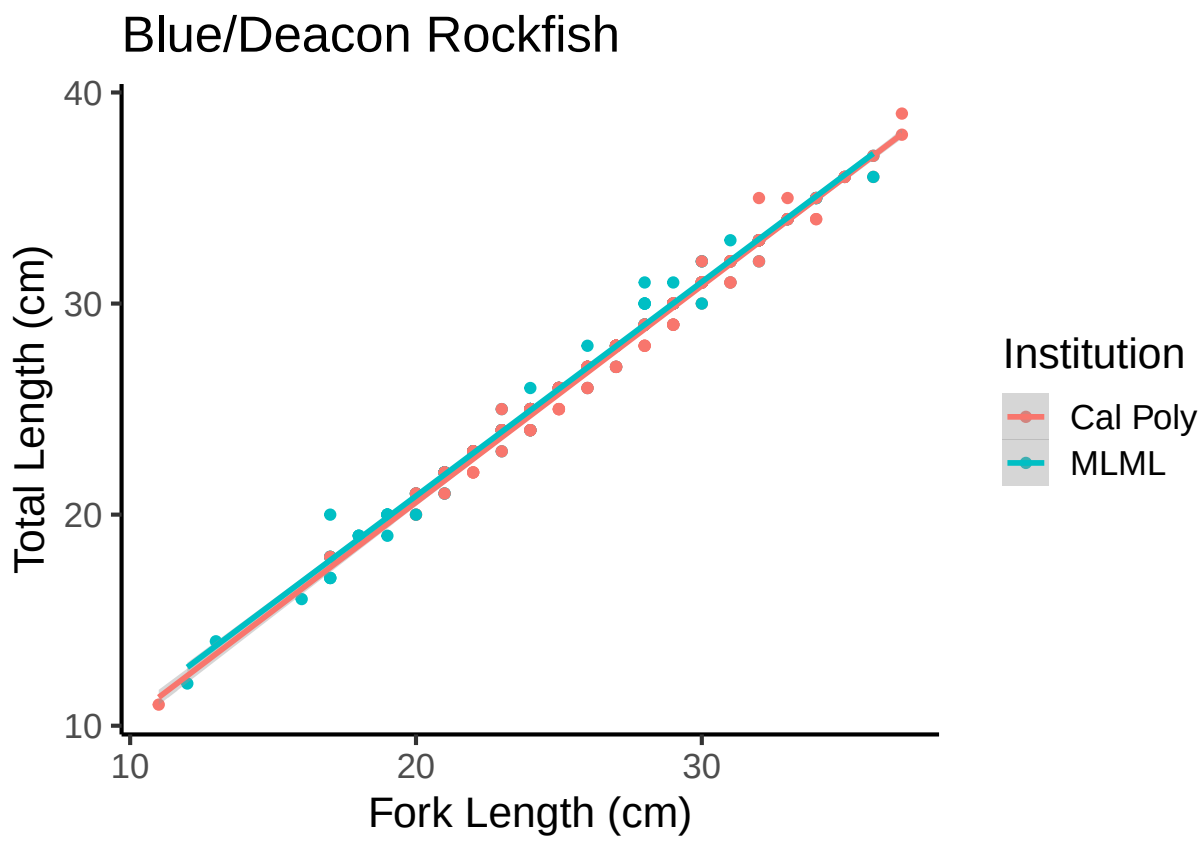
Load Data

```
length.data <-read.csv('Fork-And-Total-Length-Data.csv')
```

Blue/Deacon Rockfish

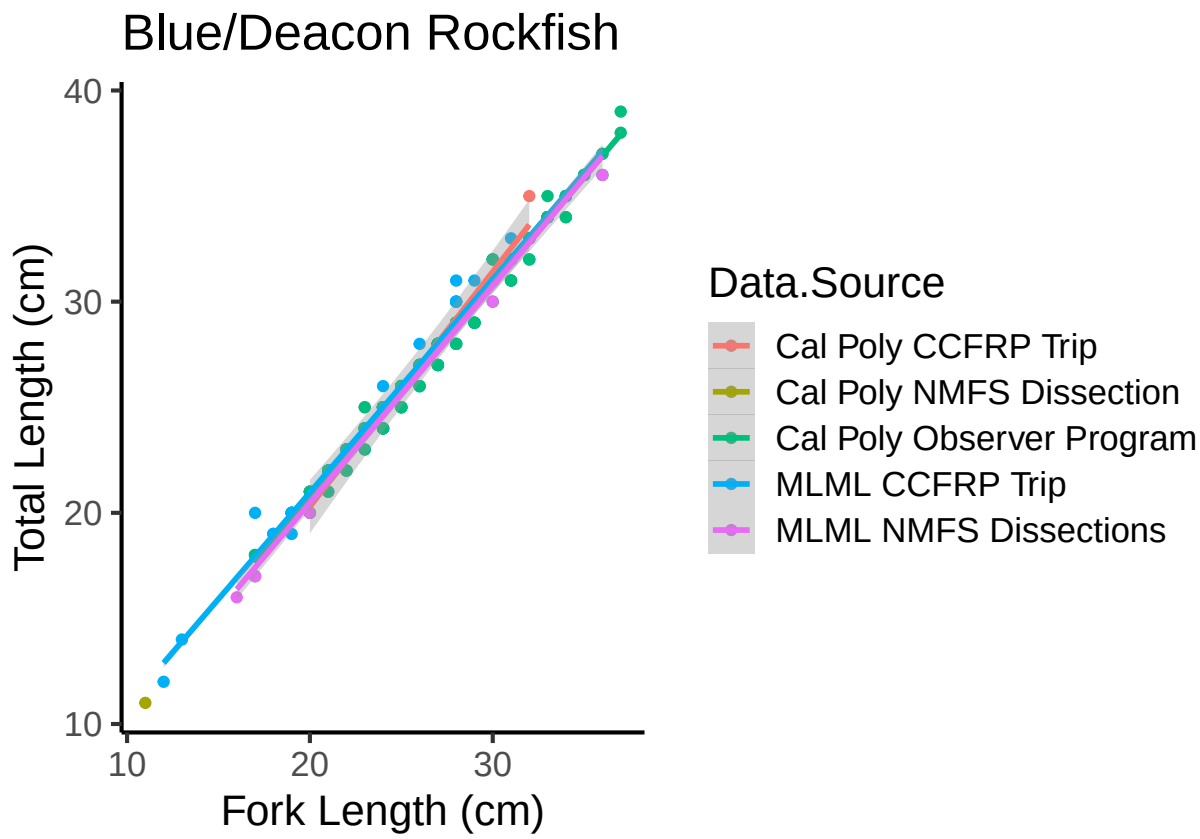
```
blue.deacon<-length.data%>%
  group_by(Institution, Species, Data.Source)%>%
  filter(Species == "Blue/Deacon Rockfish")

ggplot(blue.deacon, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Institution))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Blue/Deacon Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



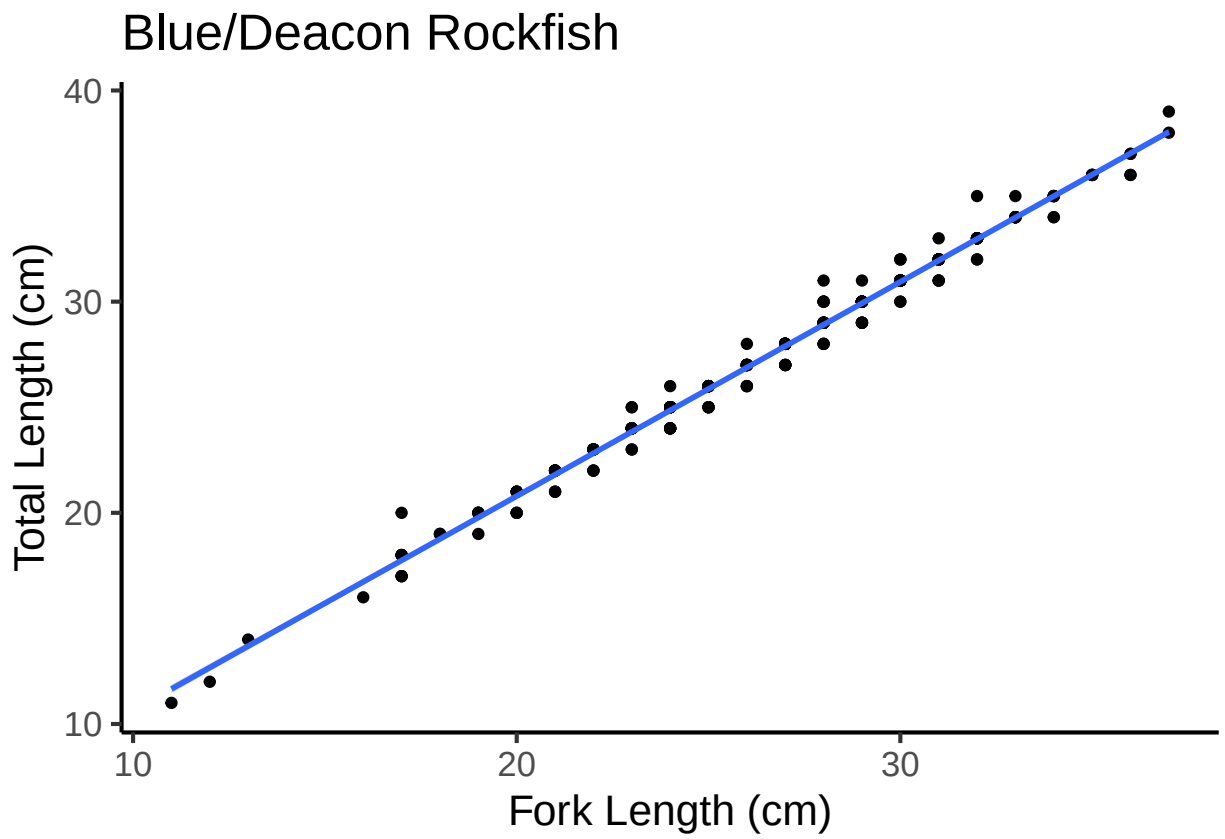

```
ggplot(blue.deacon, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Data.Source))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Blue/Deacon Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggplot(blue.deacon, aes(x=Fork.Length..cm., y=Total.Length..cm.))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Blue/Deacon Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

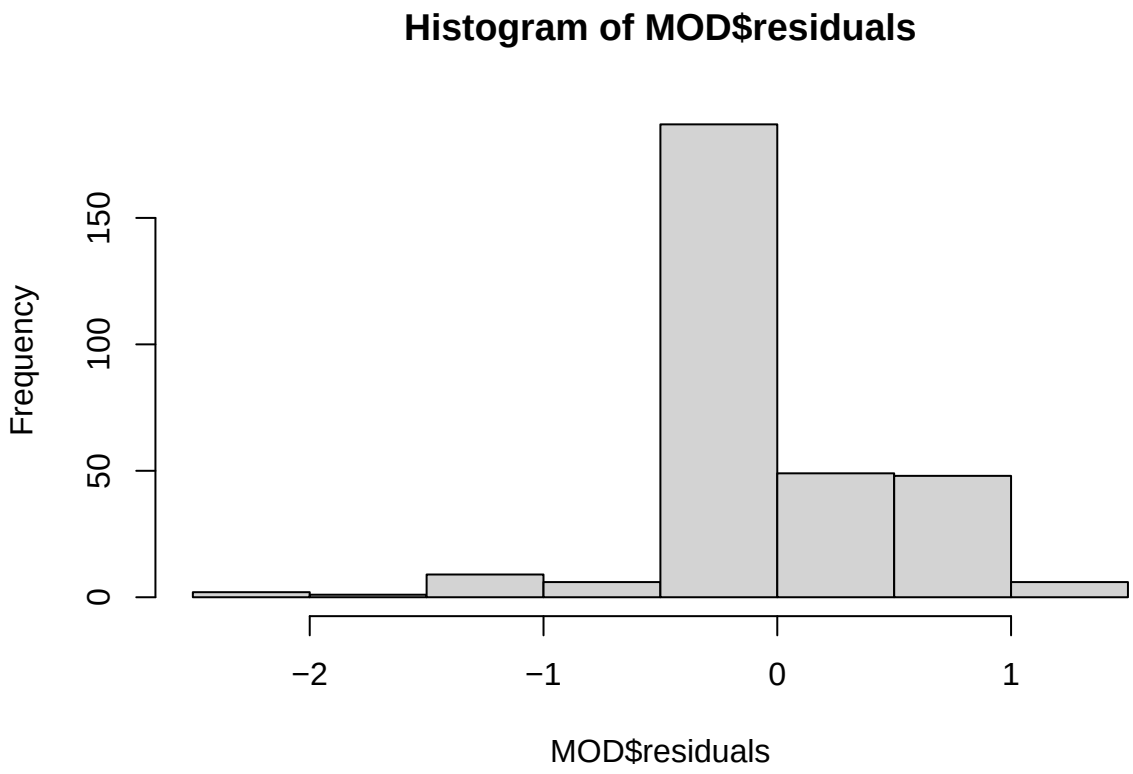
```
## `geom_smooth()` using formula = 'y ~ x'
```




```
MOD <- lm(Fork.Length..cm.~Total.Length..cm., data = blue.deacon)
  summary(MOD)
```

```
##
## Call:
## lm(formula = Fork.Length..cm. ~ Total.Length..cm., data = blue.deacon)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.30306 -0.17545 -0.07336  0.03510  1.10529
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -0.186500   0.165489  -1.127    0.261
## Total.Length..cm.  0.974478   0.005947 163.858   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4935 on 306 degrees of freedom
## Multiple R-squared:  0.9887, Adjusted R-squared:  0.9887
## F-statistic: 2.685e+04 on 1 and 306 DF,  p-value: < 2.2e-16
```

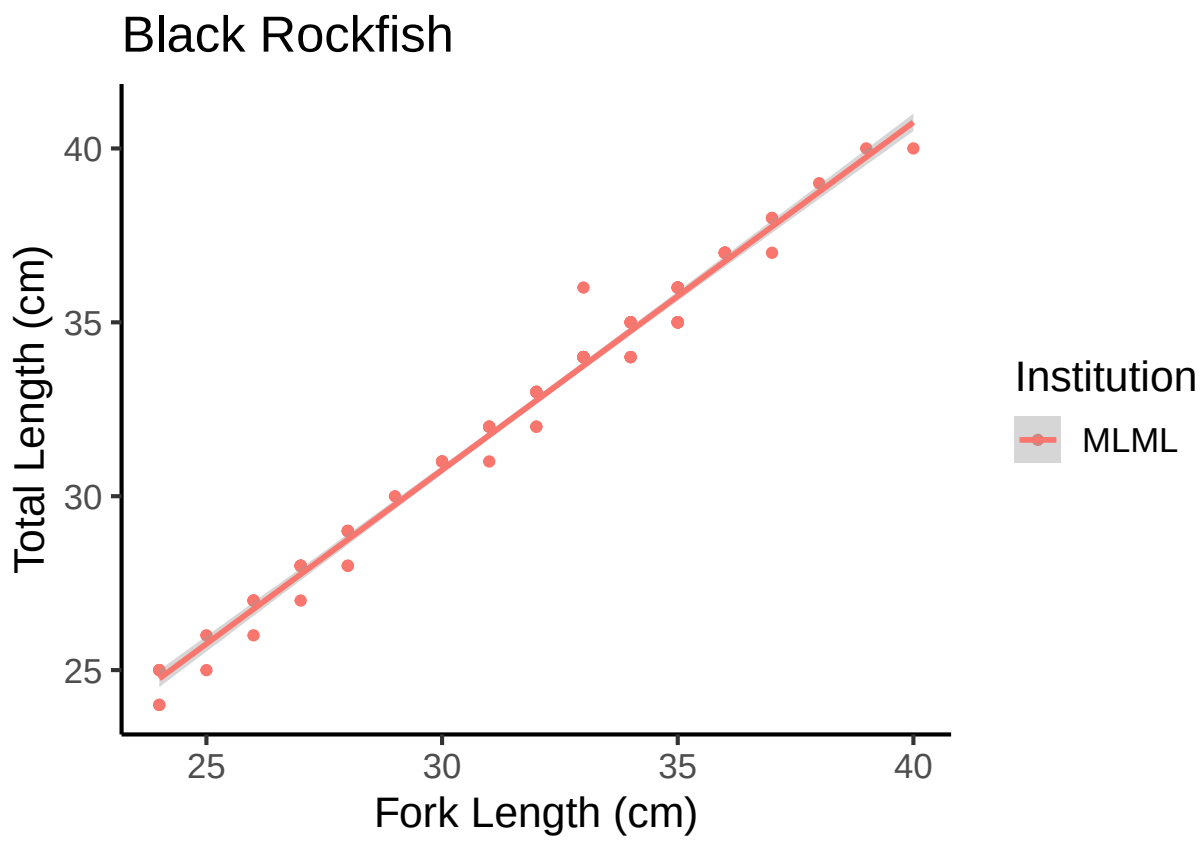
```
  hist(MOD$residuals)
```



Black Rockfish

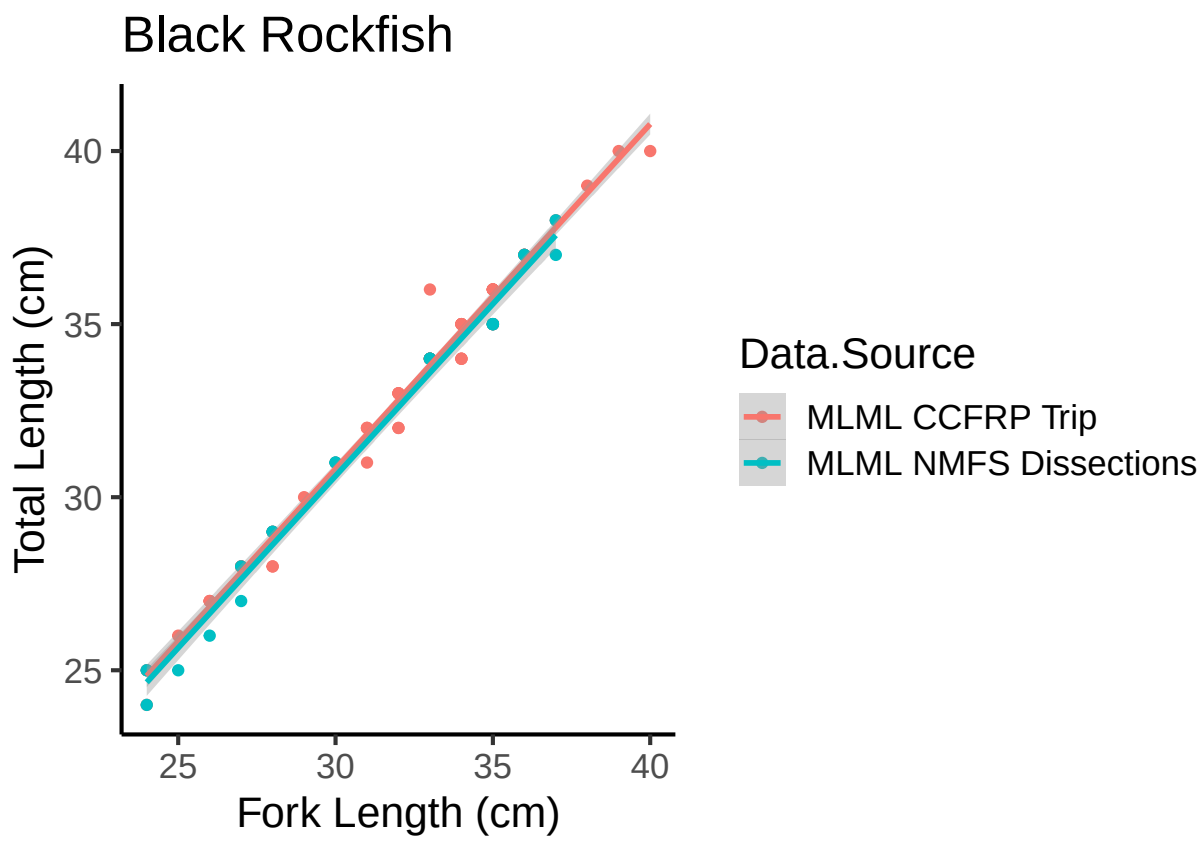
```
black<-length.data%>%
  group_by(Institution, Species, Data.Source)%>%
  filter(Species == "Black Rockfish")

ggplot(black, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Institution))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Black Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



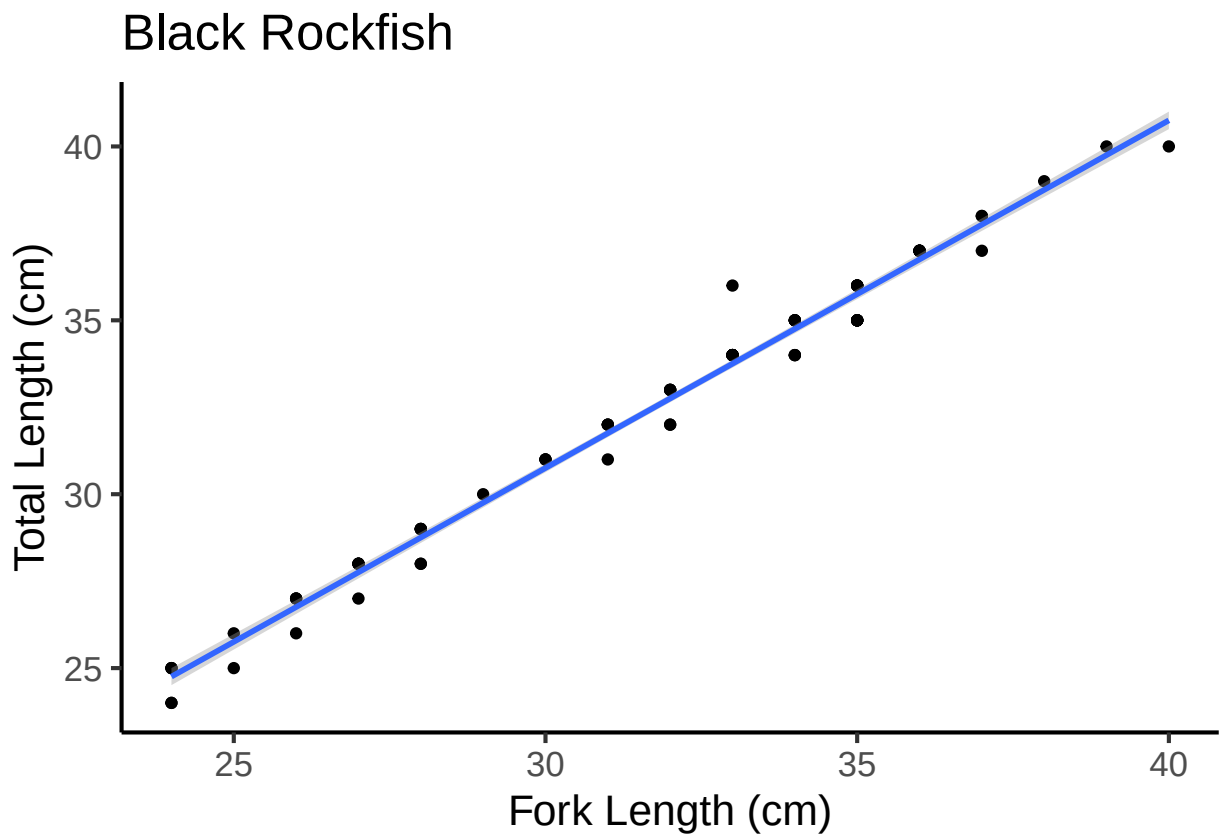

```
ggplot(black, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Data.Source))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Black Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggplot(black, aes(x=Fork.Length..cm., y=Total.Length..cm.))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Black Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

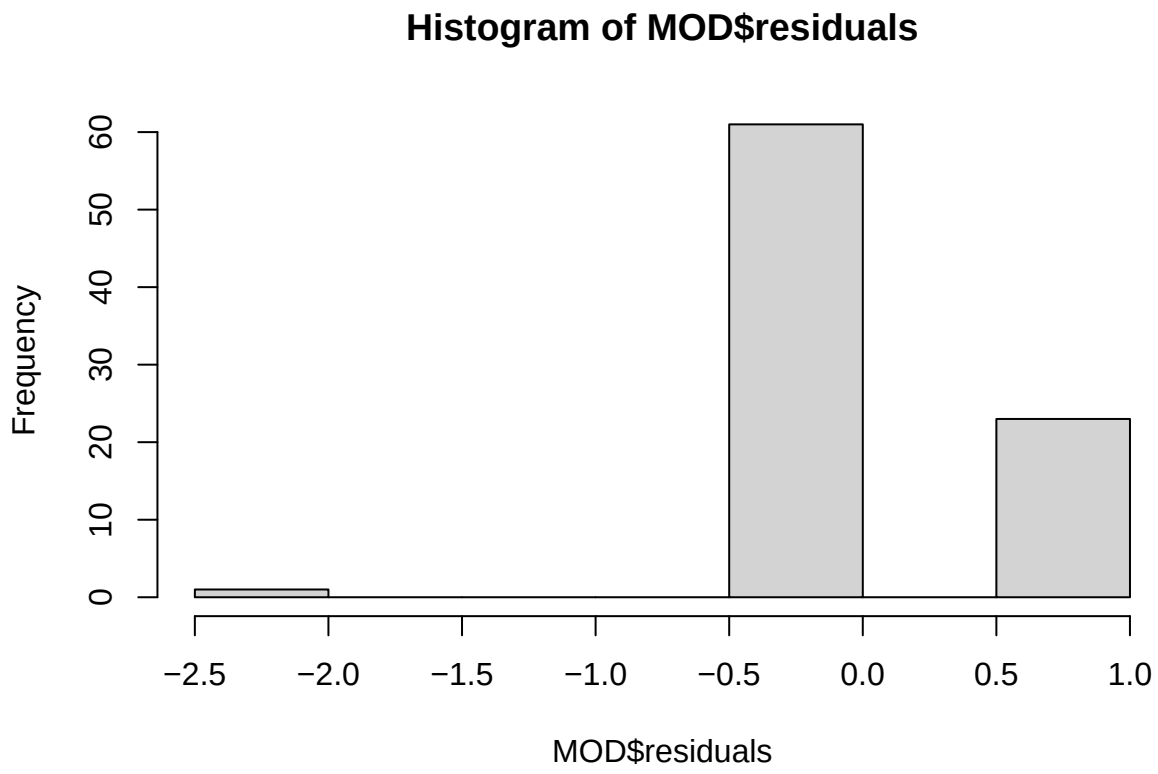
```
## `geom_smooth()` using formula = 'y ~ x'
```




```
MOD <- lm(Fork.Length..cm.~Total.Length..cm., data = black)
  summary(MOD)
```

```
##
## Call:
## lm(formula = Fork.Length..cm. ~ Total.Length..cm., data = black)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.1942 -0.2570 -0.2099  0.6174  0.8685
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -0.2407     0.4536  -0.531    0.597
## Total.Length..cm.   0.9843     0.0138  71.352   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5087 on 83 degrees of freedom
## Multiple R-squared:  0.984,  Adjusted R-squared:  0.9838
## F-statistic:  5091 on 1 and 83 DF,  p-value: < 2.2e-16
```

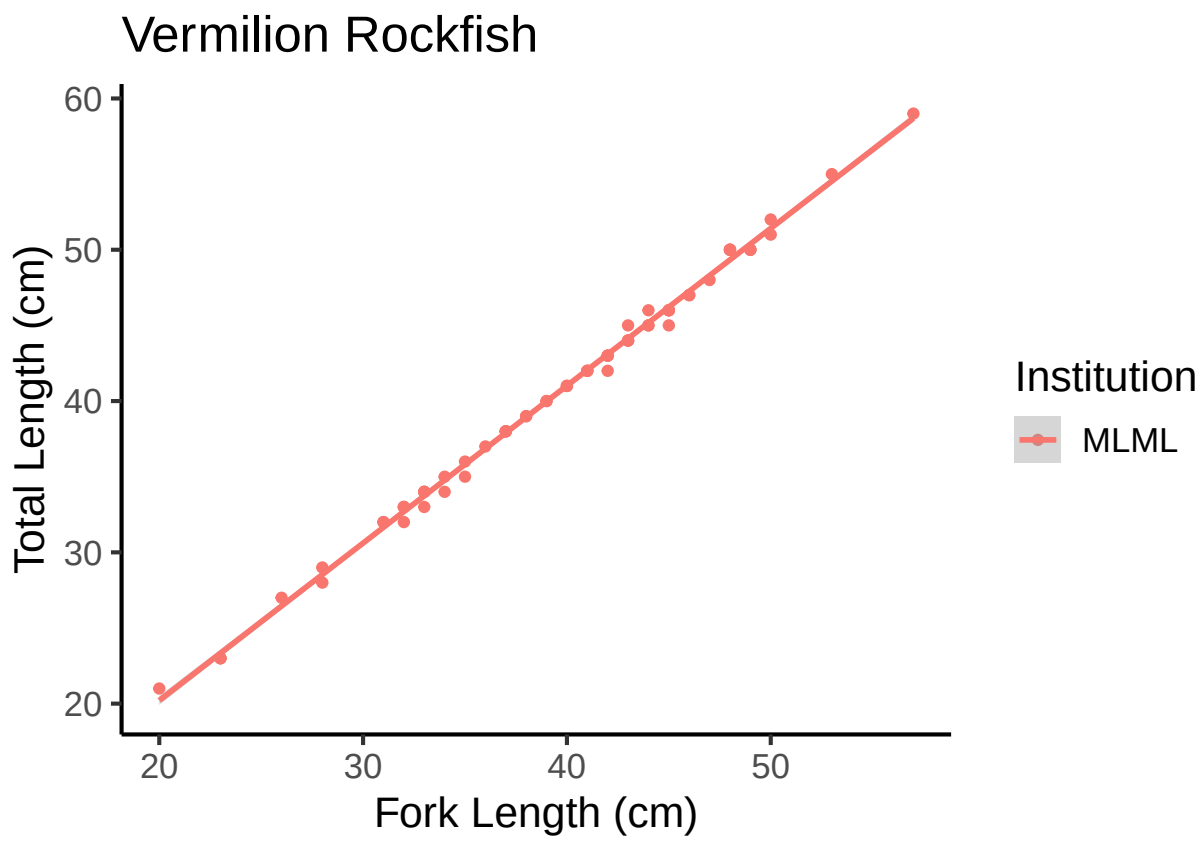
```
  hist(MOD$residuals)
```



Vermilion Rockfish

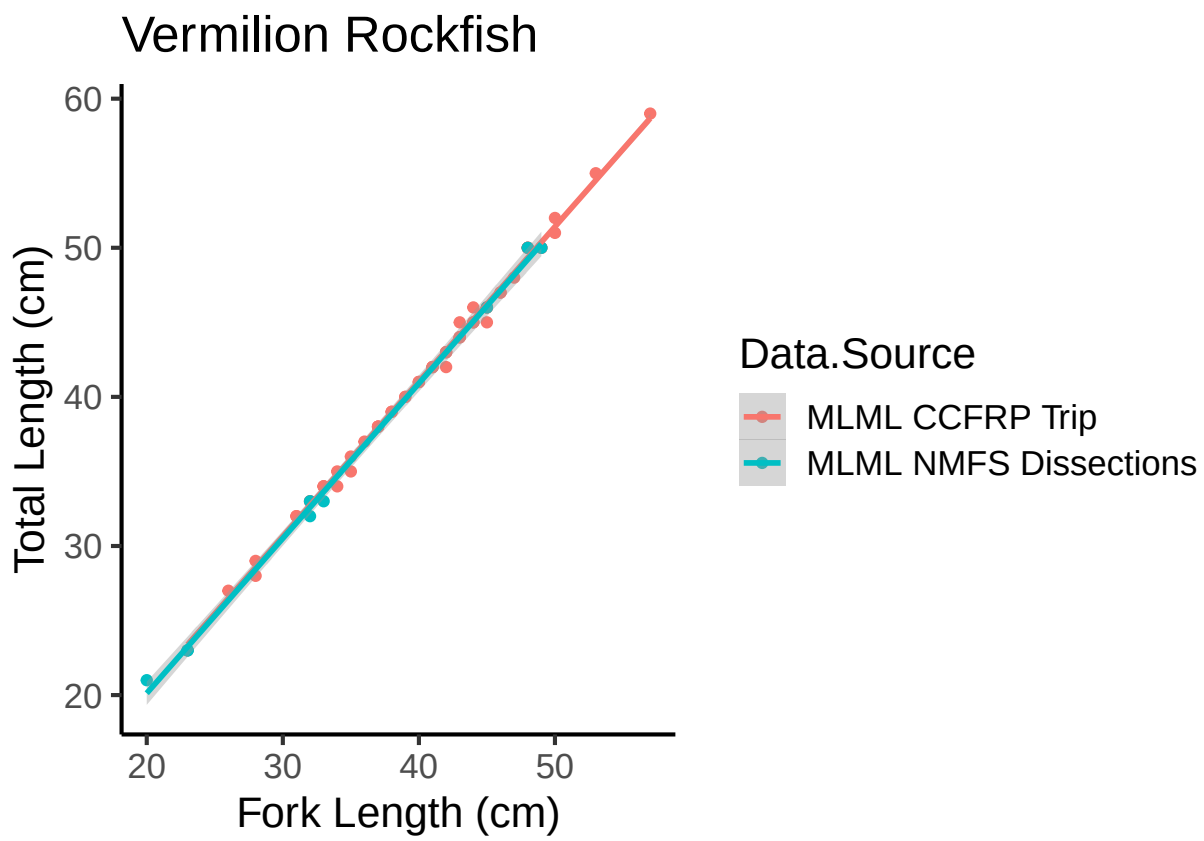
```
vermilion<-length.data%>%
  group_by(Institution, Species, Data.Source)%>%
  filter(Species == "Vermilion Rockfish")

ggplot(vermilion, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Institution))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Vermilion Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



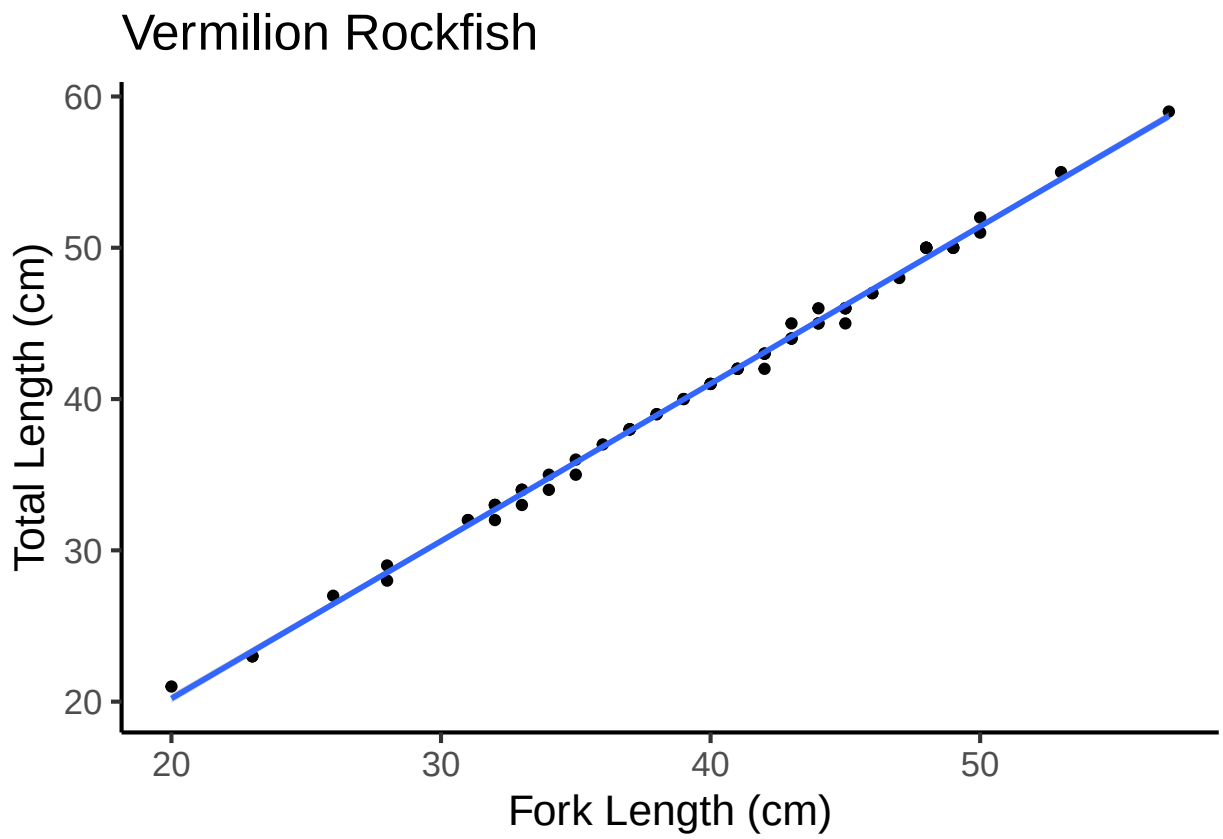

```
ggplot(vermilion, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Data.Source))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Vermilion Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggplot(vermilion, aes(x=Fork.Length..cm., y=Total.Length..cm.))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Vermilion Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

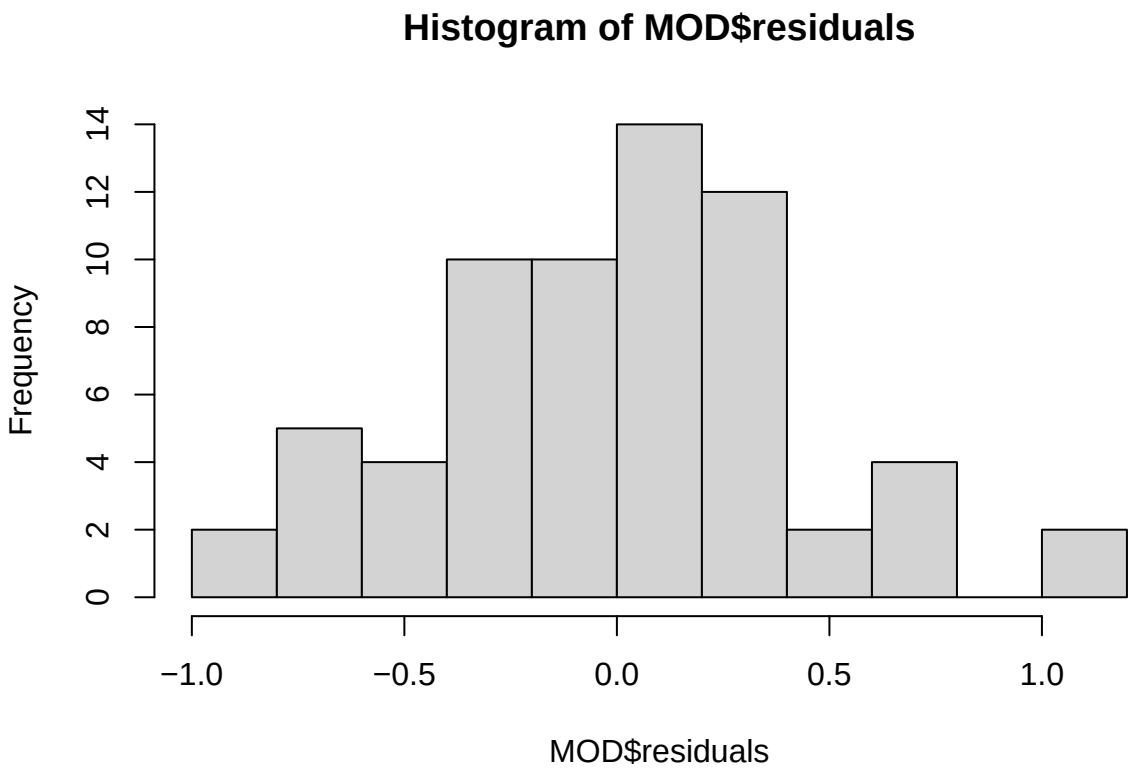
```
## `geom_smooth()` using formula = 'y ~ x'
```




```
MOD <- lm(Fork.Length..cm.~Total.Length..cm., data = vermilion)
  summary(MOD)
```

```
##
## Call:
## lm(formula = Fork.Length..cm. ~ Total.Length..cm., data = vermilion)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.81878 -0.27371  0.01579  0.26394  1.18122
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        0.67987    0.26734   2.543   0.0135 *
## Total.Length..cm.  0.95864    0.00651 147.259   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4286 on 63 degrees of freedom
## Multiple R-squared:  0.9971, Adjusted R-squared:  0.9971
## F-statistic: 2.169e+04 on 1 and 63 DF,  p-value: < 2.2e-16
```

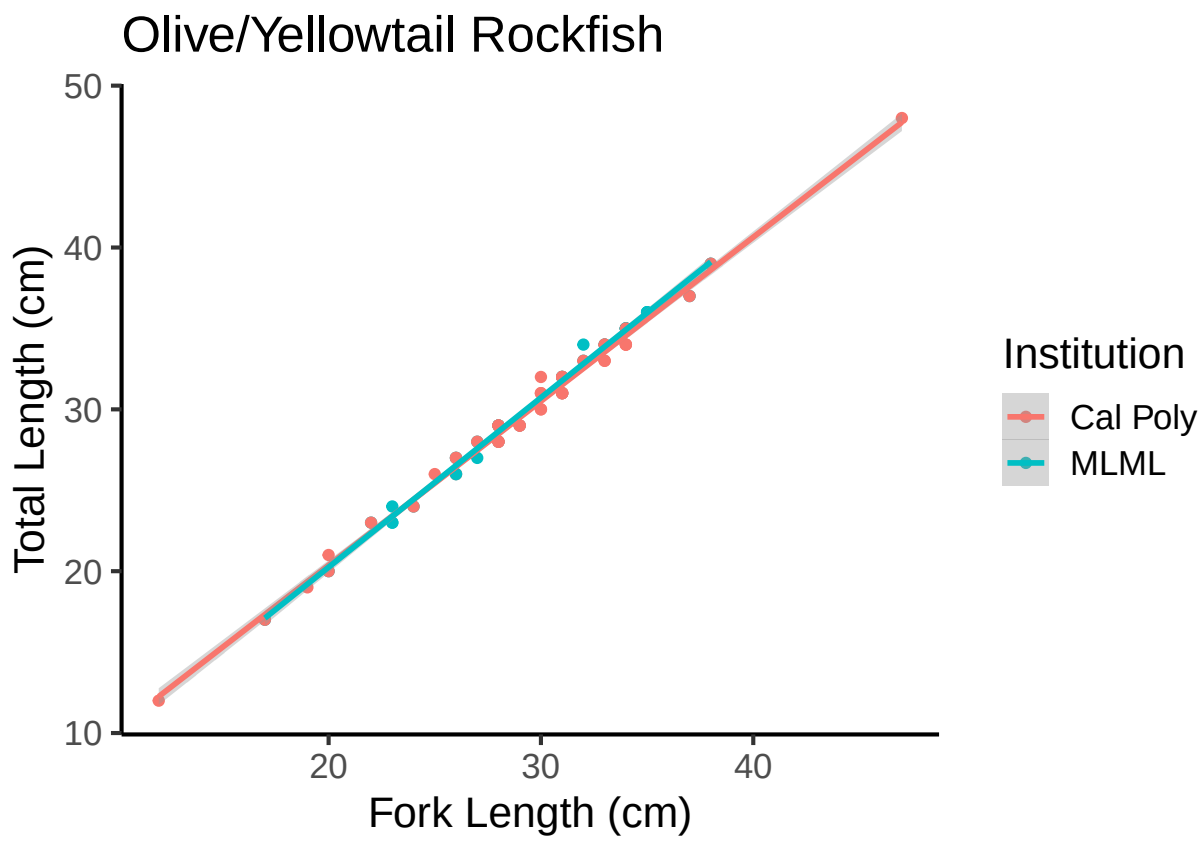
```
  hist(MOD$residuals)
```



Olive/Yellowtail Rockfish

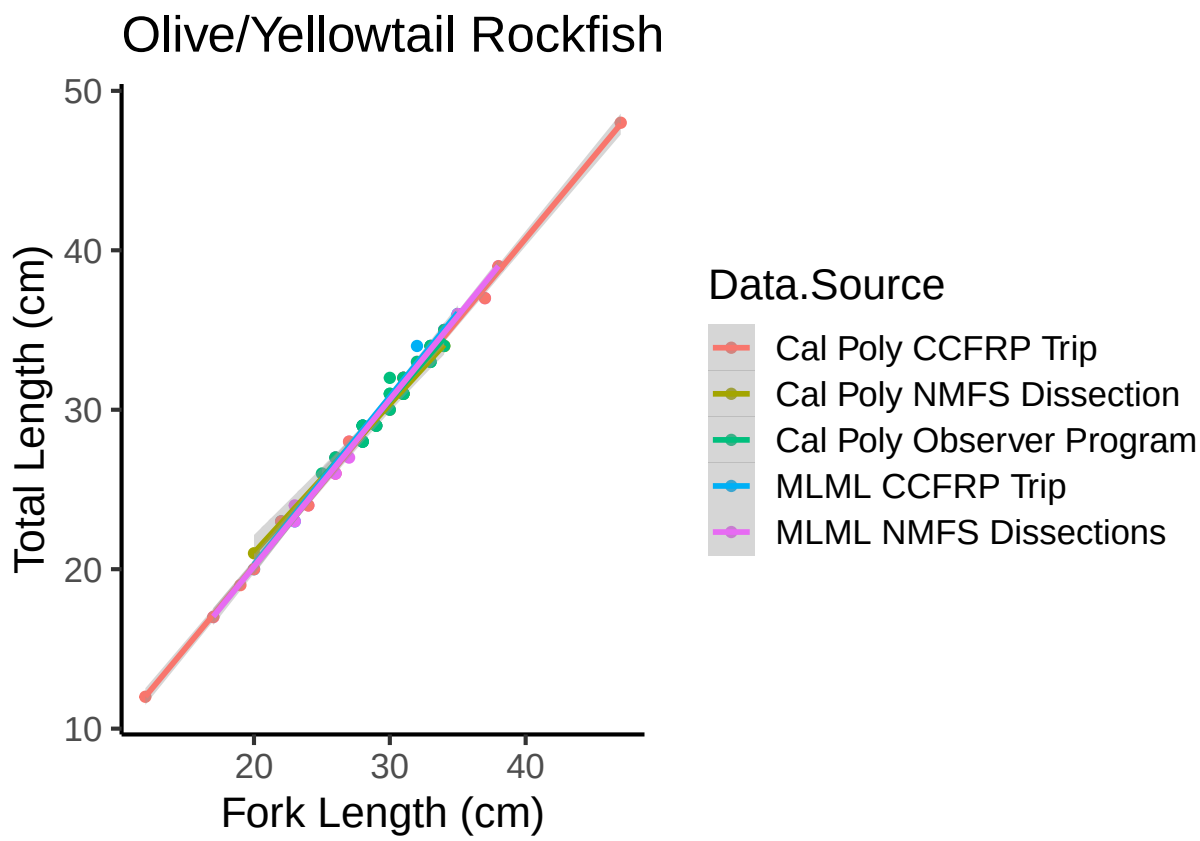
```
olive.yellowtail<-length.data%>%
  group_by(Institution, Species, Data.Source)%>%
  filter(Species == "Olive/Yellowtail Rockfish")

ggplot(olive.yellowtail, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Institution))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Olive/Yellowtail Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



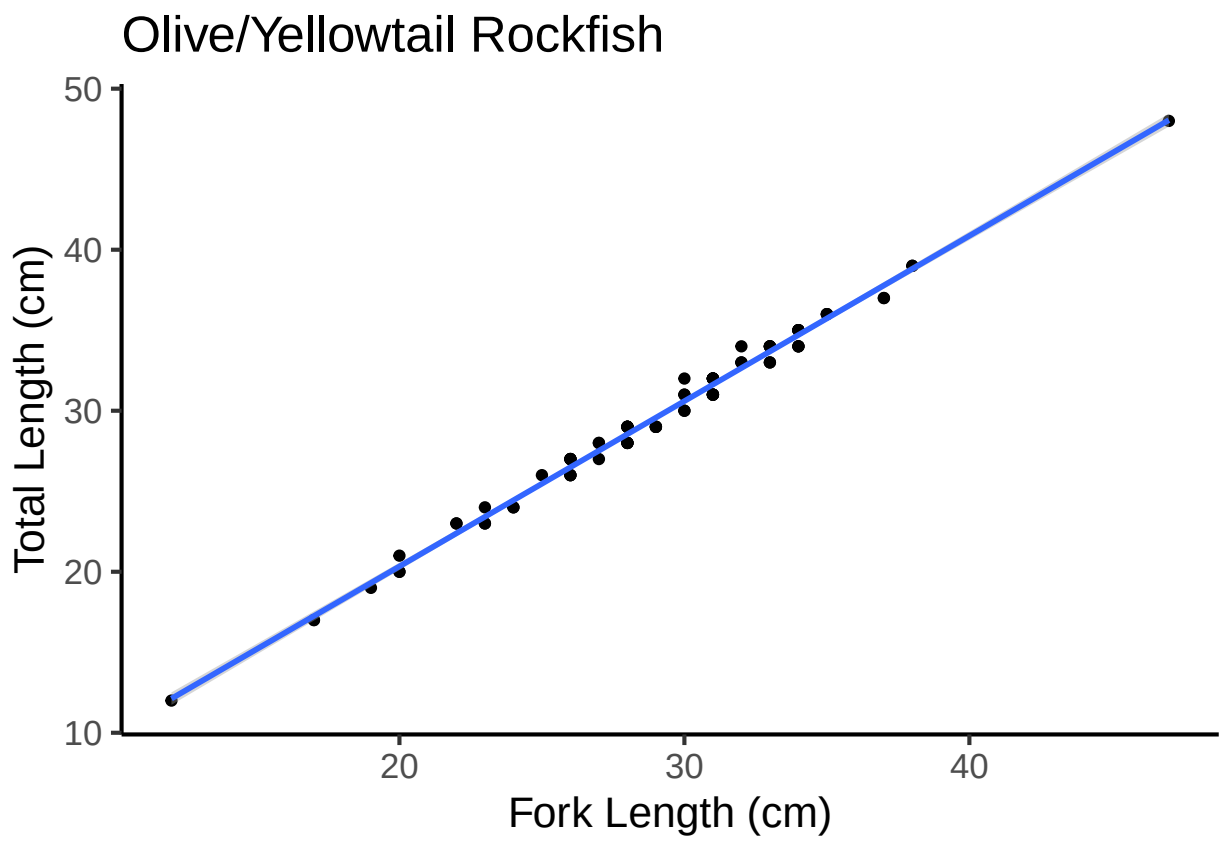

```
ggplot(olive.yellowtail, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Data.Source))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Olive/Yellowtail Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggplot(olive.yellowtail, aes(x=Fork.Length..cm., y=Total.Length..cm.))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Olive/Yellowtail Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

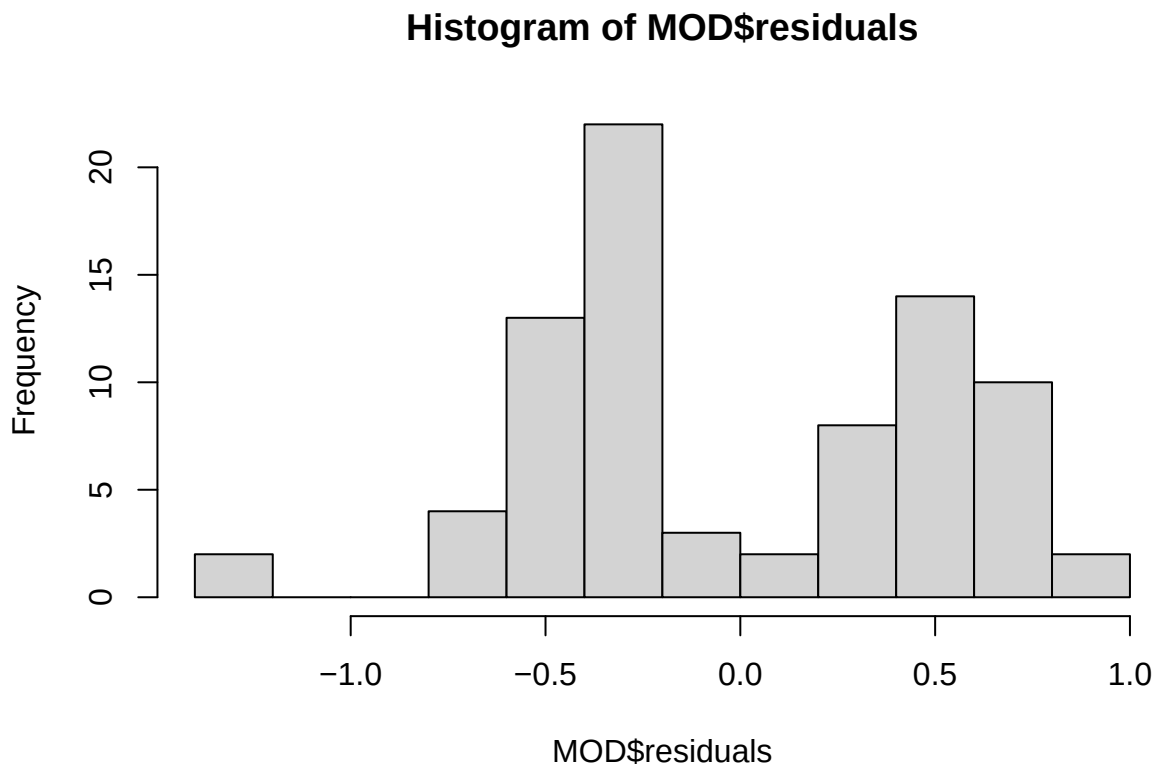
```
## `geom_smooth()` using formula = 'y ~ x'
```




```
MOD <- lm(Fork.Length..cm.~Total.Length..cm., data = olive.yellowtail)
  summary(MOD)
```

```
##
## Call:
## lm(formula = Fork.Length..cm. ~ Total.Length..cm., data = olive.yellowtail)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.3457 -0.3800 -0.2086  0.5171  0.8257
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        0.44289    0.30927   1.432    0.156
## Total.Length..cm.  0.96571    0.01024  94.344   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5138 on 78 degrees of freedom
## Multiple R-squared:  0.9913, Adjusted R-squared:  0.9912
## F-statistic:  8901 on 1 and 78 DF,  p-value: < 2.2e-16
```

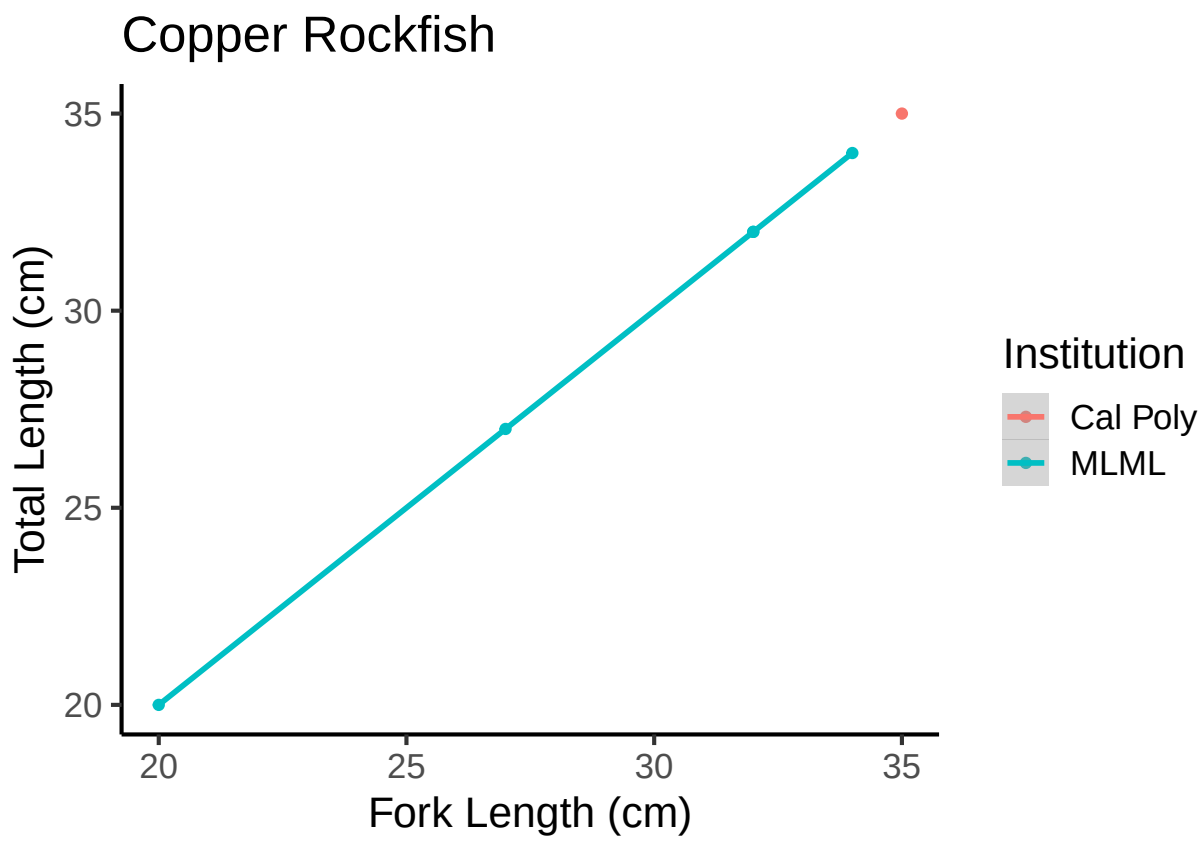
```
  hist(MOD$residuals)
```



Copper Rockfish

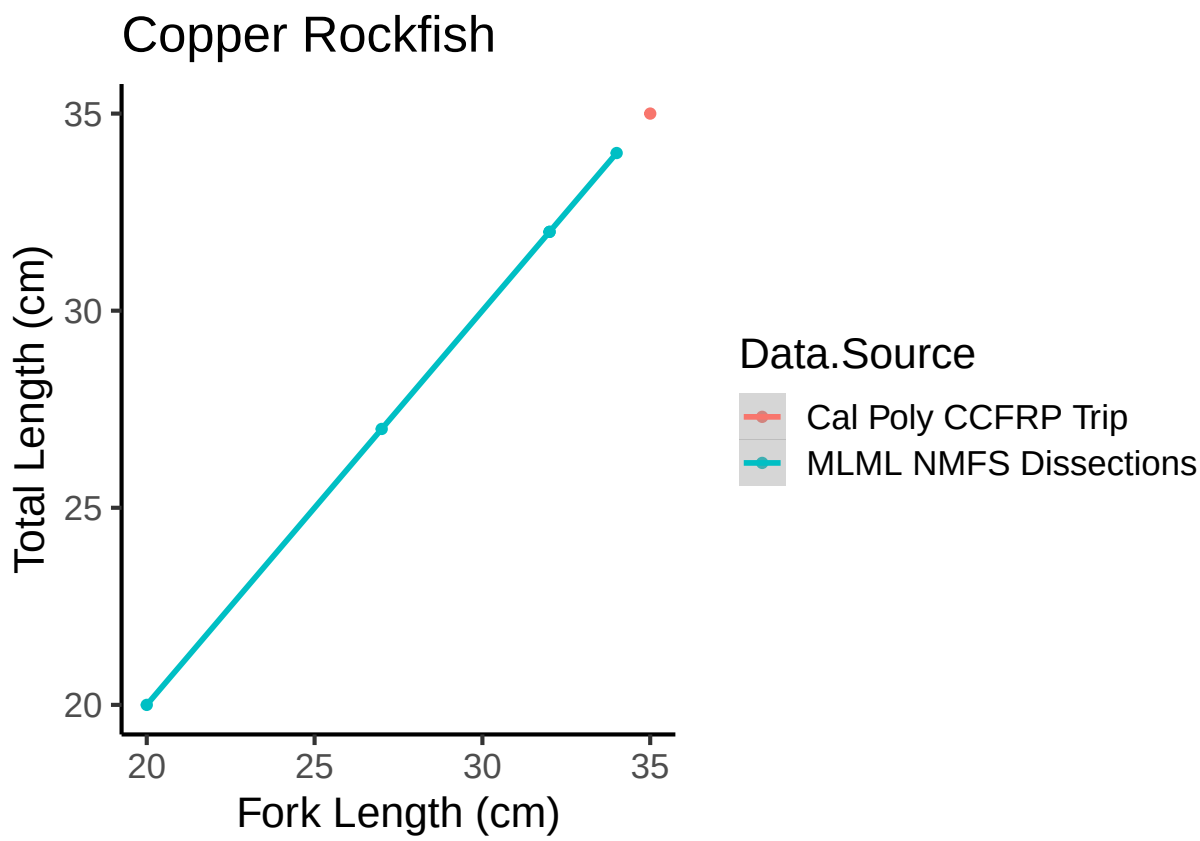
```
copper<-length.data%>%
  group_by(Institution, Species, Data.Source)%>%
  filter(Species == "Copper Rockfish")

ggplot(copper, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Institution))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Copper Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



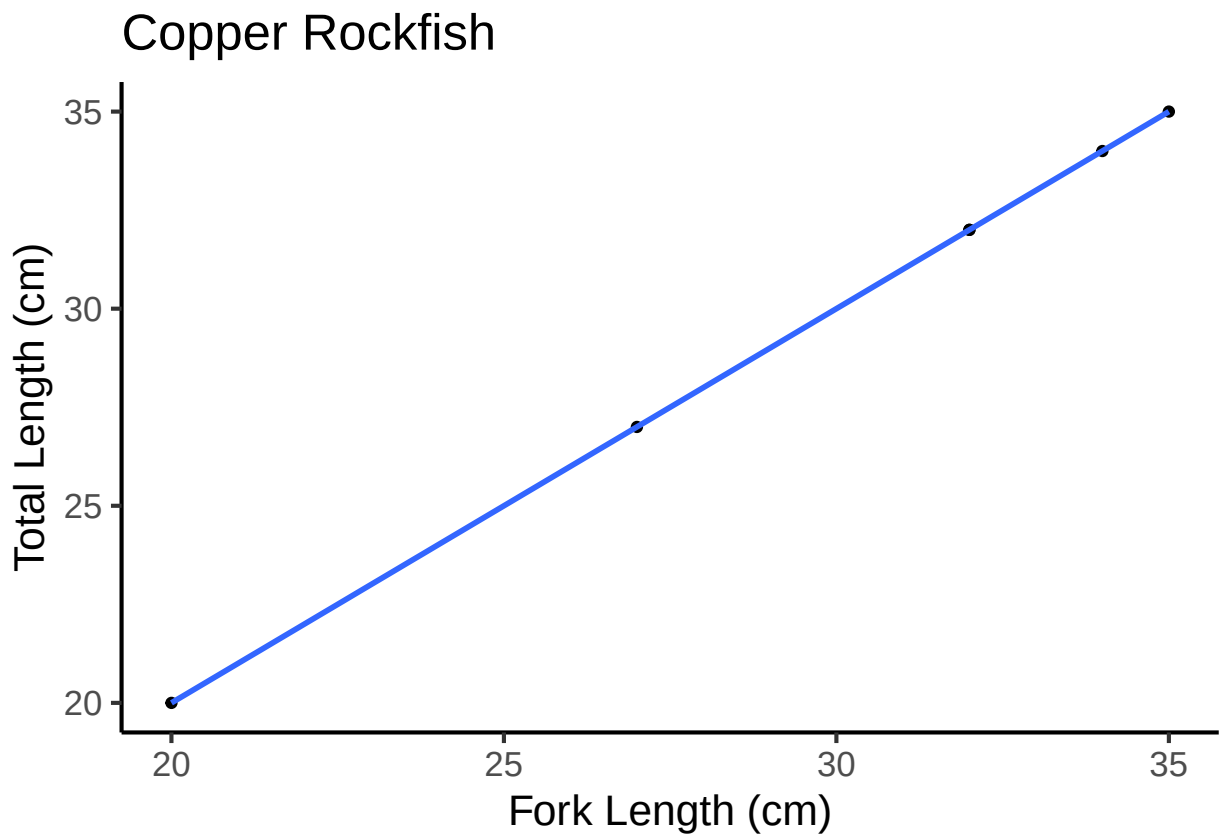

```
ggplot(copper, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Data.Source))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Copper Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggplot(copper, aes(x=Fork.Length..cm., y=Total.Length..cm.))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Copper Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

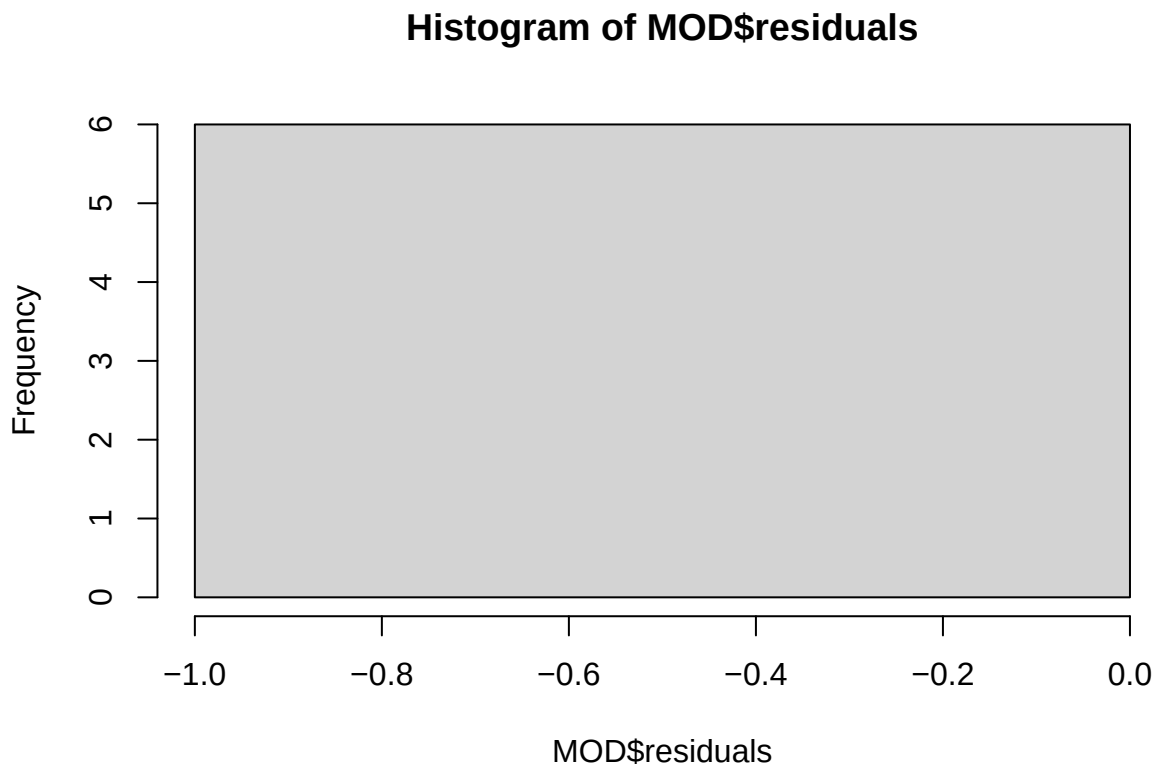
```
## `geom_smooth()` using formula = 'y ~ x'
```




```
MOD <- lm(Fork.Length..cm.~Total.Length..cm., data = copper)
  summary(MOD)
```

```
## Warning in summary.lm(MOD): essentially perfect fit: summary may be unreliable

##
## Call:
## lm(formula = Fork.Length..cm. ~ Total.Length..cm., data = copper)
##
## Residuals:
## 1 2 3 4 5 6
## 0 0 0 0 0 0
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)              0          0     NaN      NaN
## Total.Length..cm.        1          0     Inf   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0 on 4 degrees of freedom
## Multiple R-squared:      1,  Adjusted R-squared:      1
## F-statistic:   Inf on 1 and 4 DF,  p-value: < 2.2e-16
```

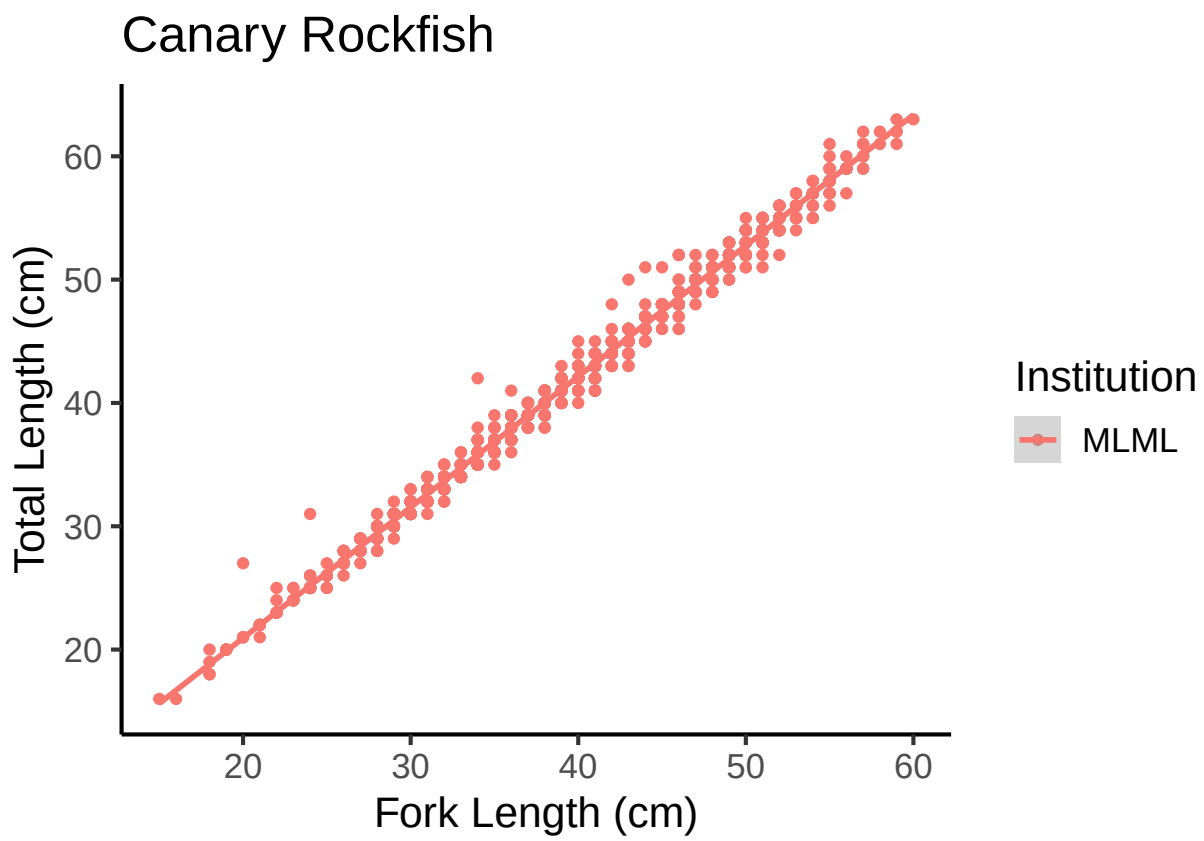
```
  hist(MOD$residuals)
```



Canary Rockfish

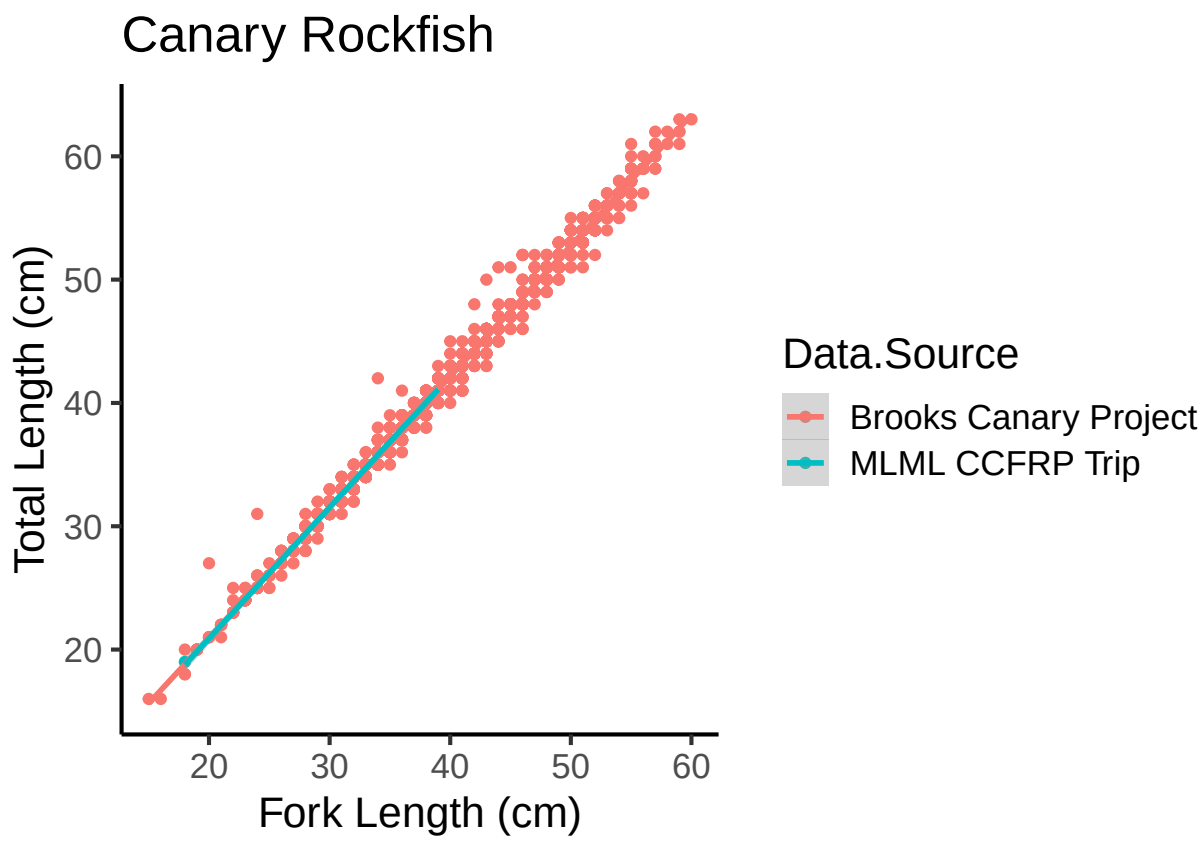
```
canary<-length.data%>%
  group_by(Institution, Species, Data.Source)%>%
  filter(Species == "Canary Rockfish")

ggplot(canary, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Institution))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Canary Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



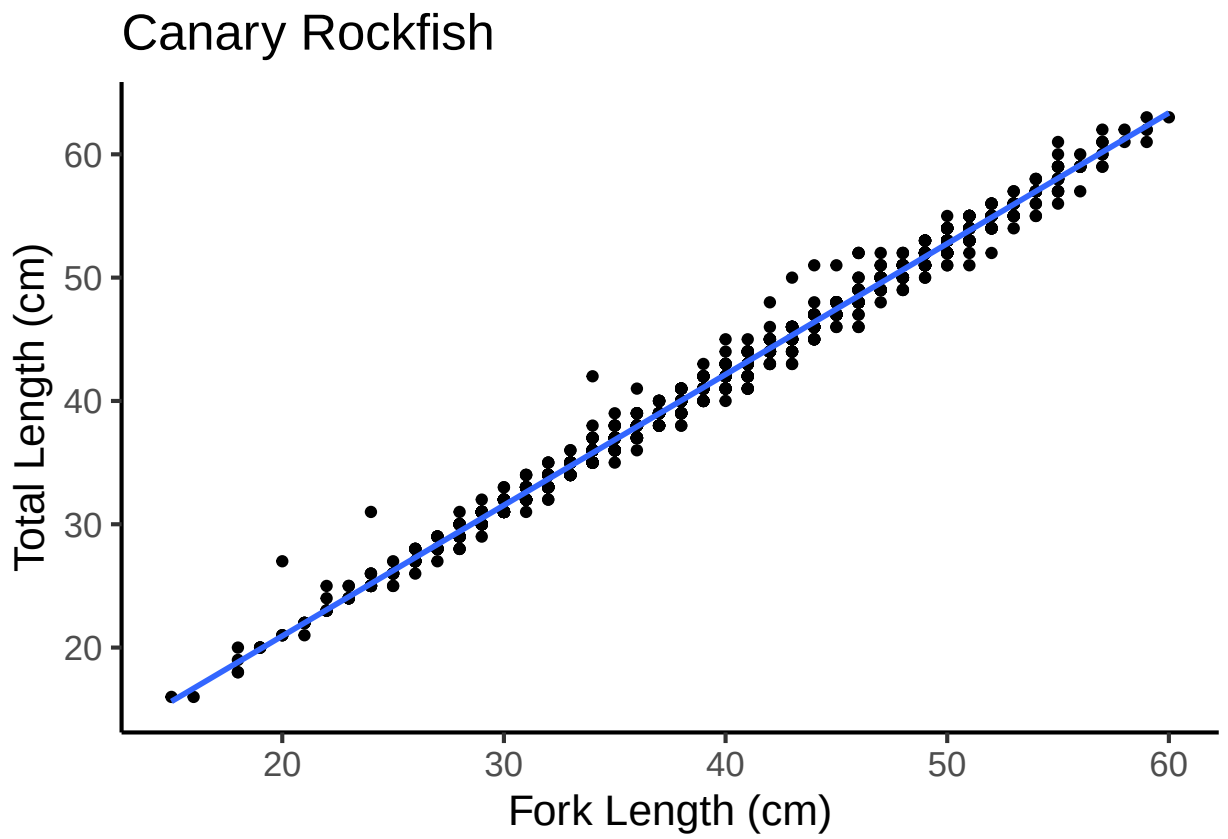

```
ggplot(canary, aes(x=Fork.Length..cm., y=Total.Length..cm., col=Data.Source))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Canary Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggplot(canary, aes(x=Fork.Length..cm., y=Total.Length..cm.))+
  geom_point()+
  geom_smooth(method = "lm")+
  ggtitle("Canary Rockfish") +
  xlab("Fork Length (cm)") + ylab("Total Length (cm)")
```

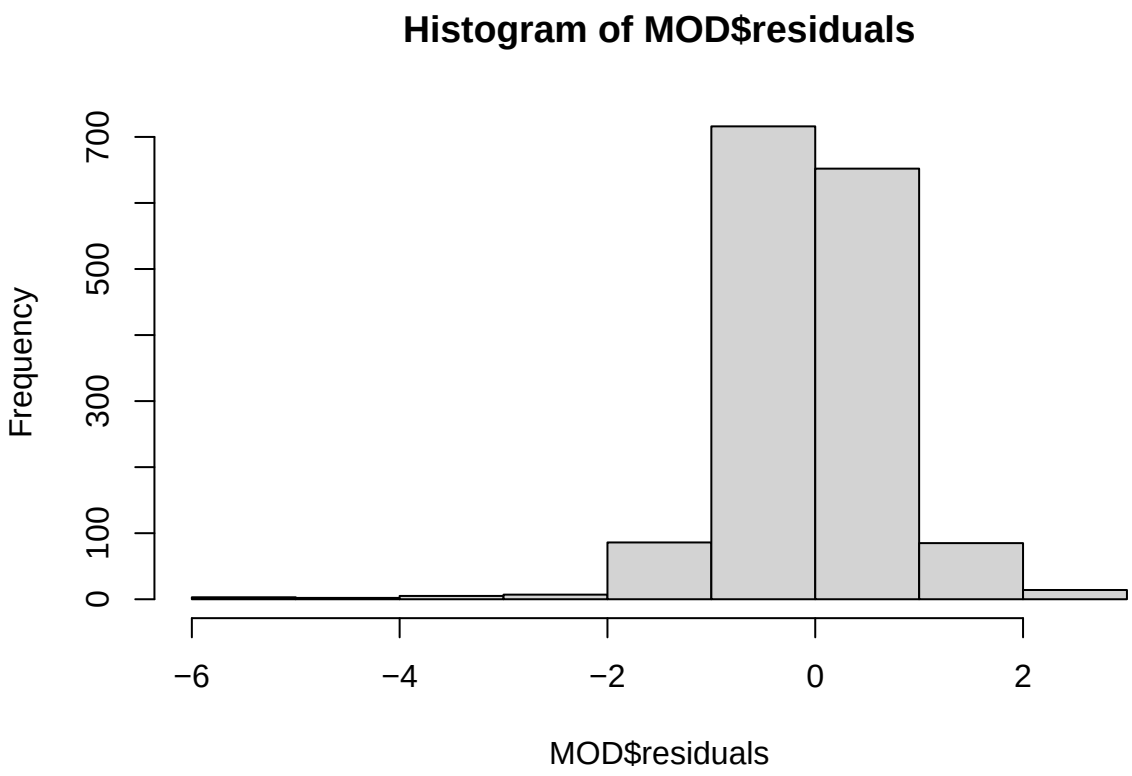
```
## `geom_smooth()` using formula = 'y ~ x'
```




```
MOD <- lm(Fork.Length..cm.~Total.Length..cm., data = canary)
  summary(MOD)
```

```
##
## Call:
## lm(formula = Fork.Length..cm. ~ Total.Length..cm., data = canary)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.8555 -0.3691 -0.0208  0.4383  2.7866
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.552121   0.086977   6.348 2.85e-10 ***
## Total.Length..cm. 0.935794   0.002048 456.853  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7459 on 1568 degrees of freedom
## Multiple R-squared:  0.9925, Adjusted R-squared:  0.9925
## F-statistic: 2.087e+05 on 1 and 1568 DF,  p-value: < 2.2e-16
```

```
  hist(MOD$residuals)
```


Histogram of MOD$residuals
Frequency
0
100
300
500
700
−6
−4
−2
0
2
MOD$residuals