

# Lecture 20 - Regression: Inference, Outliers, ~~and Intervals~~

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Sta102 / BME102

April 13, 2016

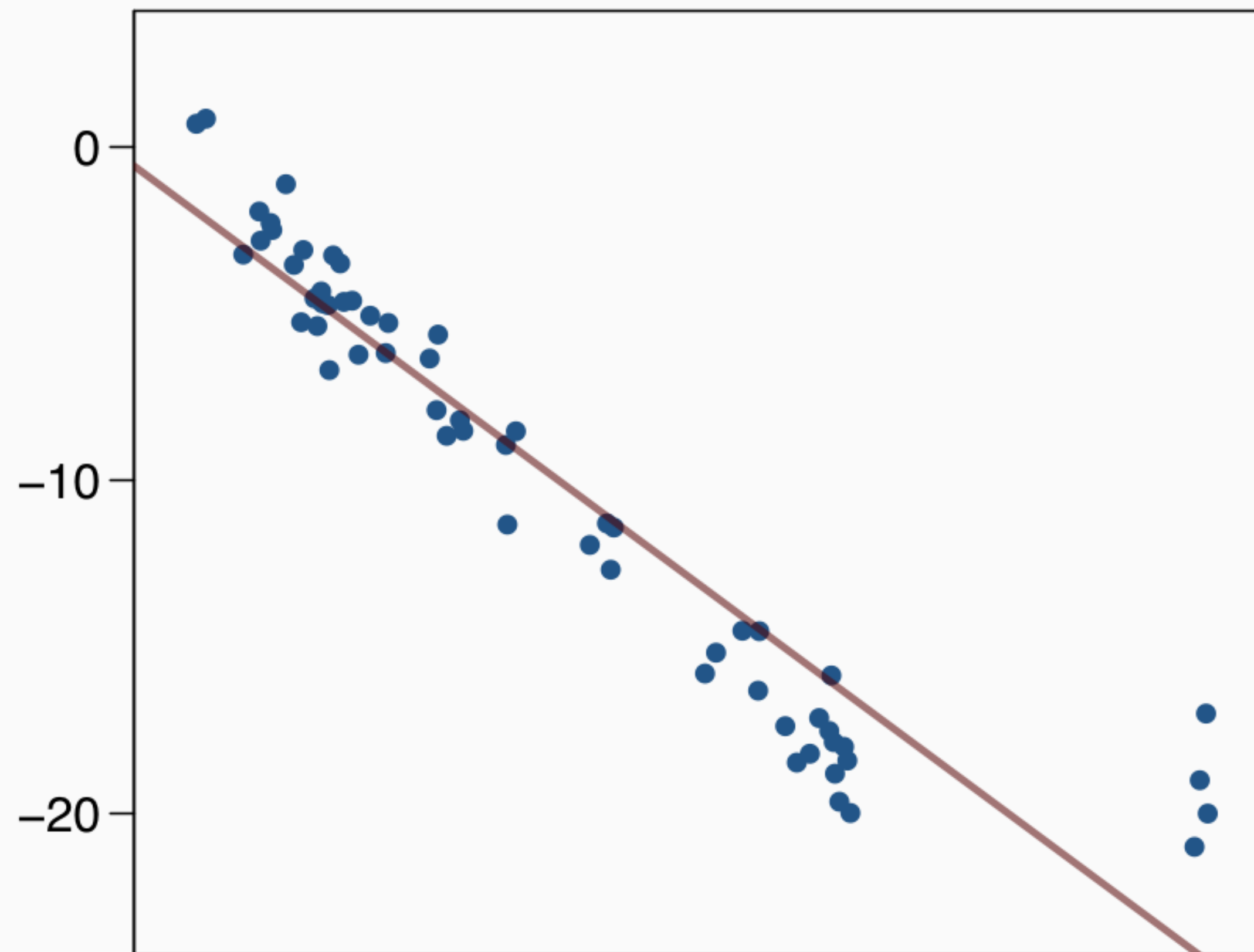
Colin Rundel

# Types of outliers in linear regression

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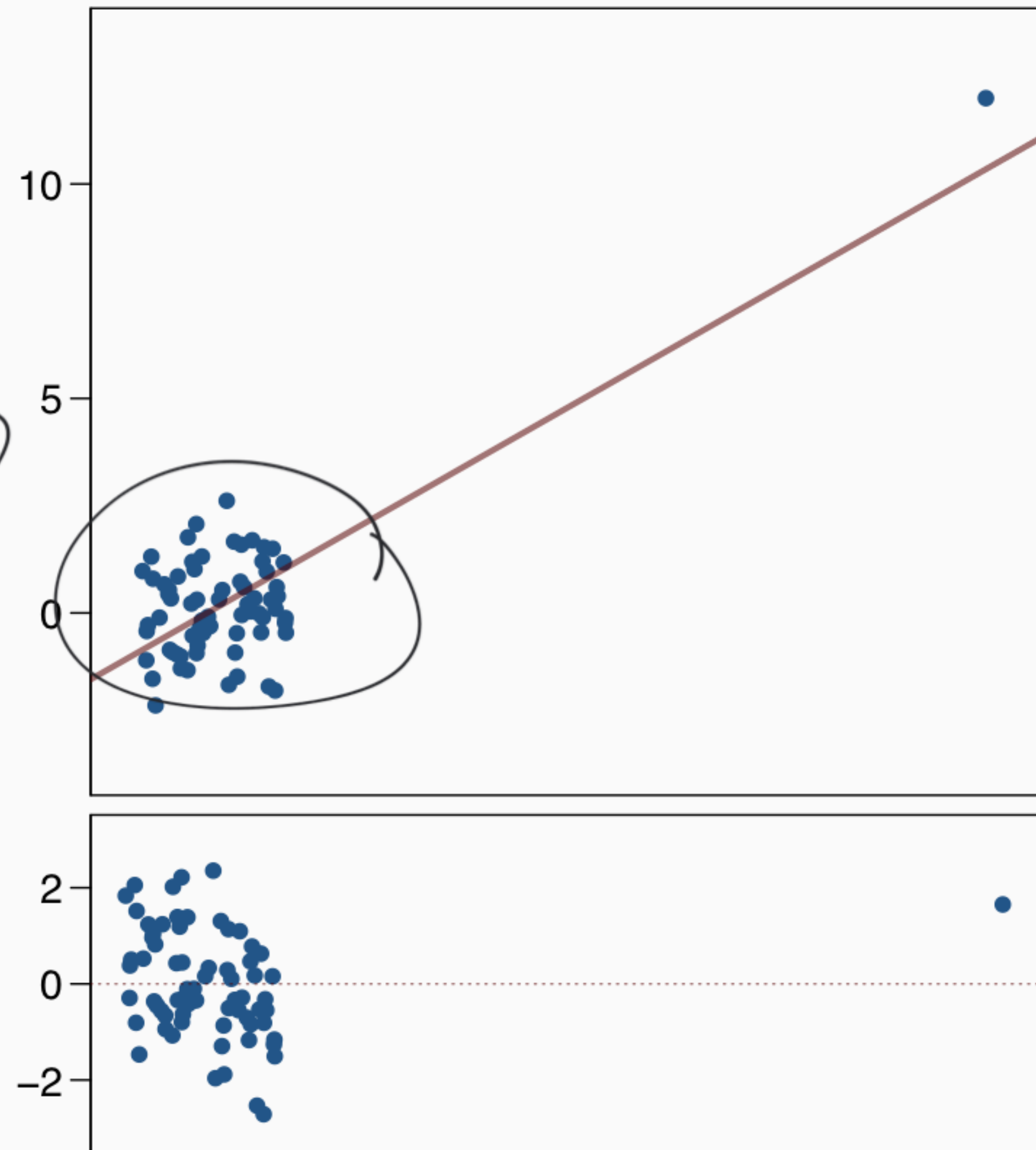
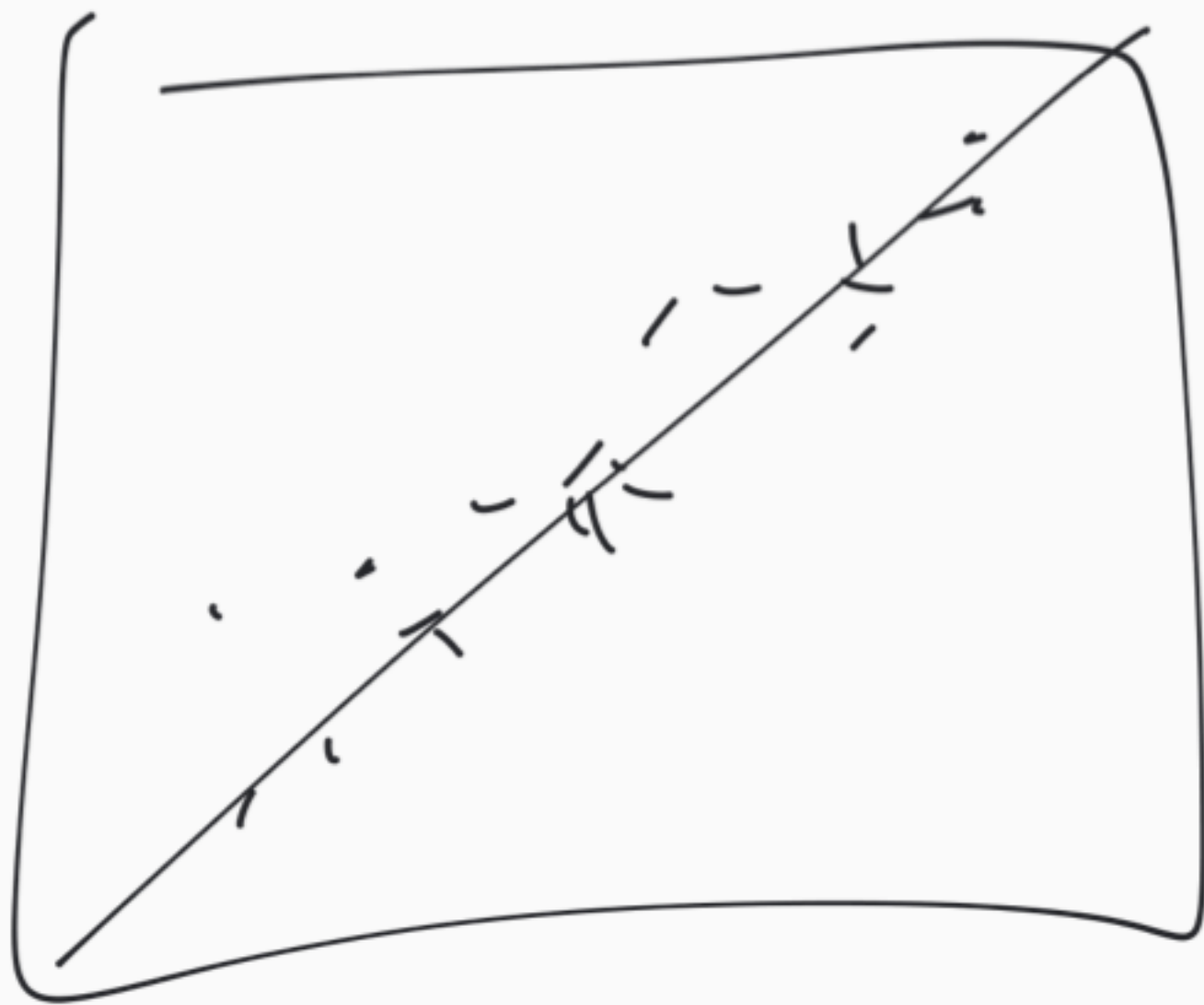
# Types of outliers

Is regression robust? Think about how the regression line would change with and without “outlier(s)”.



# Types of outliers

How does the following point influence the least squares line?

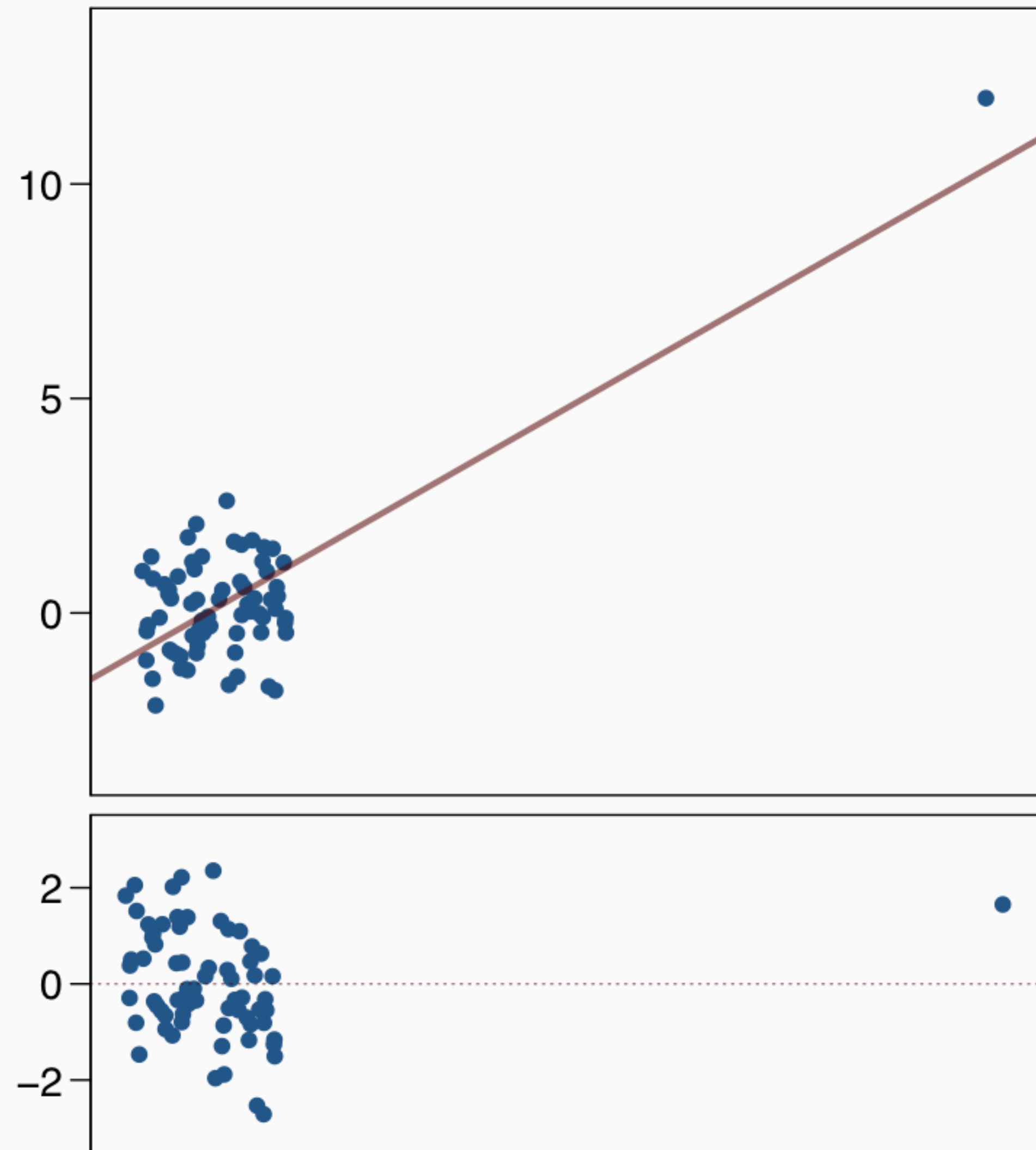




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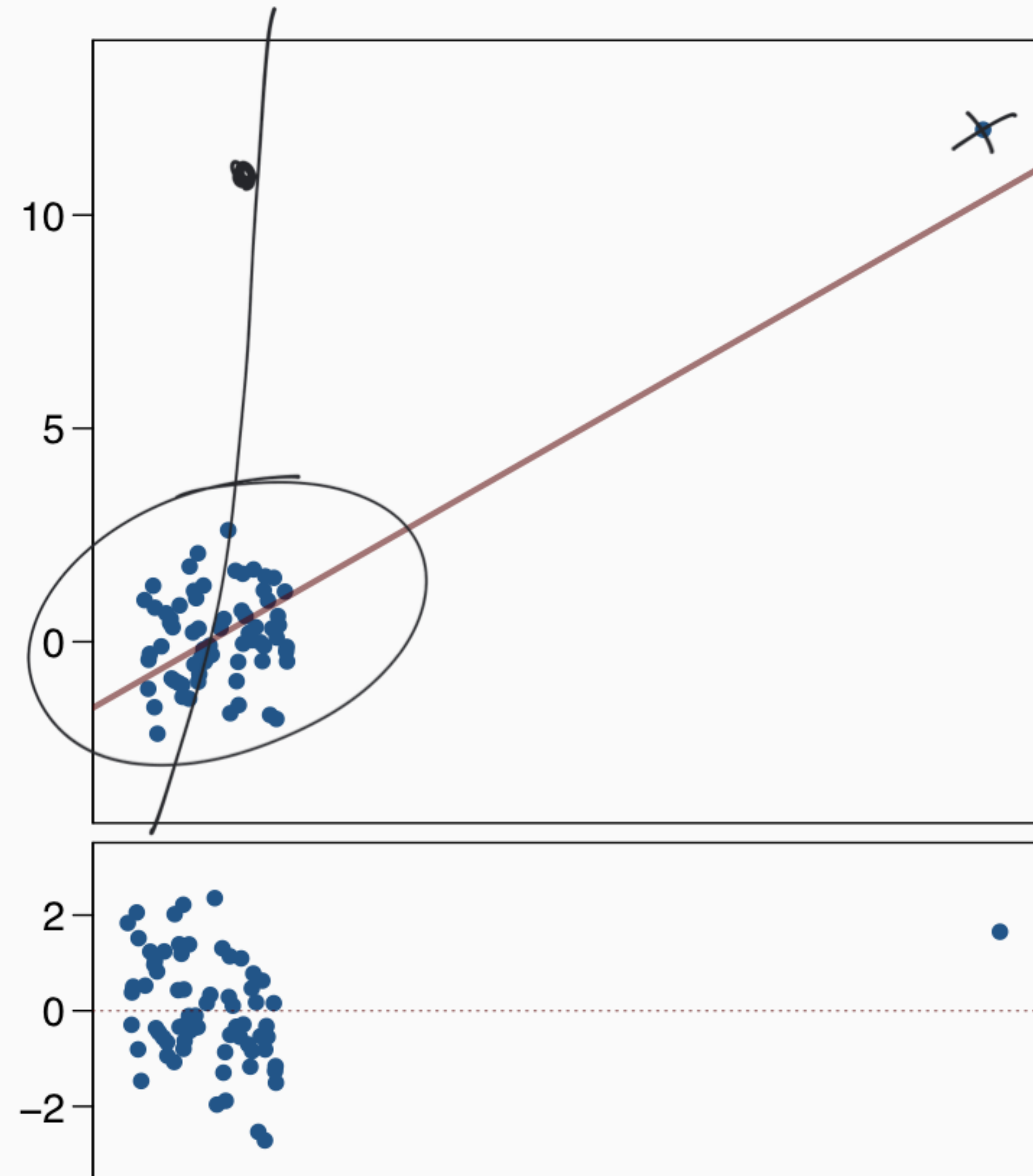
Without the outlier there is *no* relationship between  $X$  and  $Y$  ( $\text{Cor}(X, Y) = 0$ ).



# Types of outliers

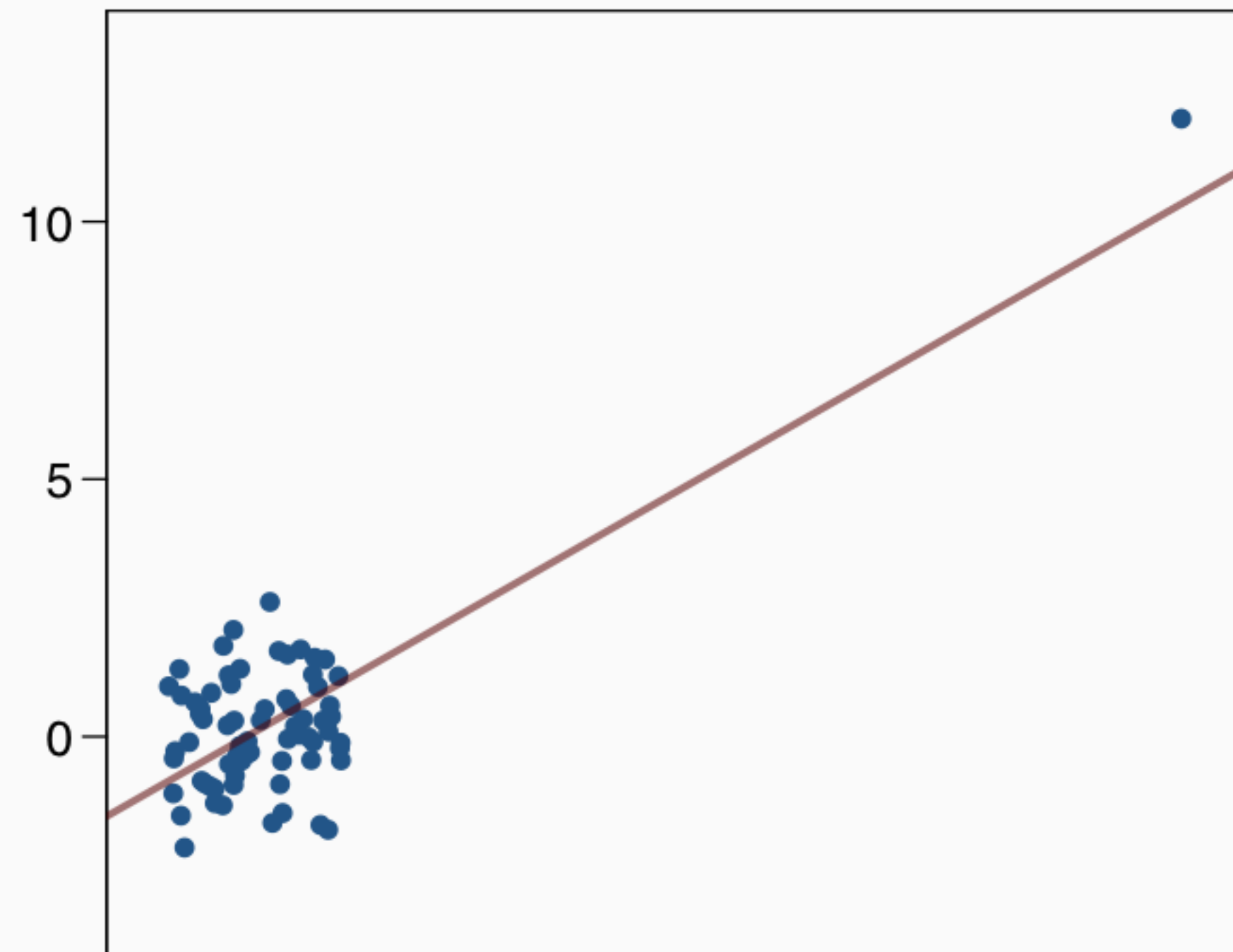
How does the following point influence the least squares line?

What would have happened if the outlier was directly above the other points?



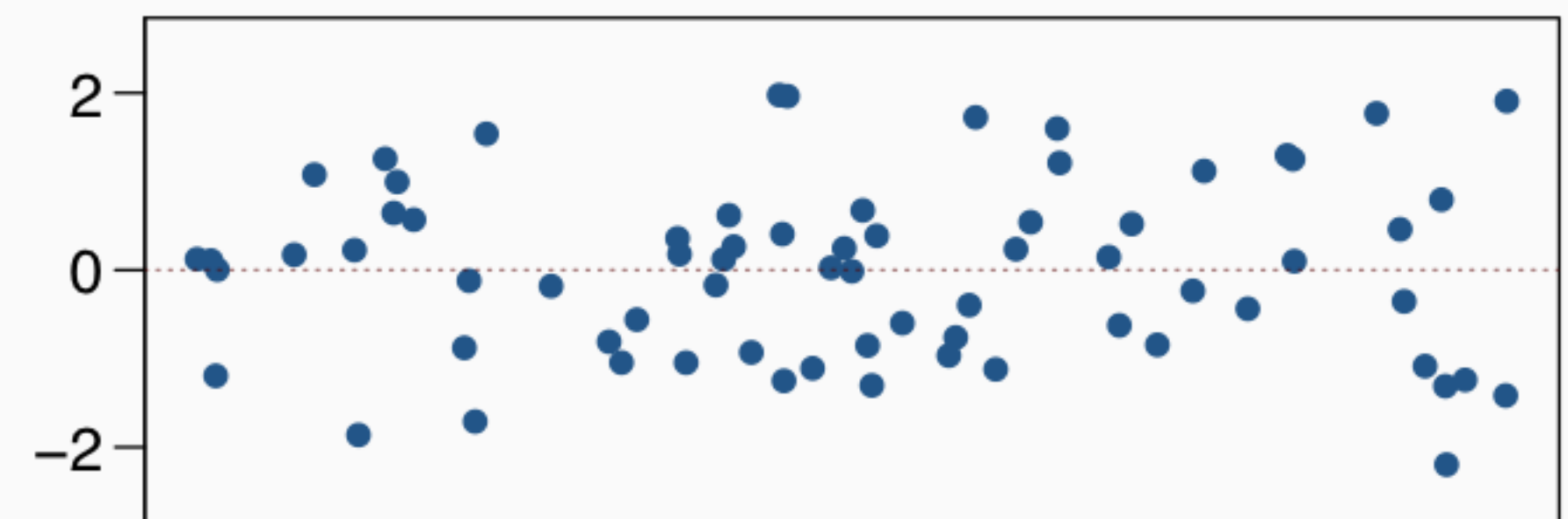
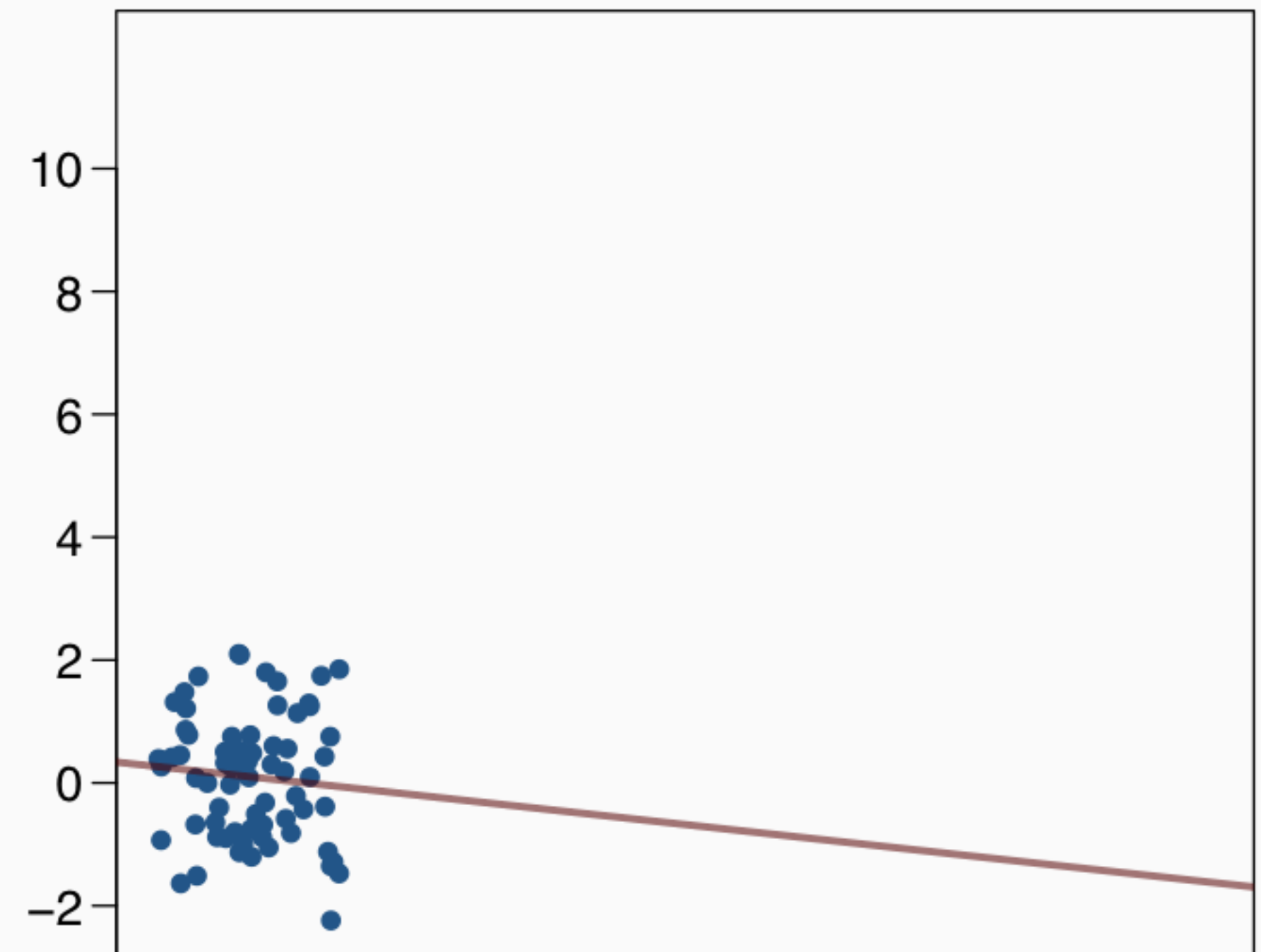
# With and without

$$R = 0.72, R^2 = 0.522$$



x

$$R = -0.091, R^2 = 0.0083$$



## Some terminology

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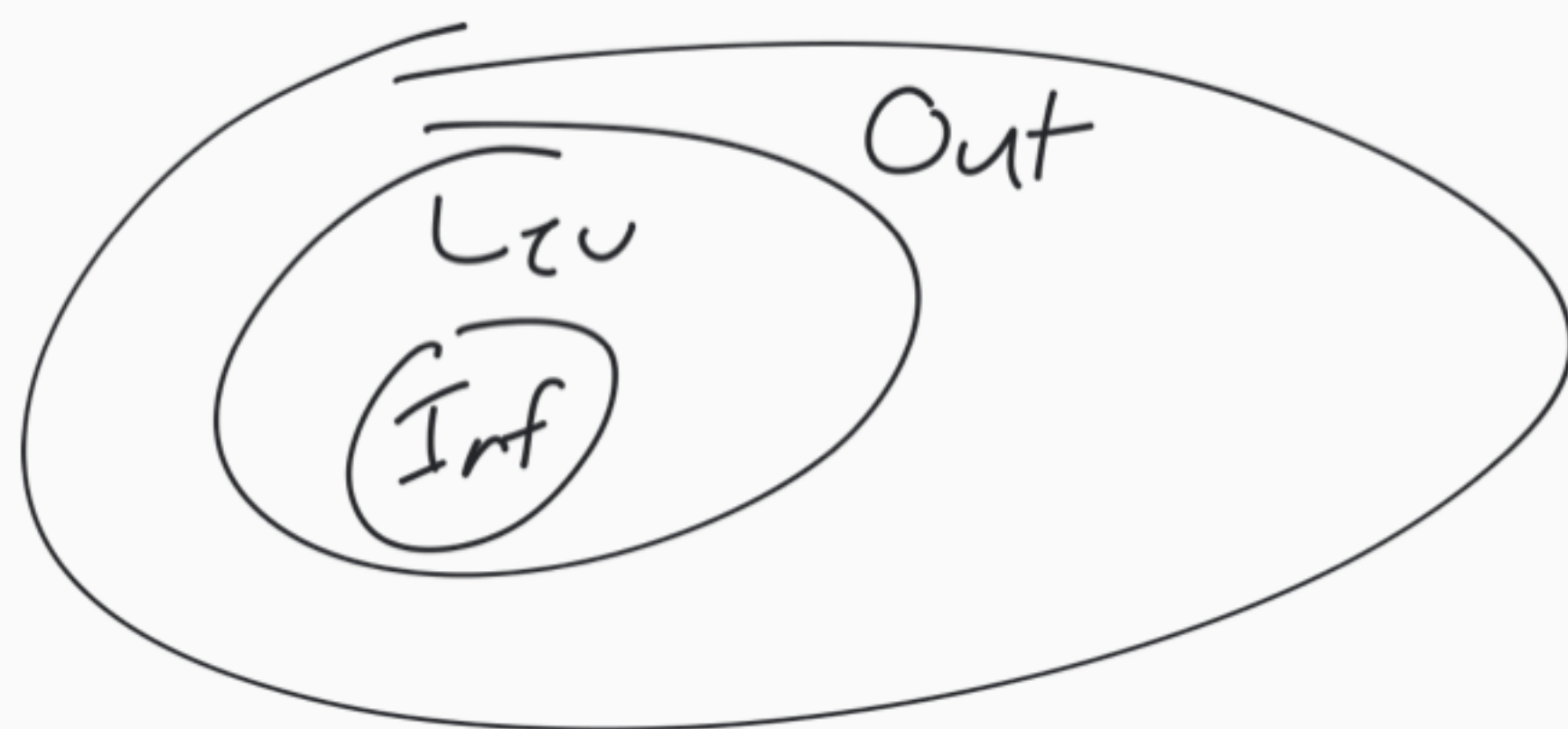
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- Outliers that are horizontally distant from the body of other points are called *leverage* points.
- Points with high leverage that actually influence the *slope* of the regression line are called *influential* points.



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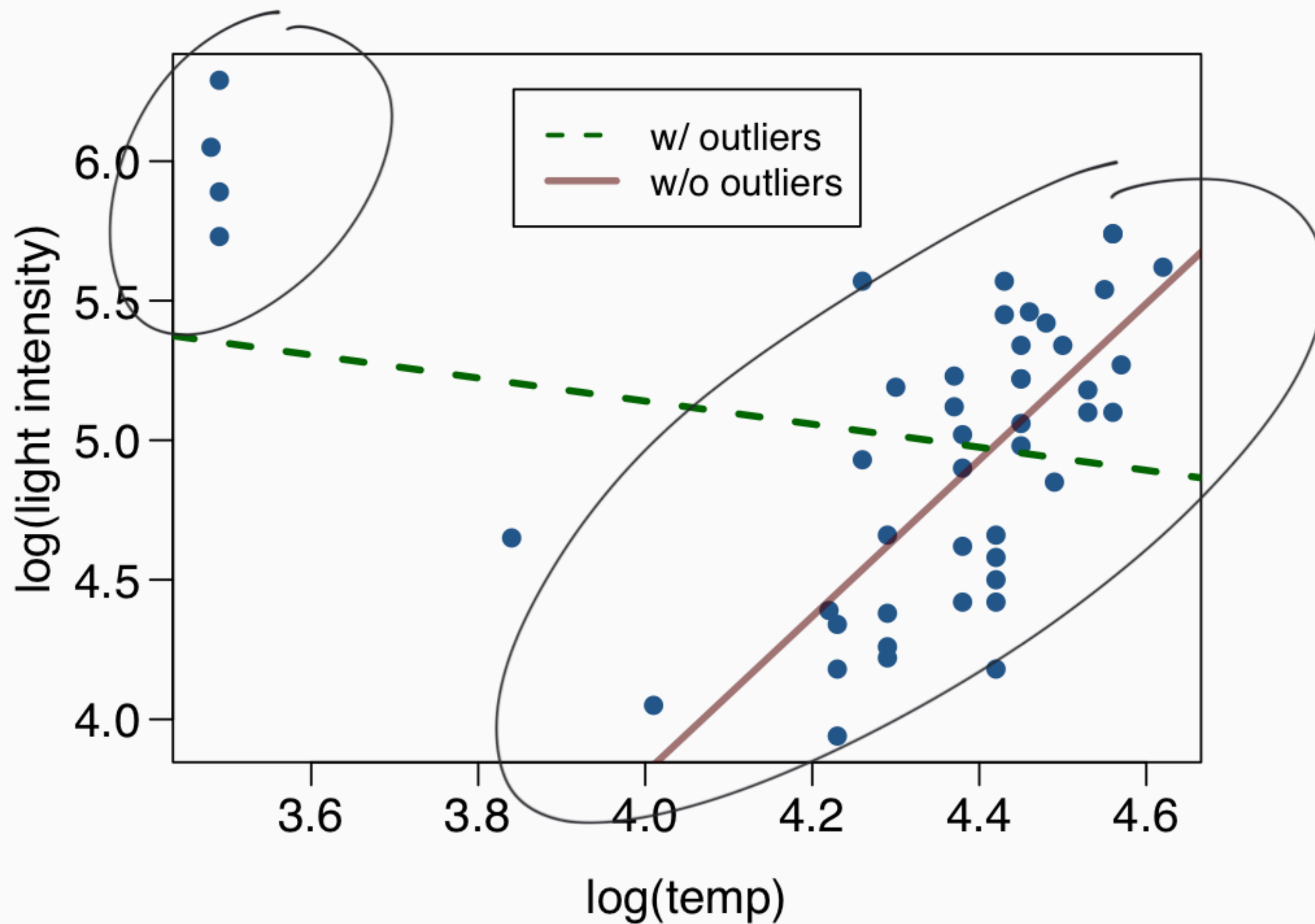
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- Outliers that are horizontally distant from the body of other points are called *leverage* points.
- Points with high leverage that actually influence the *slope* of the regression line are called *influential* points.
- In order to determine if a point is influential, visualize the regression line with and without the point. Does the slope of the line change considerably? If so, then the point is influential.



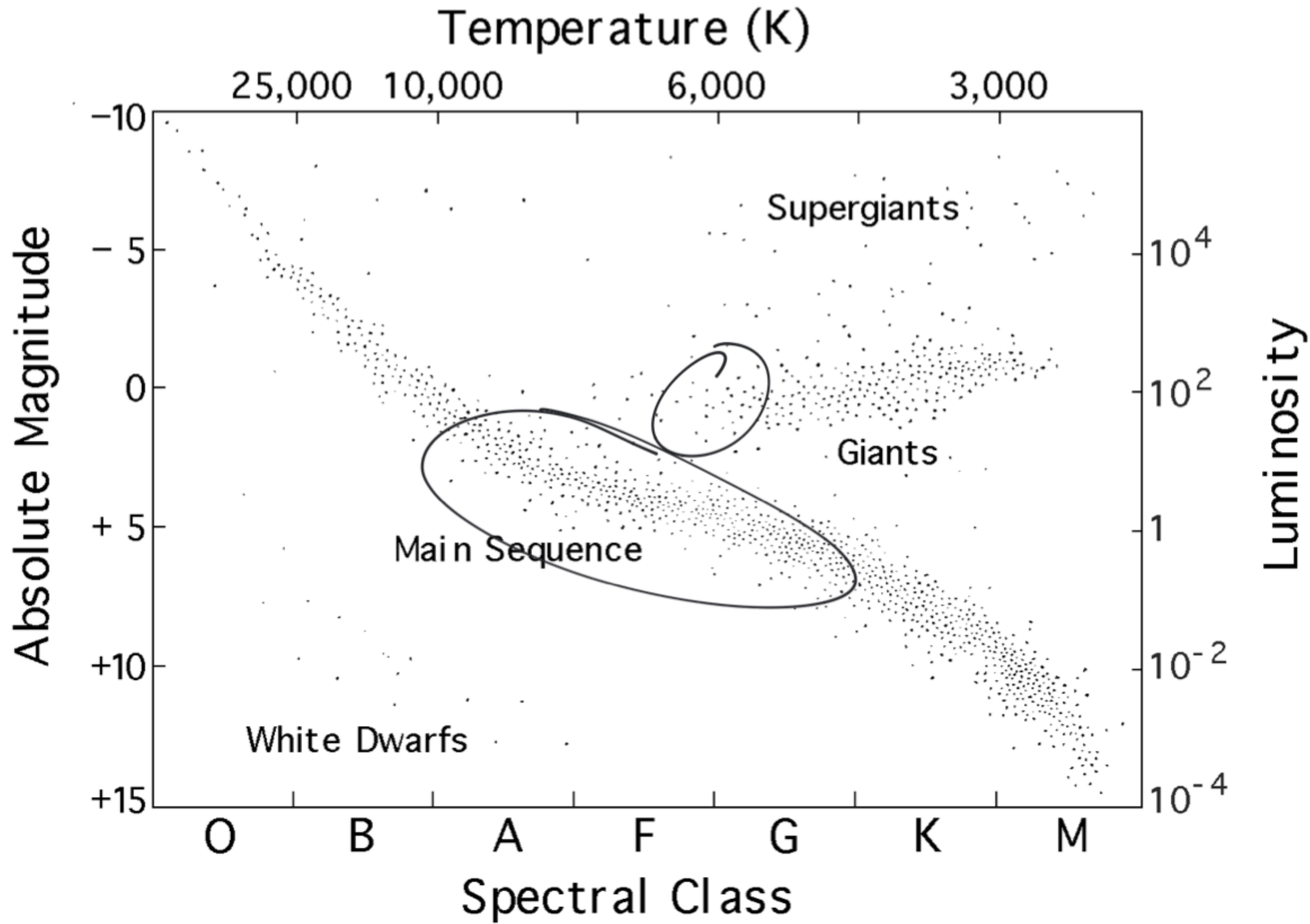
# Influential points

Data are available on the log of the surface temperature and the log of the light intensity of 47 stars in the star cluster CYG OB1.





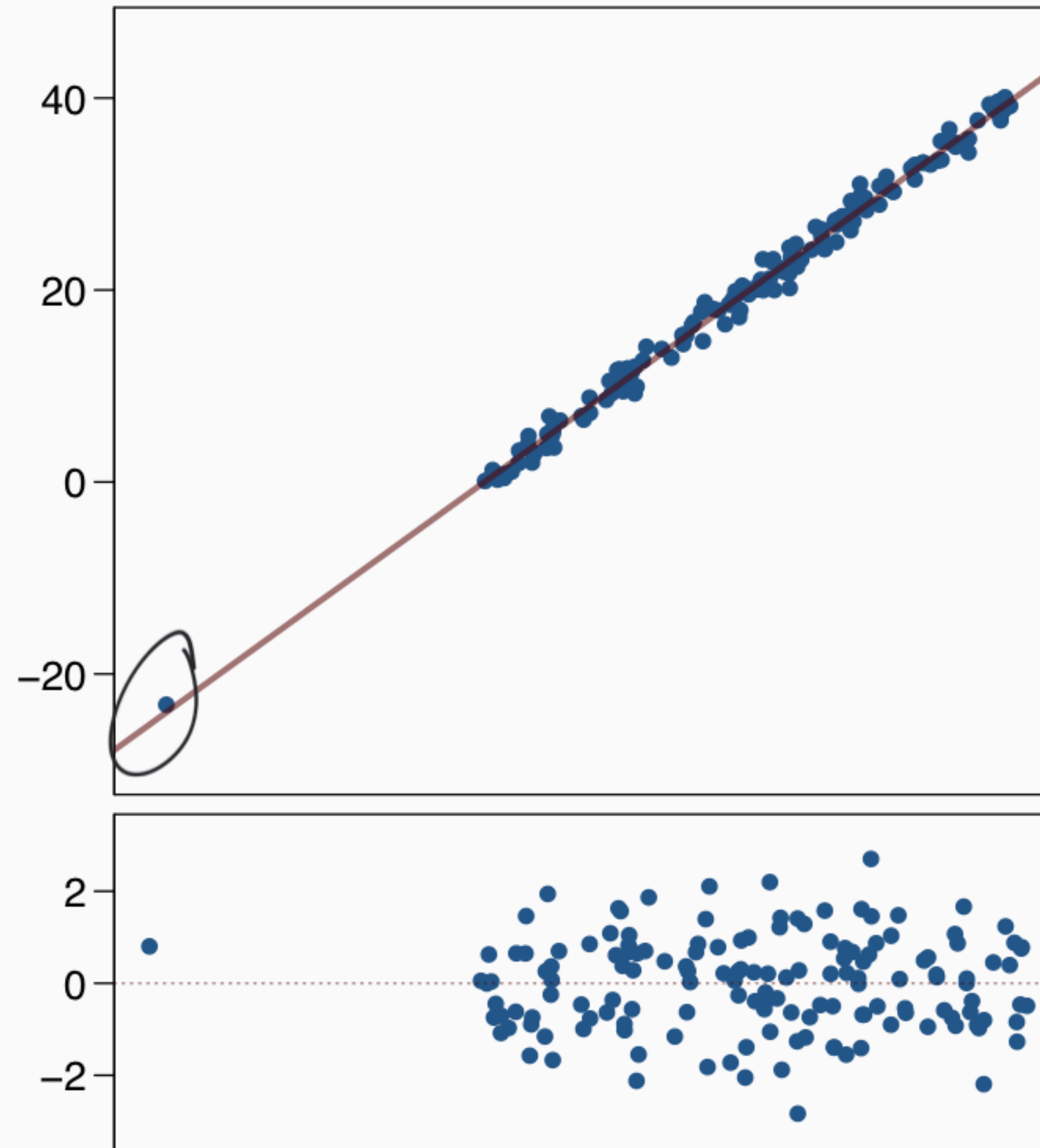
# Hertzsprung-Russell Diagram



# Types of outliers

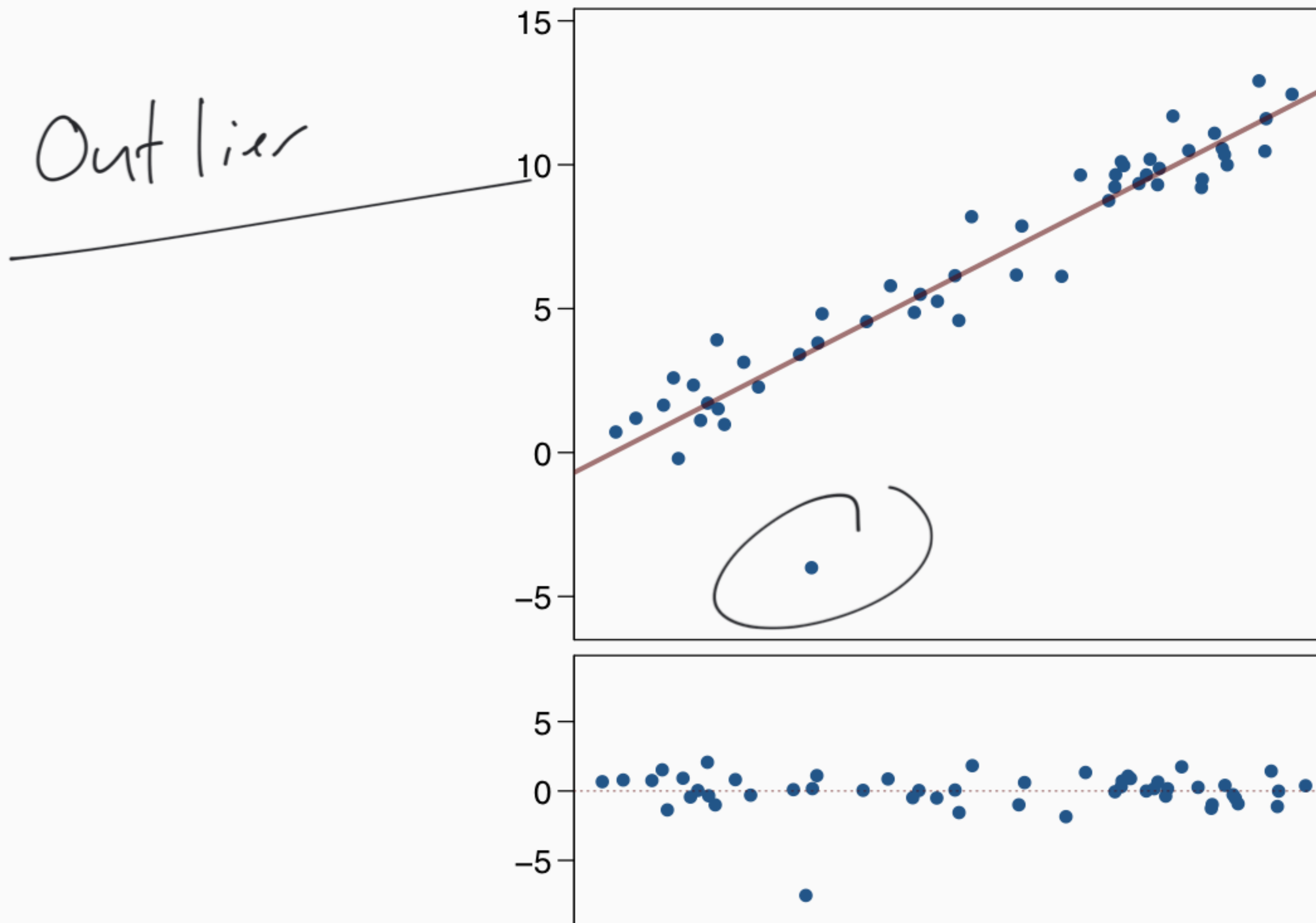
Which type of outlier is displayed below?

Leverage  
pt



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Which type of outlier is displayed below?



# Recap

Are following statements true or false?

- (1) Influential points always change the intercept of the regression line.
- (2) Influential points always reduce  $R^2$ .
- (3) It is much more likely for a high leverage point to be influential, than a low leverage point.
- (4) When the data set includes an influential point, the relationship between the explanatory variable and the response variable is always nonlinear.



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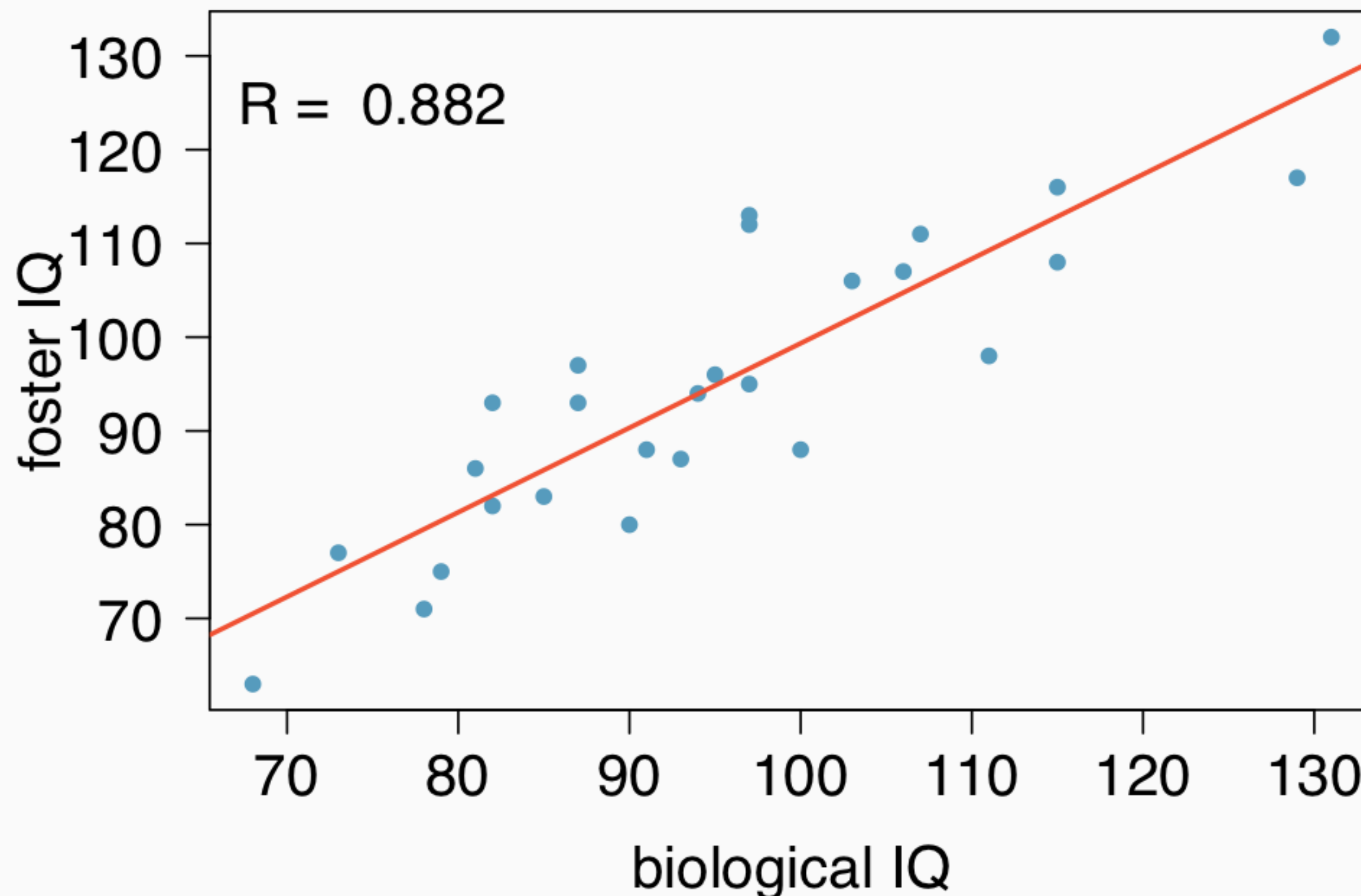


# Inference for linear regression

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# Nature vs. nurture?

In 1966 Cyril Burt published a paper called “The genetic determination of differences in intelligence: A study of monozygotic twins reared apart” The data consist of IQ scores for [an assumed random sample of] 27 identical twins, one raised by foster parents, the other by the biological parents.



# Finding the regression line

	Foster IQ (y)	Biological IQ (x)
mean	$\bar{y} = 95.11$	$\bar{x} = 95.30$
sd	$s_y = 16.08$	$s_x = 15.73$
correlation	$R = 0.8819$	

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$$b_1 = \frac{s_y}{s_x} R = \frac{16.08}{15.73} 0.8819 = 0.90$$

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$$b_0 = \bar{y} - b_1 \bar{x} = 95.11 - 0.90 \cdot 95.30 = 9.2$$



# Regression Output

```
summary(lm(twins$Foster ~ twins$Biological))

## Call:
## lm(formula = twins$Foster ~ twins$Biological)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.3512  -5.7311   0.0574   4.3244  16.3531
##
## Coefficients:
##              Estimate Std. Error t value Pr(> |t|)
## (Intercept)    9.20760    9.29990   0.990   0.332
## twins$Biological  0.90144    0.09633   9.3582 1.2e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.729 on 25 degrees of freedom
## Multiple R-squared: 0.7779, Adjusted R-squared: 0.769
## F-statistic: 87.56 on 1 and 25 DF, p-value: 1.204e-09
```

# Conditions for inference

In order to conduct *inference*, the following conditions must be met:

1. Linearity
2. Nearly normal residuals
3. Constant variability

## Conditions: (1) Linearity

- The relationship between the explanatory and the response variable should be linear.

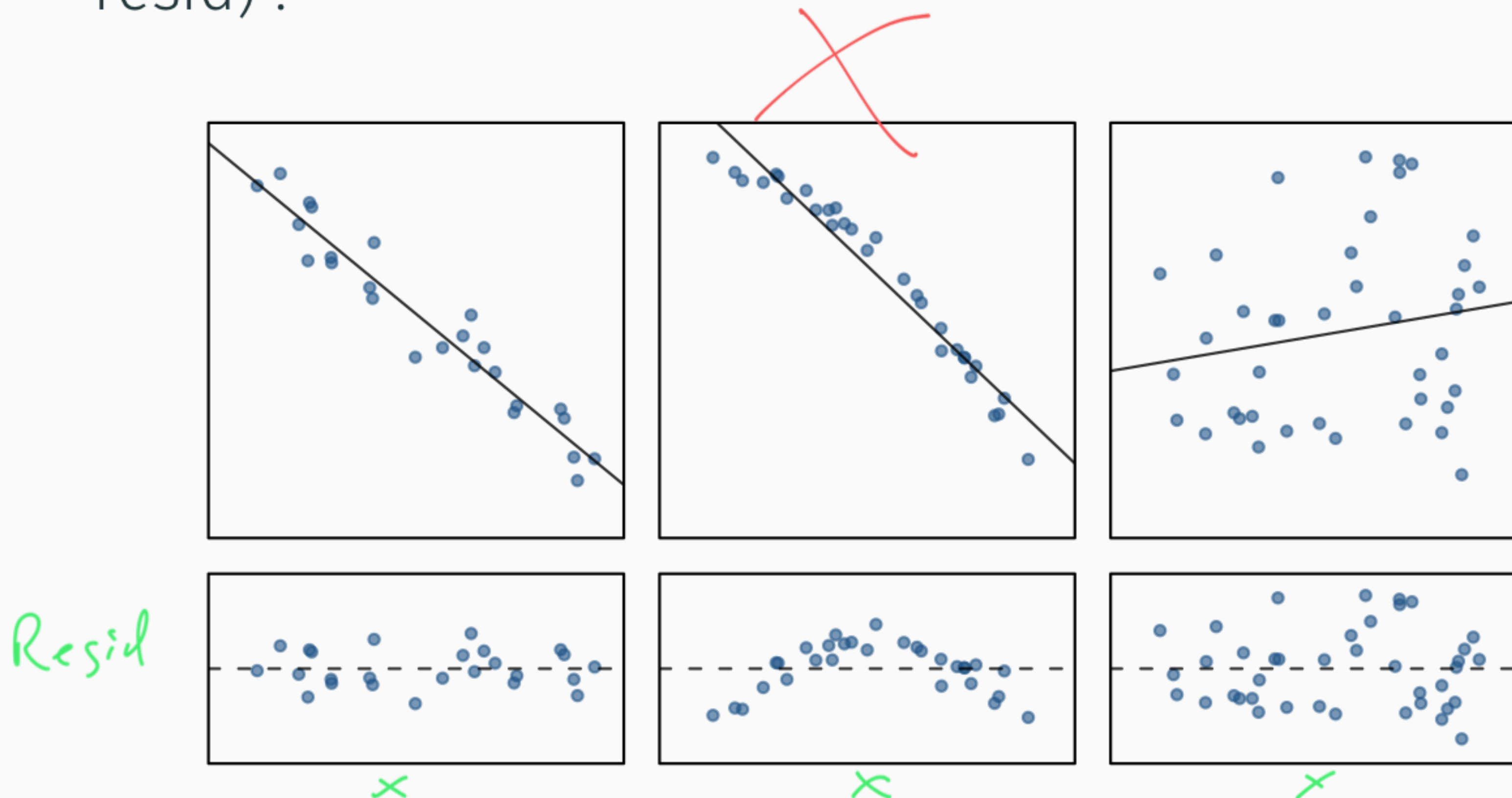


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- Check using a *scatterplot* (x vs y) or a *residual plot* (x vs resid).



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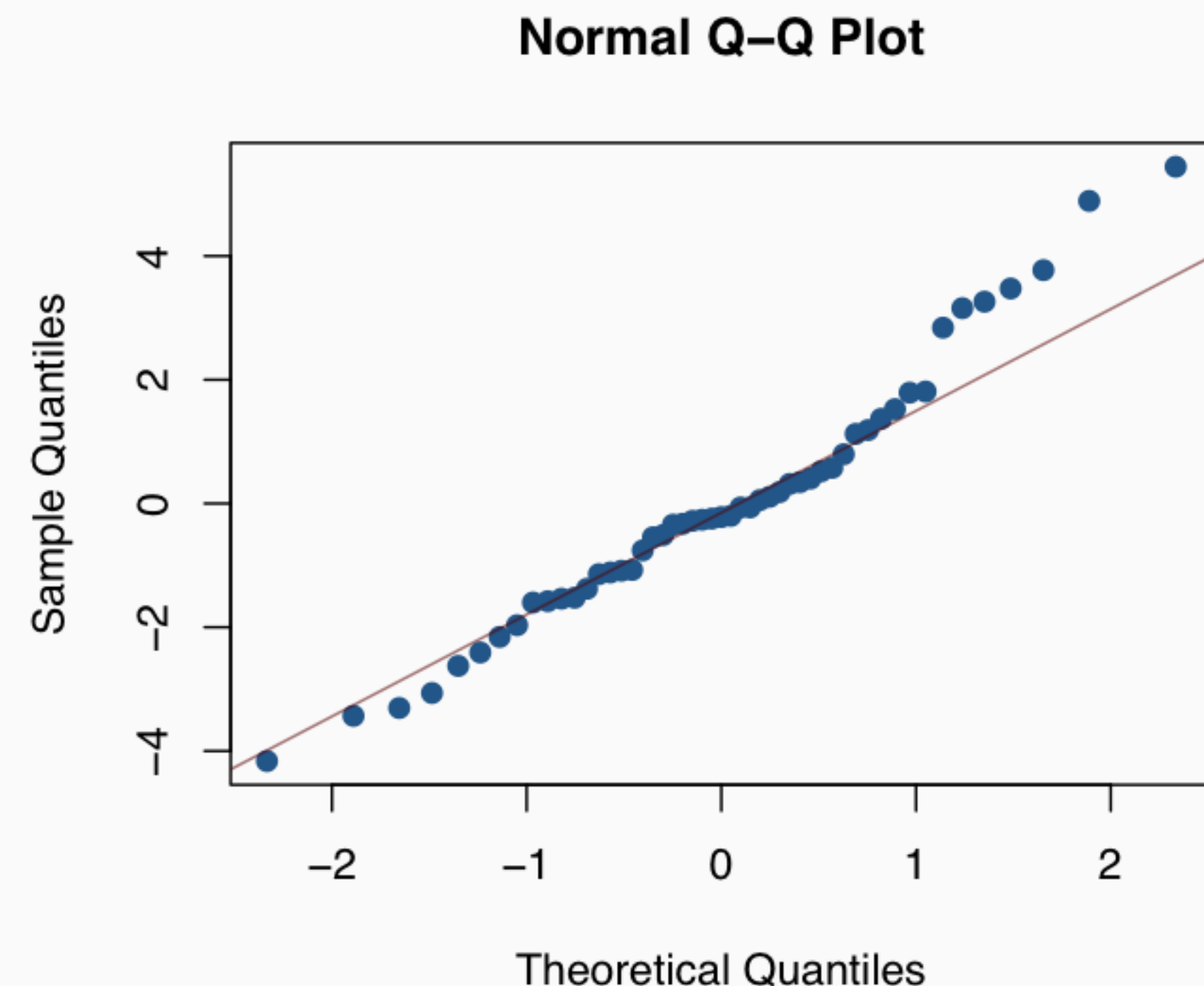
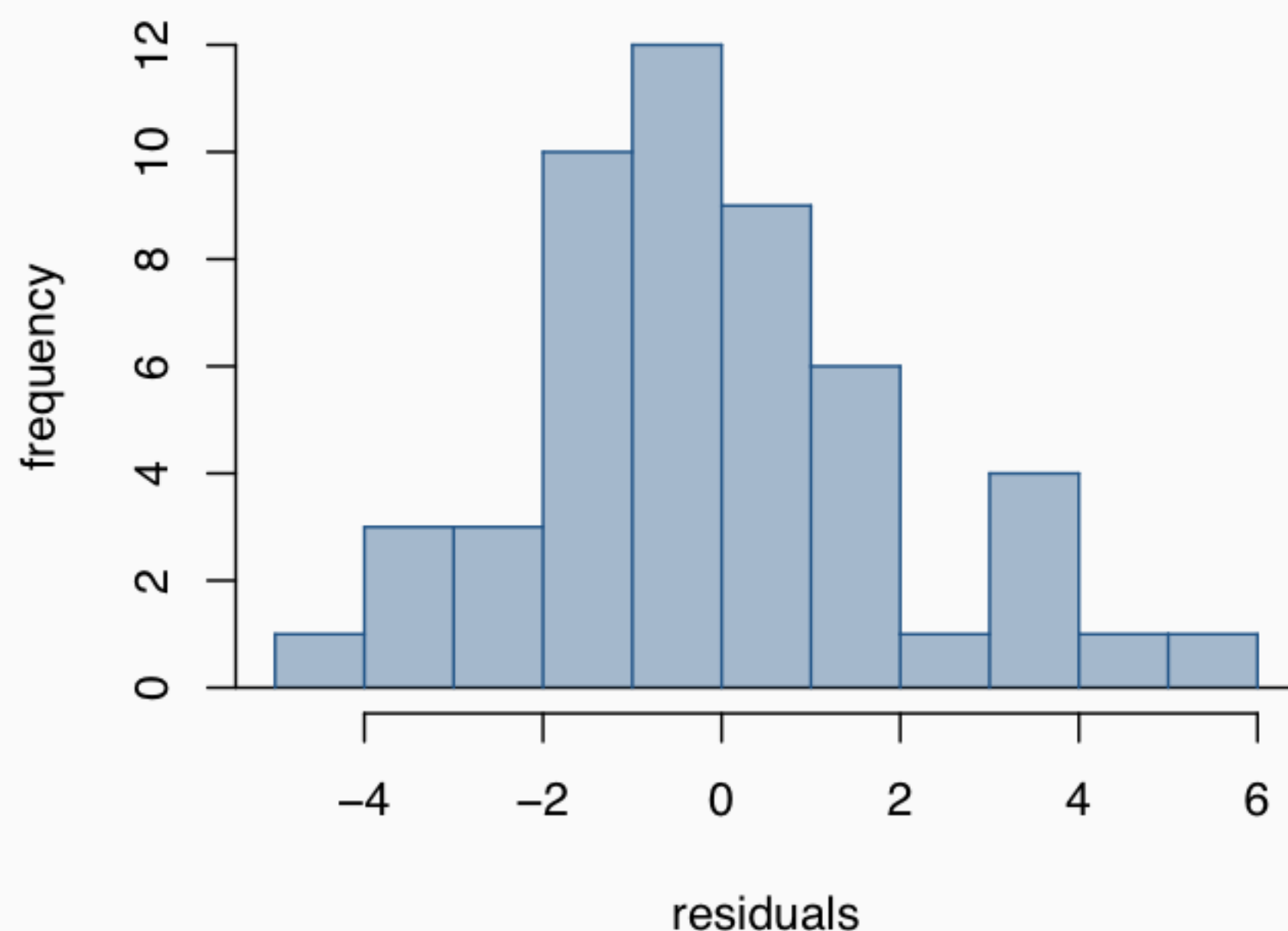
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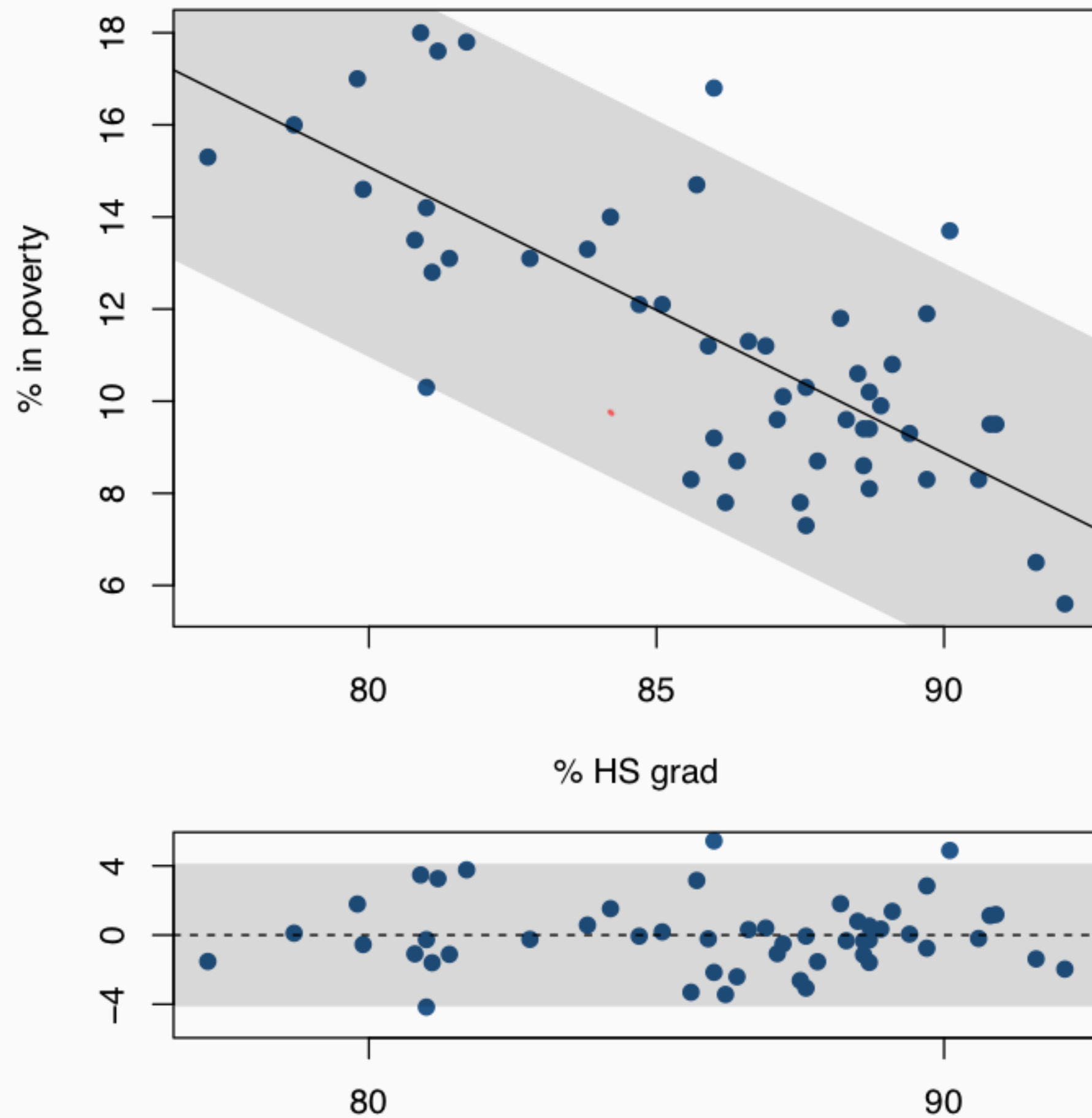


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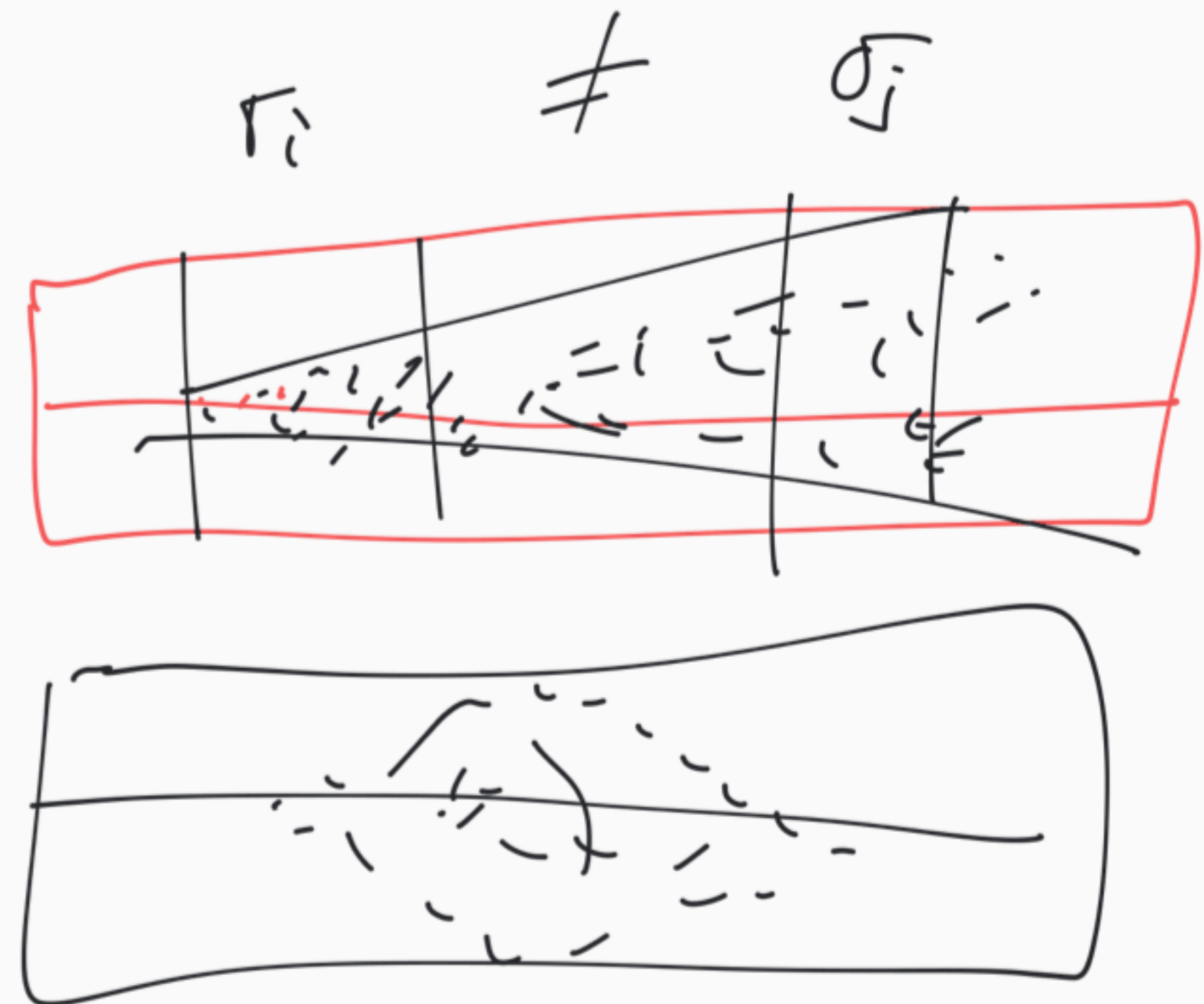
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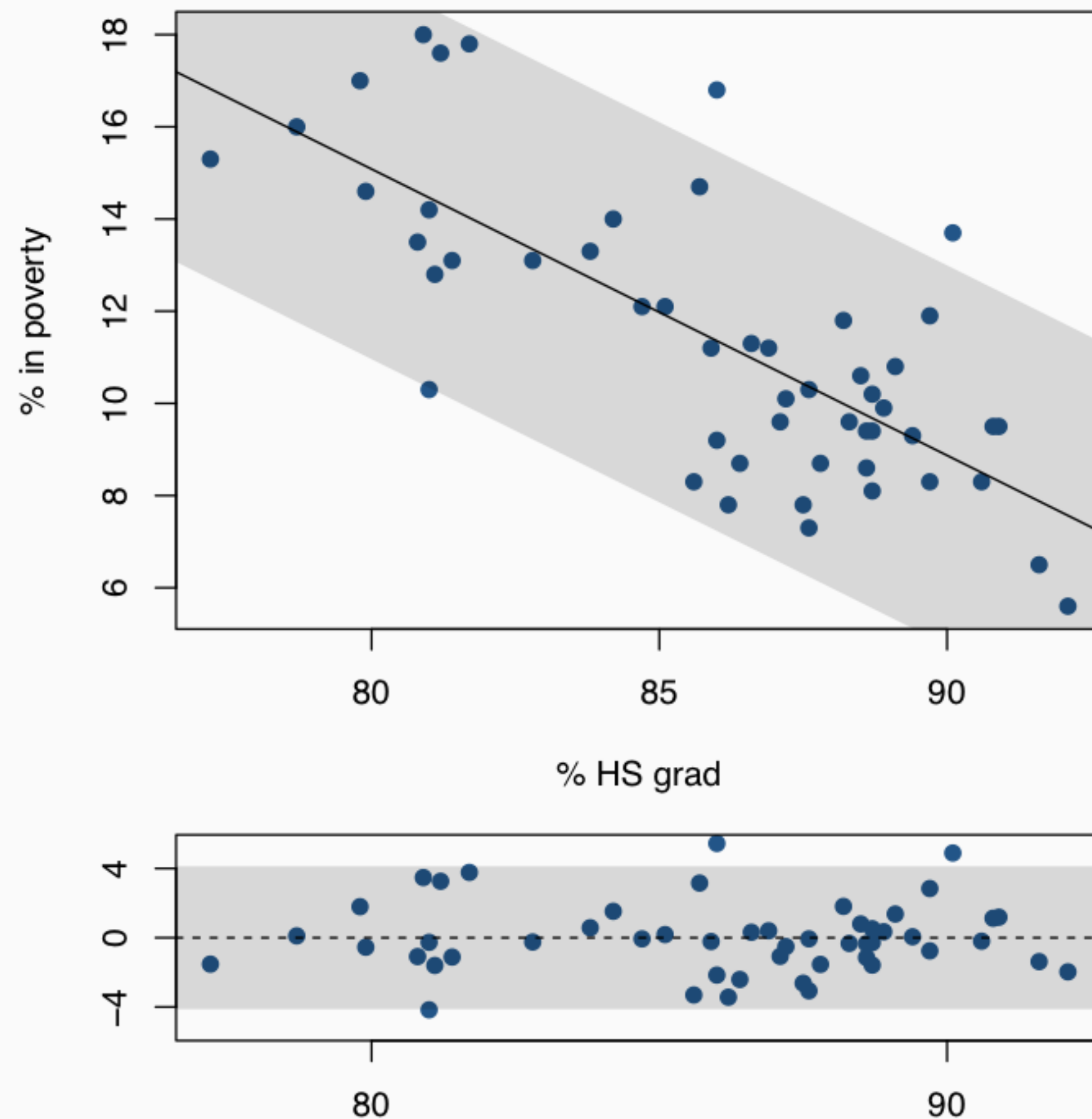
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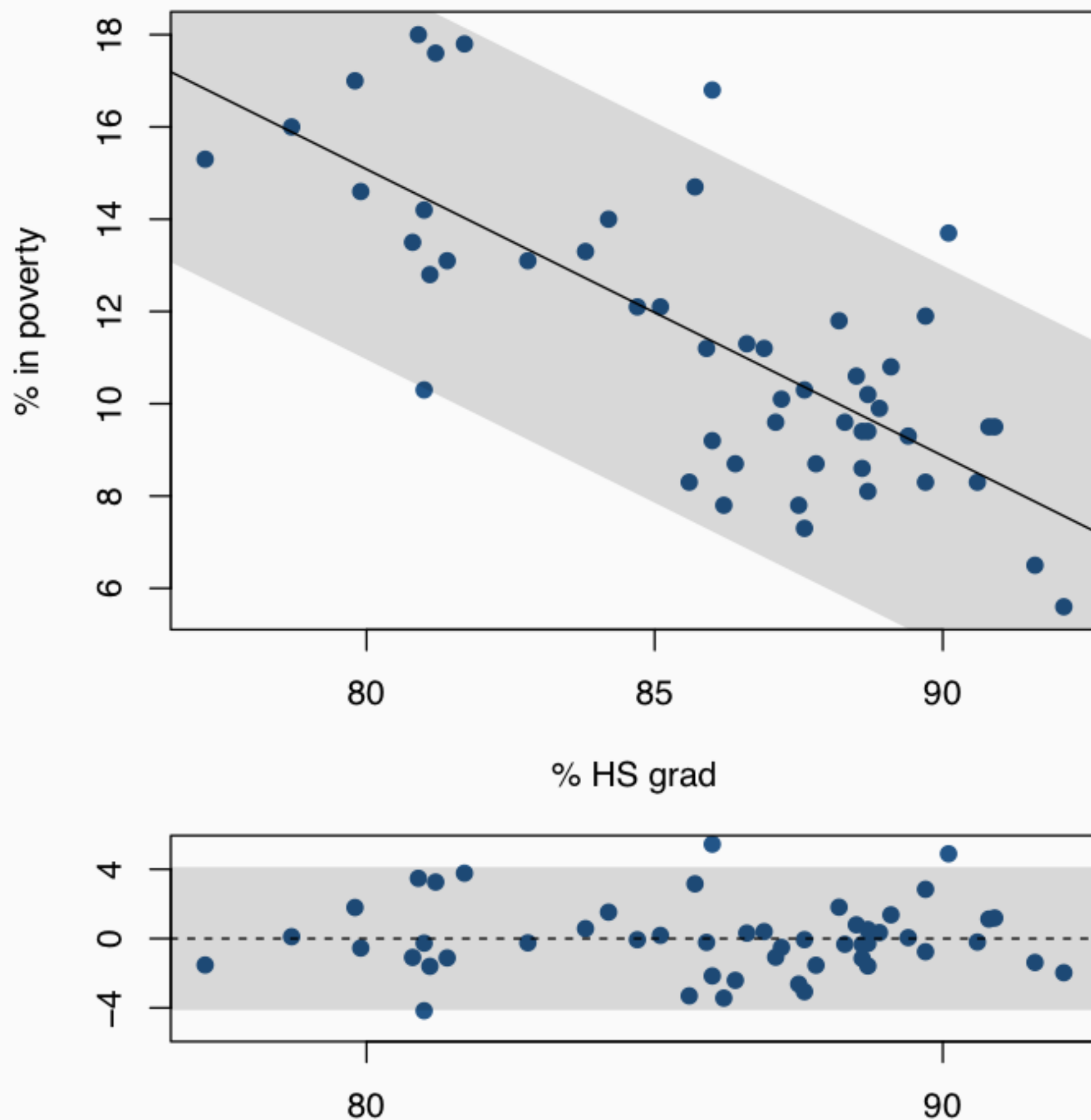
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- This implies that the variability of *any* region of the residual plot should be the same as any other region.

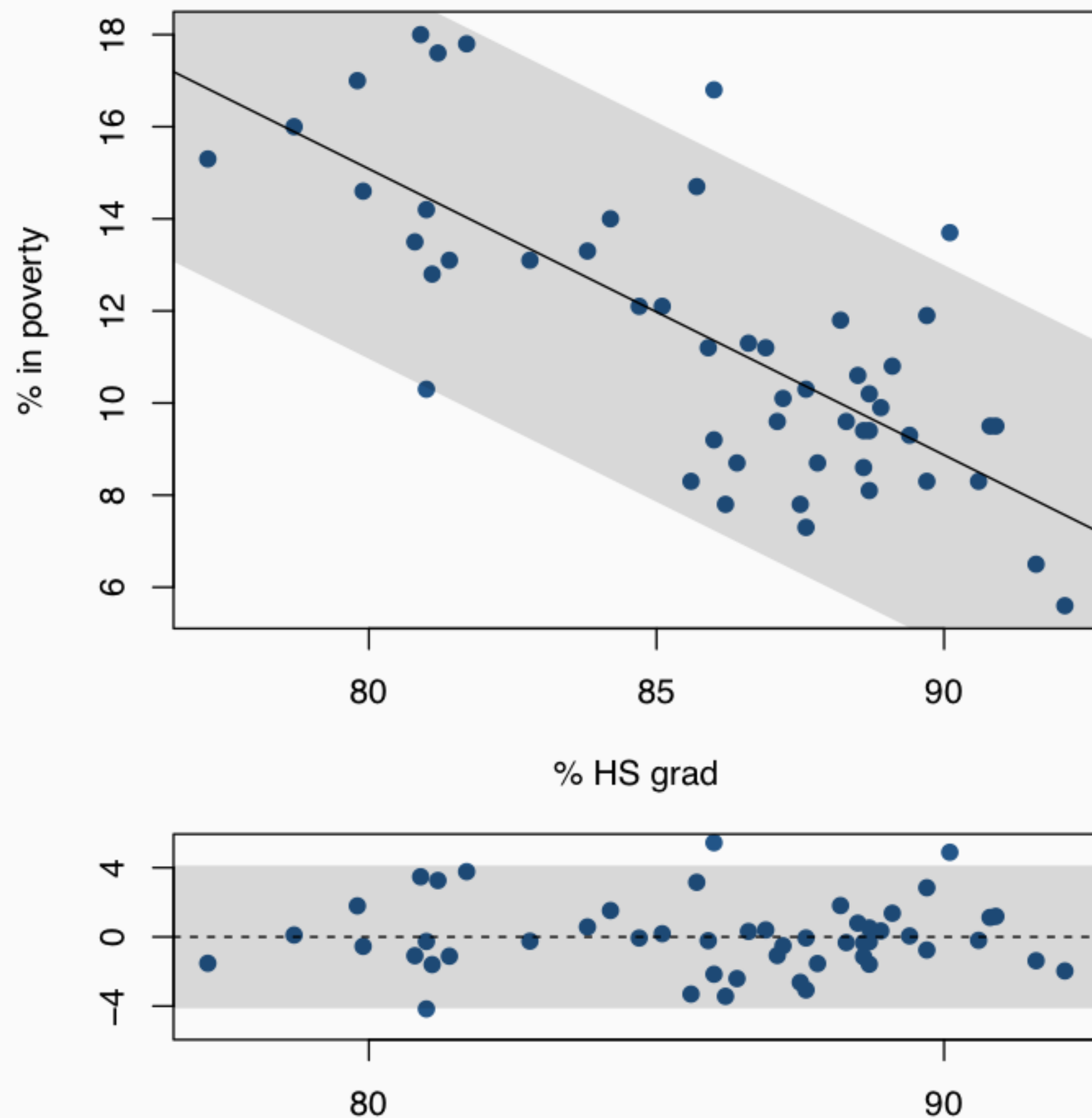


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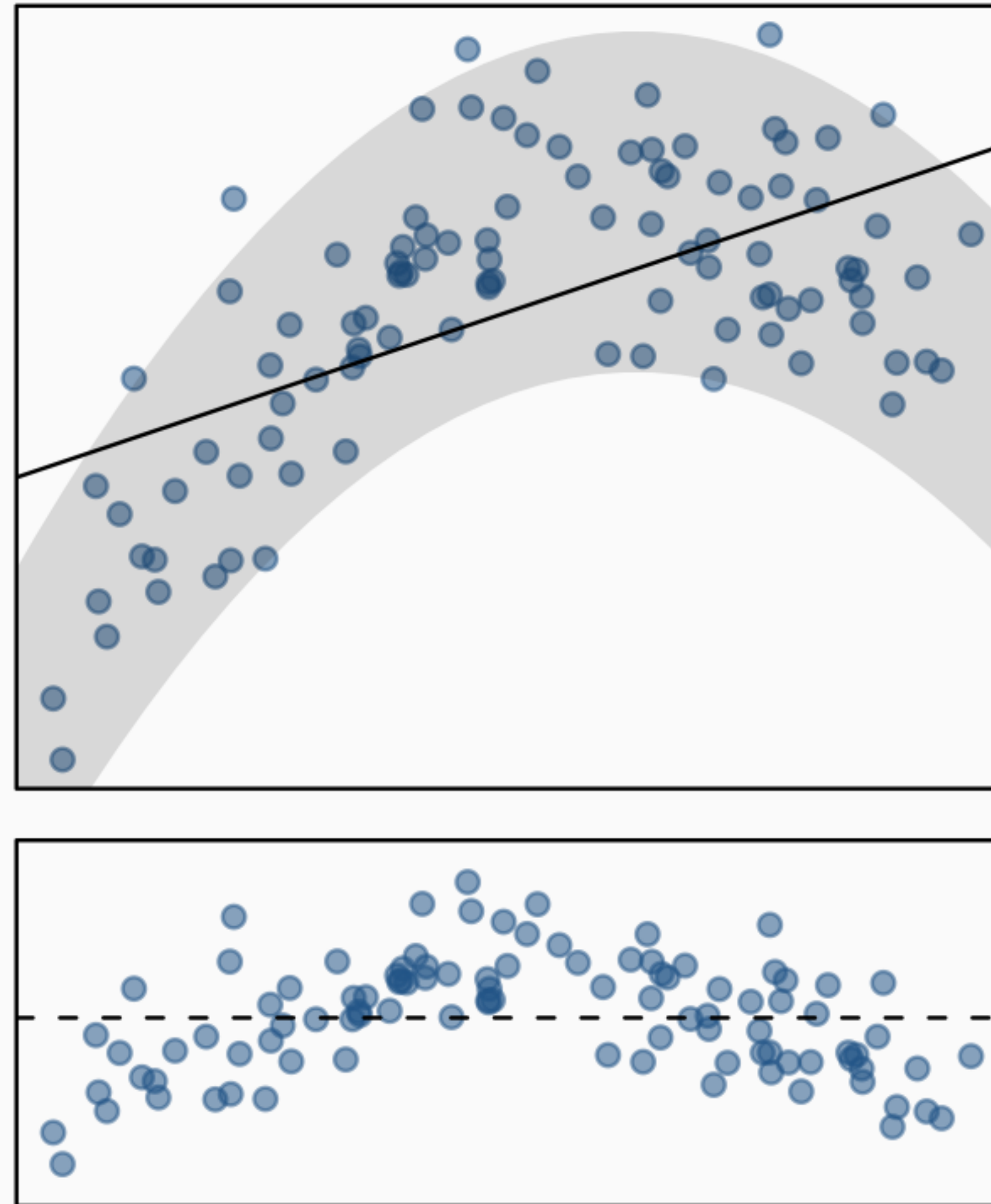
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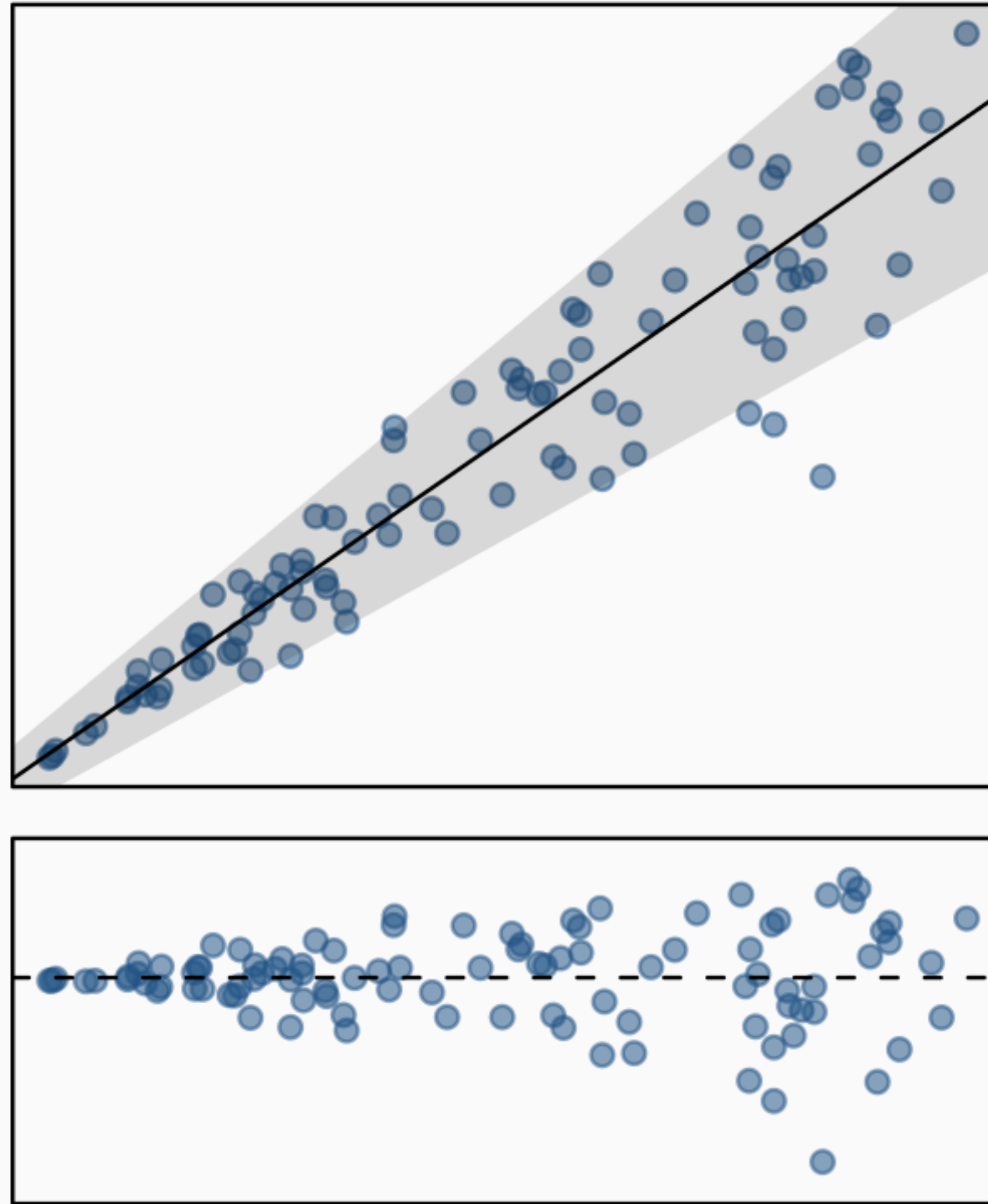
# Checking conditions

What condition is this linear model violating?



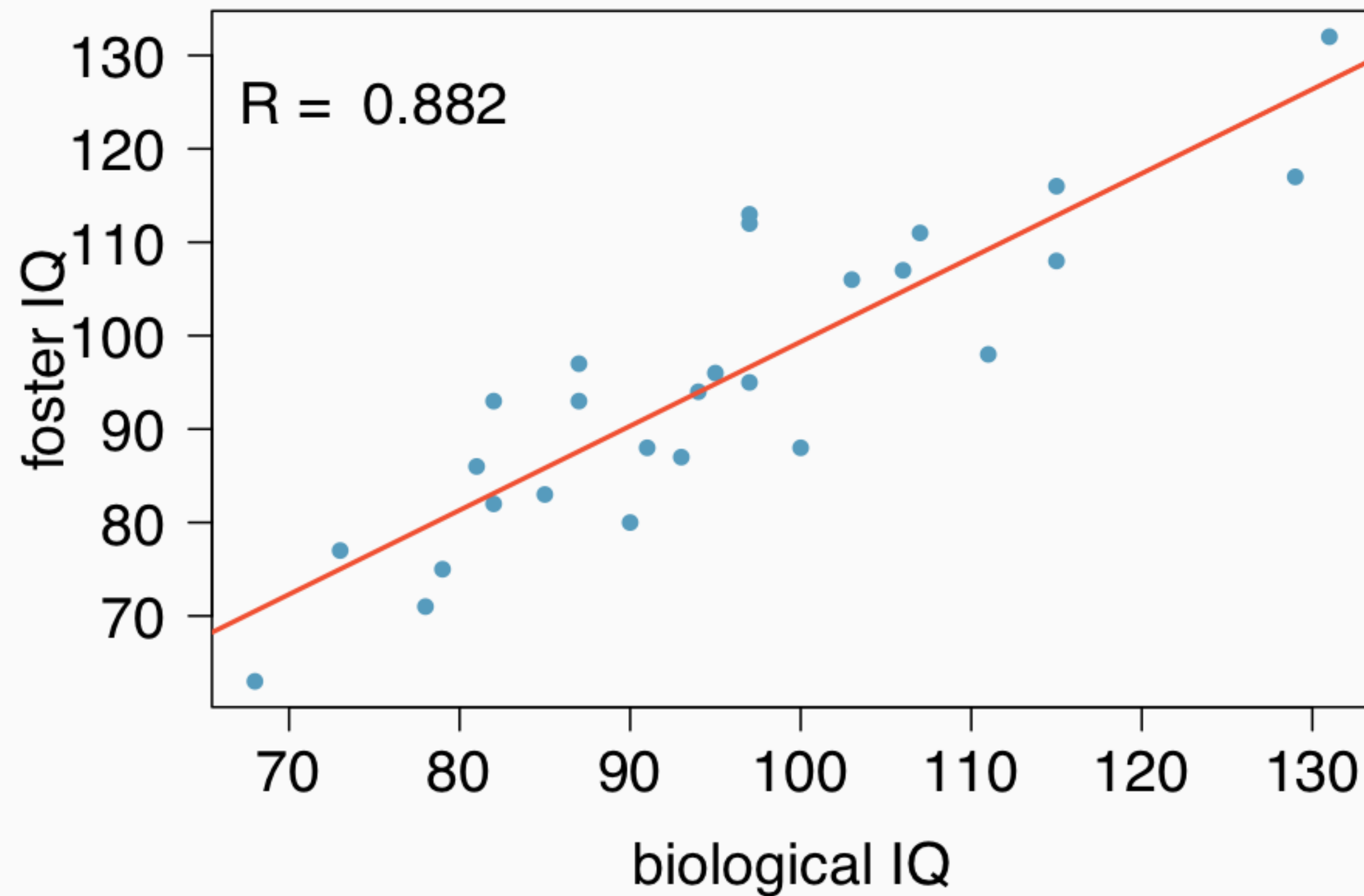
## Checking conditions (II)

What condition is this linear model obviously violating?





# Back to Nature vs nurture



	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	9.2076	9.2999	0.99	0.3316
biolIQ	0.9014	0.0963	9.36	0.0000



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$$H_0: \beta_1 = 0$$

$$H_A: \beta_1 \neq 0$$

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We are interested in inference on  $\beta_1$  which we estimate using the point estimate  $b_1$ .

It turns out that after normalizing our point estimate has a  $T$  distribution with  $n - 2$  degrees of freedom.

$$T_{df=n-2} = \frac{b_1 - \beta_1}{SE}$$

$$S_x^2 = \frac{1}{n-1} \sum (x_i - \bar{x})^2$$

$$S_e^2 = \frac{1}{n-2} \sum (e_i)^2$$

where,

$$SE_{b_1} = \frac{1}{\sqrt{n-1}} \frac{S_e}{S_x} = \frac{1}{\sqrt{n-1}} \frac{\sqrt{\frac{1}{n-2} \sum_{i=1}^n \epsilon_i^2}}{\sqrt{\frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2}}$$

# Data + Regression Output

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$$df = 27 - 2 = 25$$

$$\text{p-value} = P(|t| > 9.36) < 0.01$$

$$P(T > 9.36 \text{ or } T < -9.36)$$

$$\text{Reject } H_0 \Rightarrow \beta_1 \neq 0$$

# Confidence interval for the slope

Since we know the sampling distribution we can also construct a confidence interval:  $\text{point estimate} \pm CV \times SE$ .

What is the correct 95% confidence interval for the slope parameter?

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$$\begin{aligned} 95\% CI &= PE \pm CV \times SE = b_1 \pm t_{df=25}^* \left( \frac{1}{\sqrt{n-1}} \frac{S_e}{S_x} \right) \\ &= 0.9014 \pm 2.06 \times 0.0963 \\ &= (0.7, 1.1) \end{aligned}$$

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- The null value is almost always 0, since we are usually checking for *any* relationship between the explanatory and the response variable.
- The regression output gives  $b_1$ ,  $SE_{b_1}$ , and the *two-tailed* p-value for the  $t$ -test of the slope when the null hypothesis is  $\beta_1 = 0$



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- If you have a sample that is non-random (biased), the results will be unreliable.
- The ultimate goal is to have independent observations – and you know how to check for those by now.



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- We considered the  $t$ -test as a way to evaluate the strength of evidence for a hypothesis test for the slope of relationship between  $x$  and  $y$ .
- However, we can also consider the variability in  $y$  explained by  $x$ , compared to the unexplained variability.
- *Partitioning* the variability in  $y$  to explained and unexplained variability is something we have already done (*ANOVA*).

# Sums of Squares

$$\sum_i (y_i - \bar{y})^2 = \sum_i (\hat{y}_i - \bar{y})^2 + \sum_i (y_i - \hat{y}_i)^2$$

ANOVA Model:

$$\hat{y}_{ij} = \bar{y}_i$$

$$SST = \sum_i \sum_j (y_{ij} - \bar{y})^2$$

$$SSG = \sum_i \sum_j (\bar{y}_i - \bar{y})^2$$

$$SSE = \sum_i \sum_j (y_{ij} - \bar{y}_i)^2$$

Regression Model:

$$\hat{y}_i = b_0 + b_1 x_i$$

$$SST = \sum_i \sum_j (y_{ij} - \bar{y})^2$$

$$SSG = \sum_i \sum_j (b_0 + b_1 x_i - \bar{y})^2$$

$$SSE = \sum_i \sum_j (y_{ij} - b_0 - b_1 x_i)^2$$



# ANOVA Table - Linear Regression

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

*Sum of Squares:*  $SS_{Tot} = \sum_i (y_i - \bar{y})^2 = 6724.66$  (total variability in y)

# ANOVA Table - Linear Regression

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

*Sum of Squares:*  $SS_{Tot} = \sum_i (y_i - \bar{y})^2 = 6724.66$  (total variability in y)

$$\begin{aligned} SS_{Err} &= \sum_i (y_i - \hat{y}_i)^2 = \sum_i e_i^2 \\ &= 1493.53 \text{ (unexplained variability in residuals)} \end{aligned}$$

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$$SS_{Err} = \sum_i (y_i - \hat{y}_i)^2 = \sum_i e_i^2$$
$$= 1493.53 \text{ (unexplained variability in residuals)}$$

$$SS_{Reg} = \sum_i (\hat{y}_i - \bar{y})^2 = SS_{Tot} - SS_{Err}$$
$$= 5231.13 \text{ (explained variability in y)}$$

# ANOVA Table - Linear Regression

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
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$$SS_{Reg} = \sum_i (\hat{y}_i - \bar{y})^2 = SS_{Tot} - SS_{Err}$$

$$= 5231.13 \text{ (explained variability in y)}$$

*Degrees of freedom:*  $df_{Tot} = n - 1 = 27 - 1 = 26$



# ANOVA Table - Linear Regression

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$$= 1493.53 \text{ (unexplained variability in residuals)}$$

$$SS_{Reg} = \sum_i (\hat{y}_i - \bar{y})^2 = SS_{Tot} - SS_{Err}$$

$$= 5231.13 \text{ (explained variability in y)}$$

*Degrees of freedom:*  $df_{Tot} = n - 1 = 27 - 1 = 26$

$$df_{Reg} = 2 - 1 = 1$$

# ANOVA Table - Linear Regression

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
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Total	26	6724.66			

*Sum of Squares:*  $SS_{Tot} = \sum_i (y_i - \bar{y})^2 = 6724.66$  (total variability in y)

$$SS_{Err} = \sum_i (y_i - \hat{y}_i)^2 = \sum_i e_i^2$$

$$= 1493.53 \text{ (unexplained variability in residuals)}$$

$$SS_{Reg} = \sum_i (\hat{y}_i - \bar{y})^2 = SS_{Tot} - SS_{Err}$$

$$= 5231.13 \text{ (explained variability in y)}$$

*Degrees of freedom:*  $df_{Tot} = n - 1 = 27 - 1 = 26$

$$df_{Reg} = 2 - 1 = 1$$

$$df_{Res} = df_{Tot} - df_{Reg} = 26 - 1 = 25$$

# ANOVA output - F-test

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

*Mean sq.:*  $MS_{Reg} = \frac{SS_{Reg}}{df_{Reg}} = \frac{5231.13}{1} = 5231.13$

# ANOVA output - F-test

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

*Mean sq.:*  $MS_{Reg} = \frac{SS_{Reg}}{df_{Reg}} = \frac{5231.13}{1} = 5231.13$

$$MS_{Err} = \frac{SS_{Err}}{df_{Err}} = \frac{1493.53}{25} = 59.74$$



# ANOVA output - F-test

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
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Total	26	6724.66			

*Mean sq.:*  $MS_{Reg} = \frac{SS_{Reg}}{df_{Reg}} = \frac{5231.13}{1} = 5231.13$

$$MS_{Err} = \frac{SS_{Err}}{df_{Err}} = \frac{1493.53}{25} = 59.74$$

*F-statistic:*  $F_{(1,25)} = \frac{MS_{Reg}}{MS_{Err}} = 87.56$  (ratio of explained to unexplained variability)

# ANOVA output - F-test

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
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*Mean sq.:*  $MS_{Reg} = \frac{SS_{Reg}}{df_{Reg}} = \frac{5231.13}{1} = 5231.13$

$$MS_{Err} = \frac{SS_{Err}}{df_{Err}} = \frac{1493.53}{25} = 59.74$$

*F-statistic:*  $F_{(1,25)} = \frac{MS_{Reg}}{MS_{Err}} = 87.56$  (ratio of explained to unexplained variability)

This test compares our regression model to an intercept *only* model - which is equivalent to a null hypothesis of  $\beta_1 = 0$  and the alternative of  $\beta_1 \neq 0$ .

# Regression Output

```
summary(lm(twins$Foster ~ twins$Biological))

## Call:
## lm(formula = twins$Foster ~ twins$Biological)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.3512  -5.7311   0.0574   4.3244  16.3531
##
## Coefficients:
##              Estimate Std. Error t value Pr(> |t|)
## (Intercept)    9.20760     9.29990   0.990   0.332
## twins$Biological  0.90144     0.09633   9.358 1.2e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.729 on 25 degrees of freedom
## Multiple R-squared:  0.7779, Adjusted R-squared:  0.769
## F-statistic: 87.56 on 1 and 25 DF,  p-value: 1.204e-09
```

## ANOVA output - $R^2$ calculation

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
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## ANOVA output - $R^2$ calculation

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biolQ	1	5231.13	5231.13	87.56	0.0000
Residuals	25	1493.53	59.74		
Total	26	6724.66			

$$\begin{aligned} R^2 &= \frac{\text{explained variability}}{\text{total variability}} = \frac{SS_{Reg}}{SS_{Tot}} = \frac{5231.13}{6724.66} = 0.7779 \\ &= 1 - \frac{SS_{Err}}{SS_{Tot}} = 1 - \frac{1493.53}{6724.66} = 0.7779 \end{aligned}$$