

Topic 10 – Simple Linear Regression

ENVX1002 Statistics in Life and Environmental Sciences

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Feb 2026

Module overview

- Week
9.

Describing Relationships

- ▶ Correlation (calculation, interpretation)
- ▶ Regression (model structure, model fitting)
- ▶ What/when/why/how

- **Week 10. Simple Linear Regression**

- ▶ Can we use the model?(assumptions, hypothesis testing)
- ▶ How good is the model?(interpretation, model fit)

- Week
11.

Multiple Linear Regression

- ▶ Multiple Linear Regression (MLR) modelling
- ▶ Assumptions, interpretation and the principle of parsimony

- Week
12.

Nonlinear Regression

- ▶ Common nonlinear functions
- ▶ Transformations

Last week...

- Correlation r : a measure of the strength and direction of the linear relationship between two variables
- Is there a moderate to strong *causal* relationship?

...

Simple linear regression modelling

$$Y_i = \beta_0 + \beta_1 x_i + \epsilon_i$$

Basically, a deterministic straight line equation $y = c + mx$, with added random variation that is normally distributed

$$Y = c + mx + \epsilon$$

Fitting the line

$$Y_i = \beta_0 + \beta_1 x_i + \epsilon_i$$

$$Y = c + mx + \epsilon$$

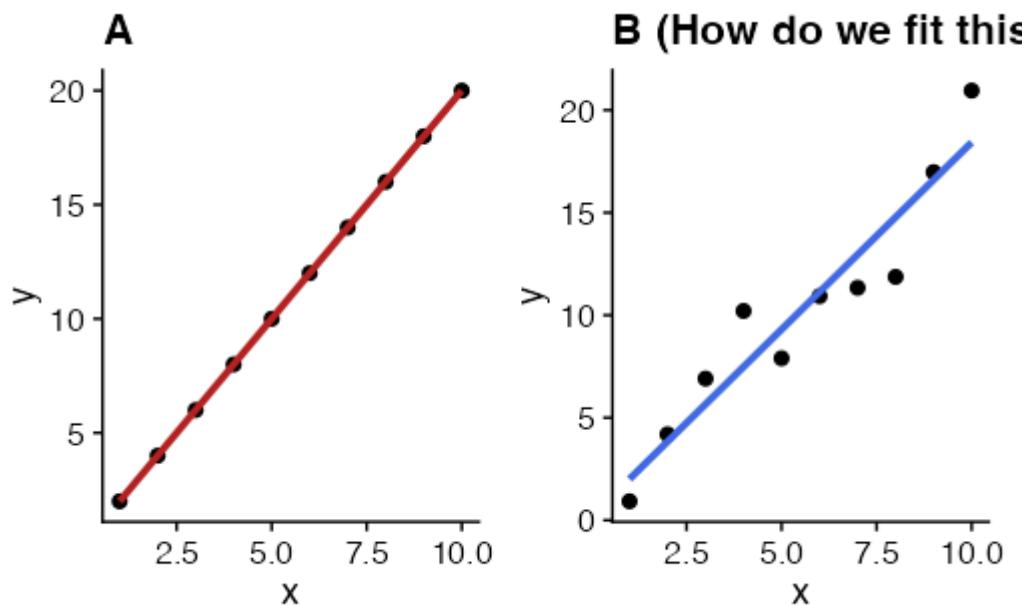
How do we fit a line to data if data are “noisy”?

```
x ← 1:10
y ← 2 * x + rnorm(10, 0, 2)
# generate y with predicted values
y_pred ← 2 * x
df ← data.frame(x, y)

p1 ← ggplot(df, aes(x, y_pred)) +
  geom_point(size = 2) +
  geom_smooth(method = "lm", se = FALSE, color = "firebrick") +
  labs(x = "x", y = "y", title = "A")

p2 ← ggplot(df, aes(x, y)) +
  geom_point(size = 2) +
  geom_smooth(method = "lm", se = FALSE, color = "royalblue") +
```

```
labs(x = "x", y = "y", title = "B (How do we fit this?)")  
  
library(patchwork)  
p1 + p2 + plot_layout(ncol = 2)
```



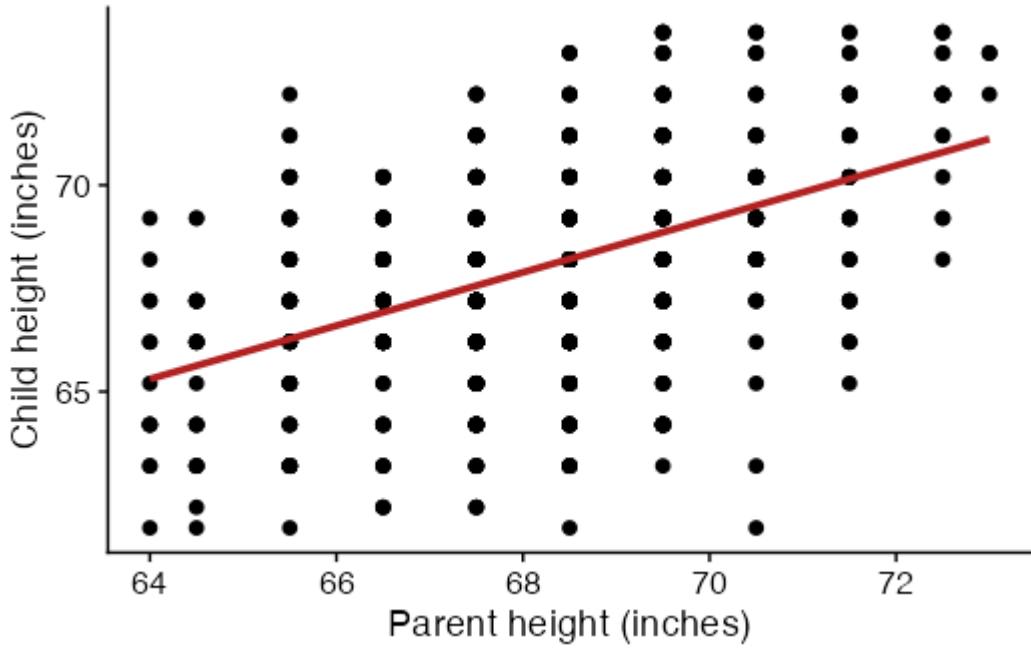
Usage of least squares

- Student's t-test (indirectly)
- linear regression
- ...
- nonlinear regression (logistic, polynomial, exponential, etc.)
- analysis of variance (ANOVA)
- generalised linear model
- principle component analysis
- machine learning models
- etc...

Galton's data revisited

- Galton's data on the heights of parents and their children.
- Is there a relationship between the heights of parents and their children?

```
library(HistData)
data(Galton)
fit ← lm(child ~ parent, data = Galton)
ggplot(Galton, aes(x = parent, y = child)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "firebrick") +
  labs(x = "Parent height (inches)", y = "Child height (inches)")
```



How did we end up with the line in the plot above?

How do we analytically fit a line?

We calculate slope (β_1):

$$\beta_1 = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^n (x_i - \bar{x})^2} = \frac{Cov(x, y)}{Var(x)} = \frac{SS_{xy}}{SS_{xx}}$$

Then substitute below to get the intercept (β_0):

$$\beta_0 = \bar{y} - \beta_1 \bar{x}$$

Imagine a dataset with a million points - this would be computationally taxing.

How do we numerically fit a line?

- *Minimise* the sum of the squared residuals via trial and error
- Most common method used via computers (gradient-descent)
- Can be done by hand (but not recommended)

$$\operatorname{argmin}_{\beta_0, \beta_1} \sum_{i=1}^n (y_i - (\beta_0 + \beta_1 x_i))^2$$

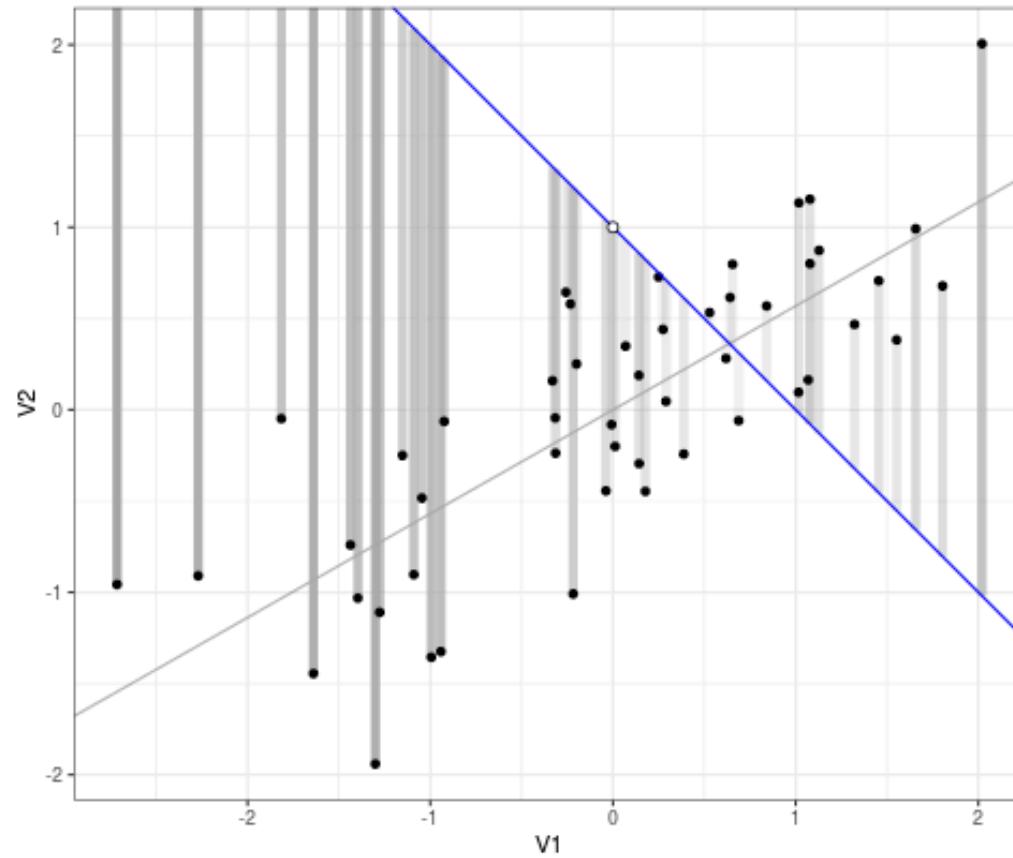


Figure 1: Source

Fitting a linear model in R

Is there a relationship between the heights of parents and their children?

```
fit ← lm(child ~ parent, data = Galton)  
fit
```

Call:
`lm(formula = child ~ parent, data = Galton)`

Coefficients:
(Intercept) parent
23.9415 0.6463

$$\widehat{child} = 23.9 + 0.646 \cdot parent$$

...

Do we trust our model? How good is the model? How can we interpret the results?

Steps for Regression

1. Understand the variables
2. Explore data
3. Fit model
4. Check assumptions
5. Assess model fit
6. Interpret output

Assumptions

- | The data **must** meet certain criteria for linear regression, which we often call *assumptions*.

Assumptions - LINE

- **L**inearity. The relationship between y and x is linear.
 - **I**ndependence. The errors ϵ are independent.
 - **N**ormal. The errors ϵ are normally distributed.
 - **E**qual Variance of errors ϵ . At each value of x , the variance of y is the same i.e. homoskedasticity, or constant variance.
- ...

Why do we care?

- If the assumptions are met, then we can be confident that the model is a good representation of the data.
- If they are *not* met, the results are still presented, but our interpretation of the model is likely to be flawed.
 - ▶ Hypothesis test results are unreliable
 - ▶ Standard error is unreliable
 - ▶ Poor estimates of coefficients = poor predictions

How do we check the assumptions?

Recall that the linear model is a **deterministic straight line equation** $y = c + mx$ plus some **random noise** ϵ :

$$Y_i = \beta_0 + \beta_1 x + \epsilon$$

- If the only source of variation in y is ϵ , then we can check our assumptions by just looking at the residuals $\hat{\epsilon}$.

...



Tip

All but the independence assumption can be assessed using diagnostic plots. R will not warn you if the assumptions are not met. It is up to you to check them!

How do we get the residuals?

- Fit the model!
- Residuals need to be calculated from the model, not from the raw data.
- In R, these values are stored automatically.

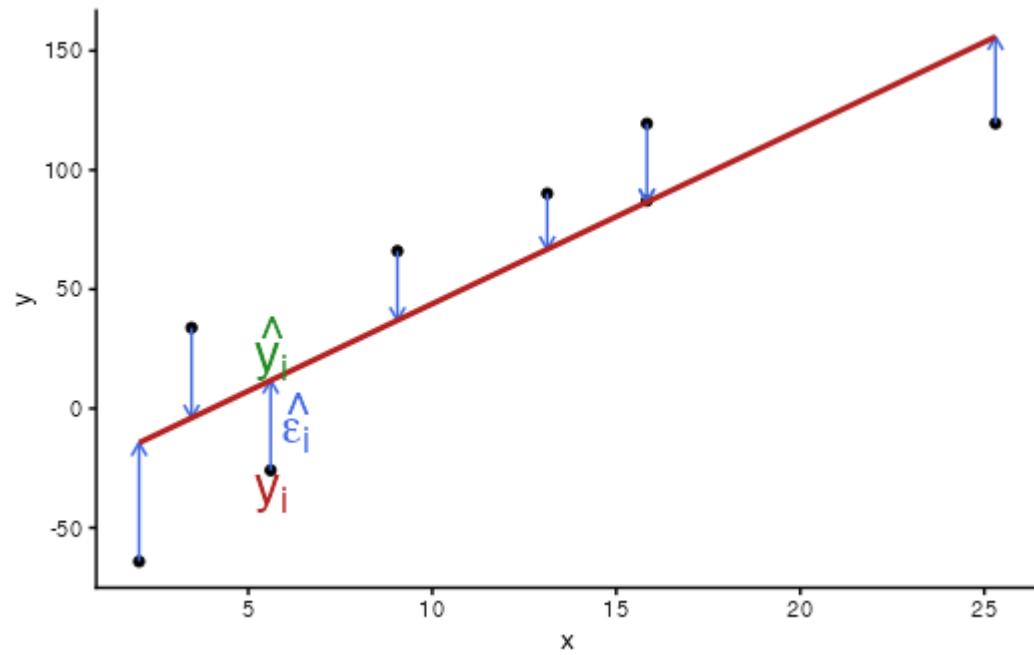
$$\hat{\epsilon}_i = y_i - \hat{y}_i$$

```
# simulate example data
set.seed(340)
x ← runif(8, 0, 30)
y ← 5 * x + rnorm(8, 0, 40)
df ← data.frame(x, y)

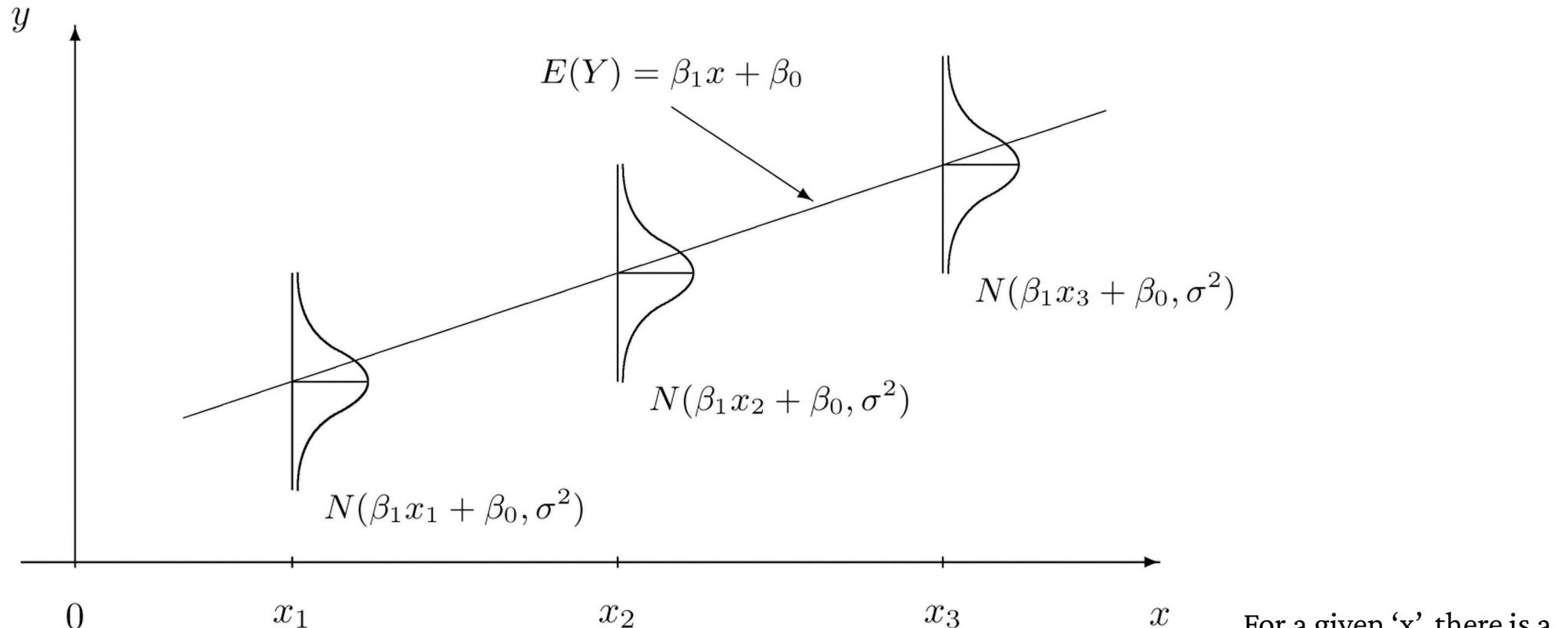
# fit linear model, add residual vertical lines as arrows
mod ← lm(y ~ x, data = df)
p1 ← ggplot(df, aes(x, y)) +
  geom_point() +
  geom_segment(aes(xend = x, yend = fitted(mod)),
    arrow = arrow(length = unit(0.2, "cm")),
    color = "royalblue"
```

```
) +
  labs(x = "x", y = "y")

p1 +
  geom_smooth(method = "lm", se = FALSE, color = "firebrick") +
  annotate("text",
    x = 6.3, y = -6, size = 7,
    label = expression(hat(epsilon[i])), colour = "royalblue"
  ) +
  annotate("text",
    x = 5.6, y = 25, size = 7,
    label = expression(hat(y[i])), colour = "forestgreen"
  ) +
  annotate("text",
    x = 5.6, y = -36, size = 7,
    label = expression(y[i]), colour = "firebrick"
  ) +
  theme_classic()
```



Another way to look at residuals



- e.g. For a given parent height, there is a range of child heights that are possible.

Checking assumptions

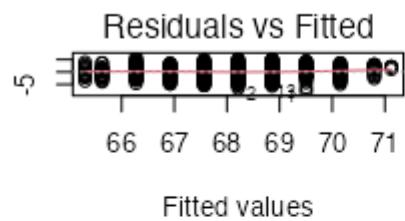
linearity | normality | equal variance | outliers

1-step

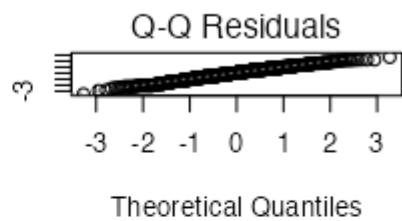
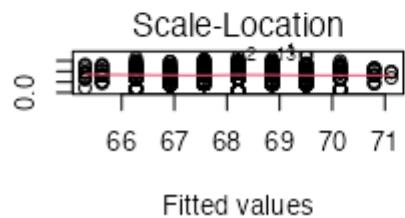
- **Residuals vs. Fitted**: check for linearity, equal variance.
- **Q-Q Residuals**: check for normality.
- **Scale-Location**: check for equal variance (standardised).
- **Residuals vs. Leverage**: check for outliers (influential points).

```
par(mfrow = c(2, 2)) # need to do this to get 4 plots on one page
plot(fit)
```

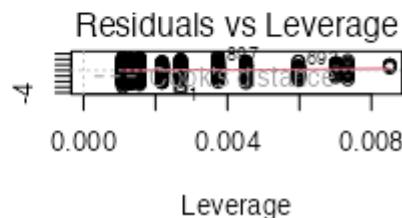
Residuals



Standardized residuals

 $\sqrt{|\text{Standardized residuals}|}$ 

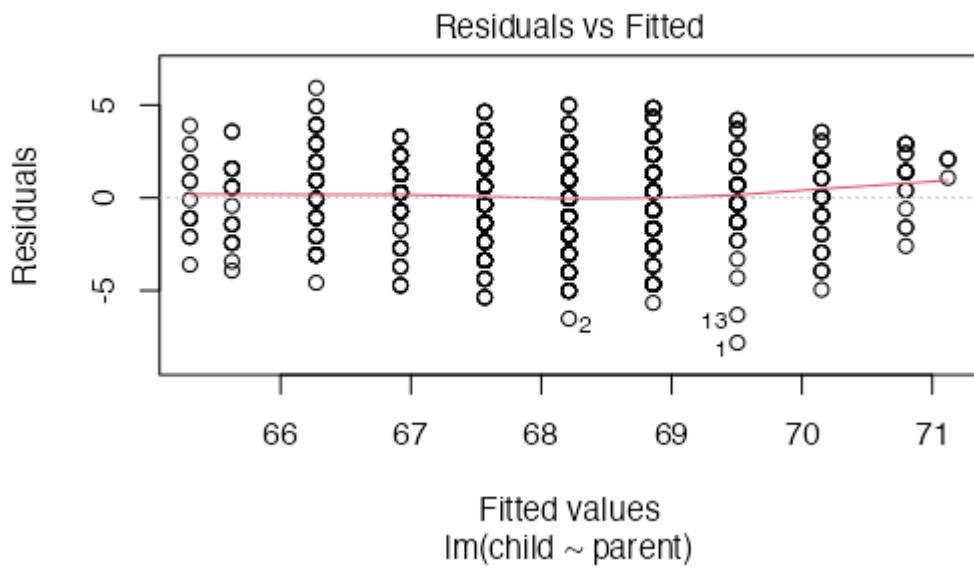
Standardized residuals



Assumption: Linearity

- Residuals vs. fitted plot looks at the relationship between the residuals and the fitted values.
- If the relationship is linear:
 - ▶ Residuals should be randomly scattered around the horizontal axis.
 - ▶ The red line should be reasonably straight.
- Could also look at a scatterplot of x and y!

```
plot(fit, which = 1)
```



Examples

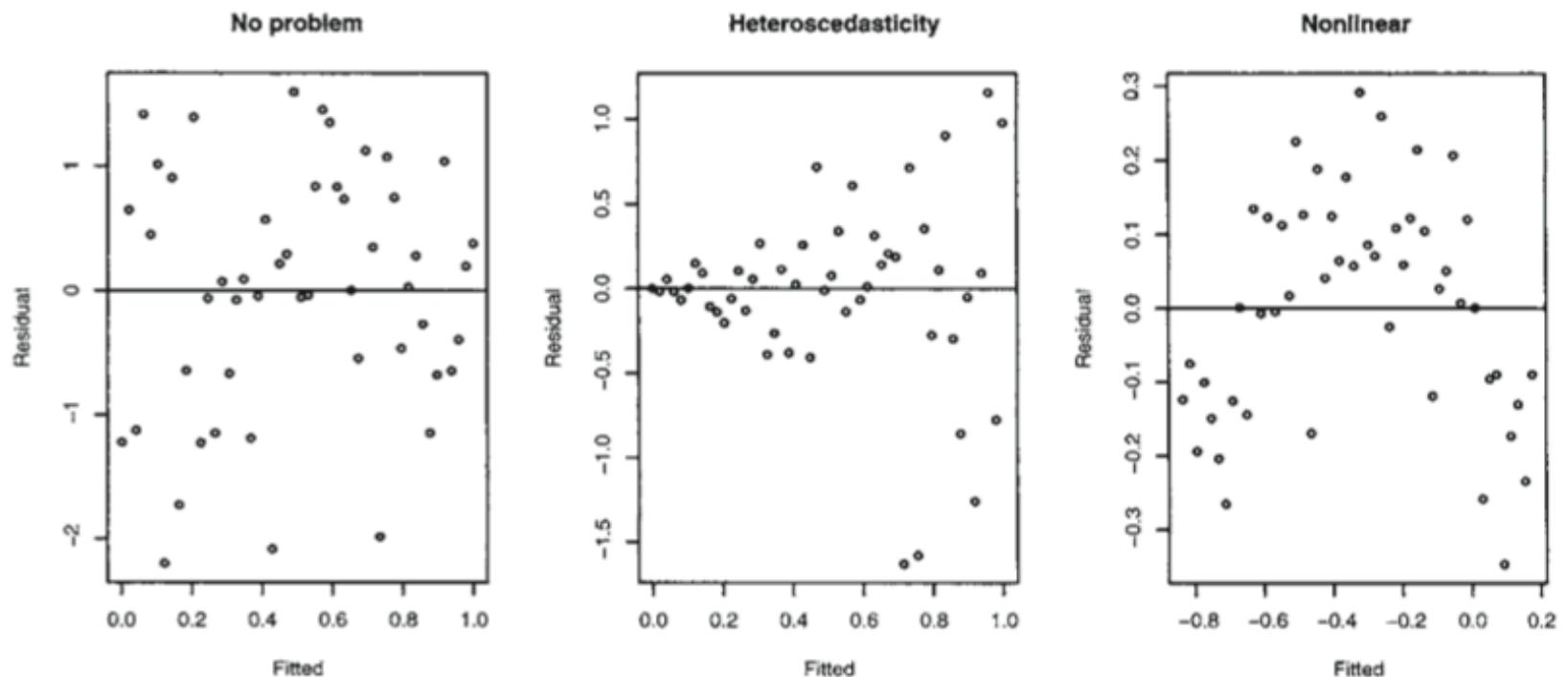


Figure 4.1 *Residuals vs. fitted plots—the first suggests no change to the current model while the second shows nonconstant variance and the third indicates some nonlinearity, which should prompt some change in the structural form of the model.*

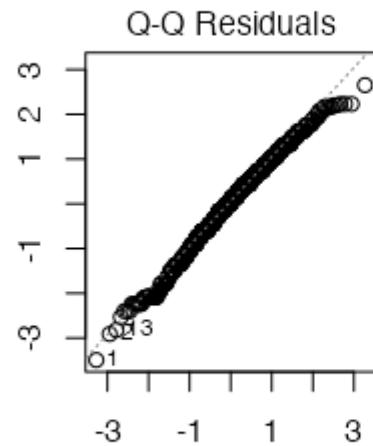
Linear Models with R (Faraway 2005, p59)

Assumption: Normality

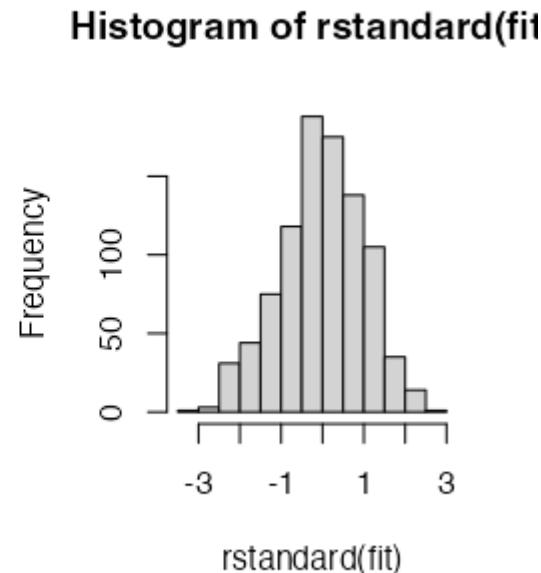
- Q-Q plot looks at the distribution of the residuals against a normal distribution function (the dotted line).
- Sometimes, a histogram is still useful to see the shape of the distribution.

```
par(mfrow = c(1, 2))
plot(fit, which = 2)
hist(rstandard(fit))
```

Standardized residuals



Theoretical Quantiles



Assumption: Normality

- If **normally distributed**, the points should follow the red line.
 - Deviation from the red line is common in the tails (i.e. the ends), but not in the middle.
- ...

Tips

- **Light-tailed**: small variance in residuals, resulting in a narrow distribution.
- **Heavy-tailed**: many extreme positive and negative residuals, resulting in a wide distribution.
- **Left-skewed** (n shape): more data falls to the left of the mean.
- **Right-skewed** (u shape): more data falls to the right of the mean.

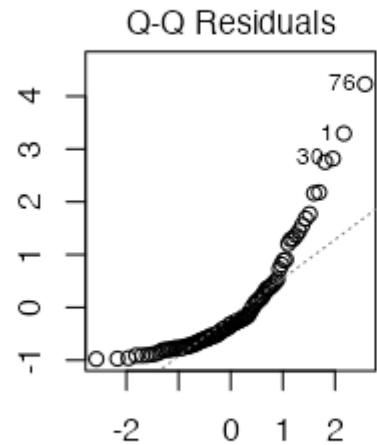


Left or right-skewed? Look at where the tail points.

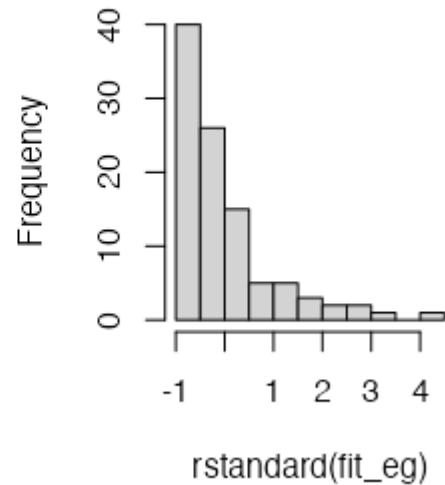
Examples

```
set.seed(915)
x ← rnorm(100)
y ← 2 + 5 * x + rchisq(100, df = 2)
df ← data.frame(x, y)
fit_eg ← lm(y ~ x, data = df)
par(mfrow = c(1, 2))
plot(fit_eg, which = 2)
hist(rstandard(fit_eg))
```

Standardized residuals

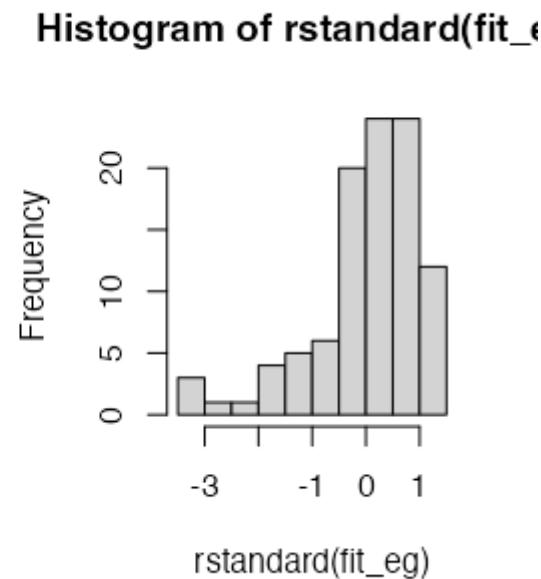
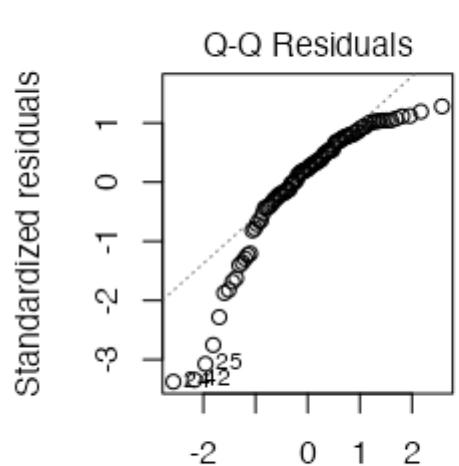


Histogram of rstandard(fit_eg)



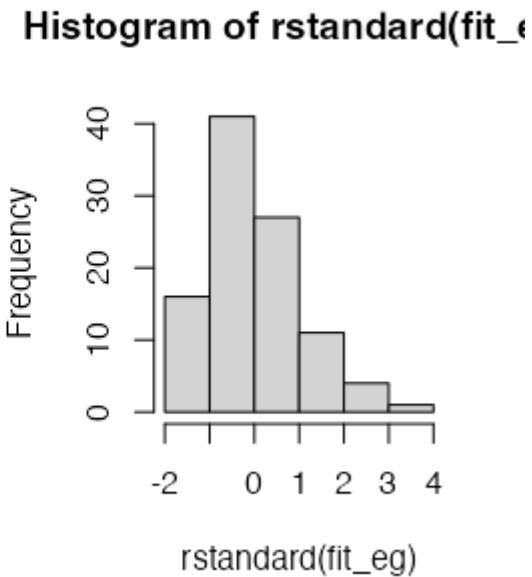
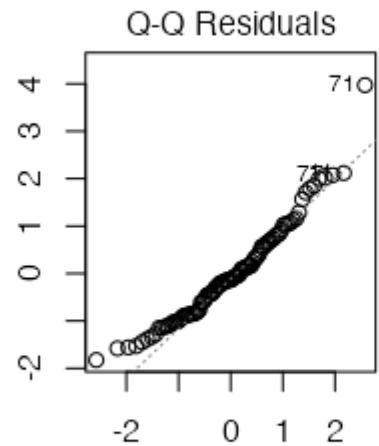
```
set.seed(1028)
x ← rnorm(100)
y ← 2 + 5 * x + rchisq(100, df = 3) * -1
df ← data.frame(x, y)
```

```
fit_eg ← lm(y ~ x, data = df)
par(mfrow = c(1, 2))
plot(fit_eg, which = 2)
hist(rstandard(fit_eg))
```



```
set.seed(1028)
x ← rnorm(100)
y ← 2 + 5 * x + rnbinom(100, 10, .5)
df ← data.frame(x, y)
fit_eg ← lm(y ~ x, data = df)
par(mfrow = c(1, 2))
plot(fit_eg, which = 2)
hist(rstandard(fit_eg))
```

Standardized residuals



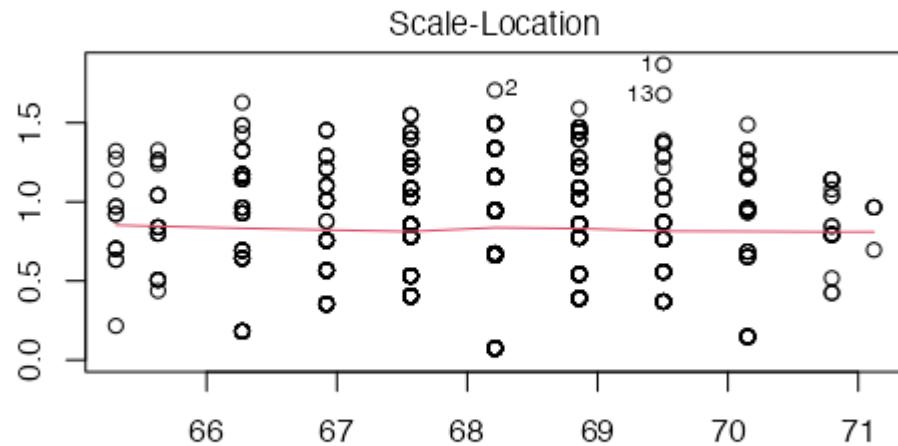
Assumption: Equal Variances

Equal variances

- Look at the **scale-location plot**.
- If variances are equal, the points should be randomly scattered around the horizontal axis.
- The red line should be more or less horizontal.

```
plot(fit, which = 3)
```

$\sqrt{|\text{Standardized residuals}|}$

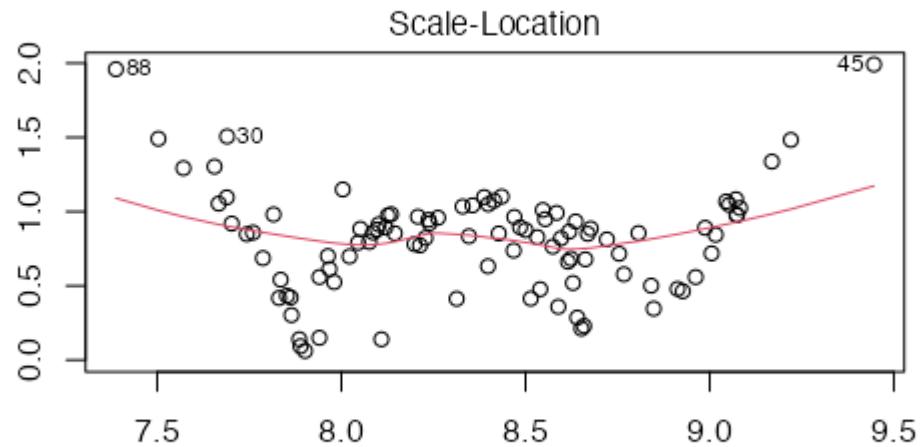


Equal variances

- If variances are not equal we *may* see:
 - A funnel shape, where the points are more spread out at the ends than in the middle. Sometimes also called “fanning”.
 - Patterns in the scale-location plot, such as a curve or a wave, indicating that the variance is changing.
- Look at the red line for a general trend, **but don't depend on it too much.**

```
set.seed(915)
x ← rnorm(100)
y ← 2 + 5 * x^2 +rchisq(100, df = 2)
df ← data.frame(x, y)
fit_eg ← lm(y ~ x, data = df)
plot(fit_eg, which = 3)
```

$\sqrt{|\text{Standardized residuals}|}$



Fitted values
 $\text{Im}(y \sim x)$

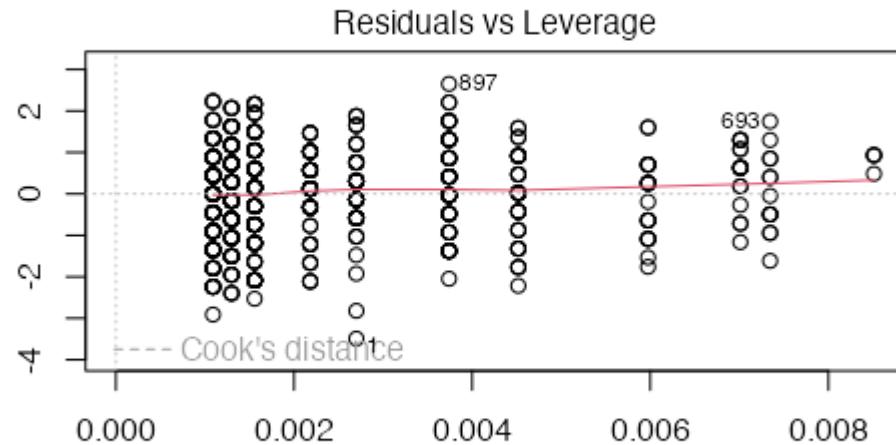
Outliers

- **Leverage** is a measure of how far away the predictor variable is from the mean of the predictor variable.
 - The Residuals vs Leverage plot shows the relationship between the residuals and the leverage of each point.
 - **Cook's distance** is a measure of how much the model would change if a point was removed.
-

In general, points with **high leverage** and **high Cook's distance** are considered outliers.

```
plot(fit, which = 5)
```

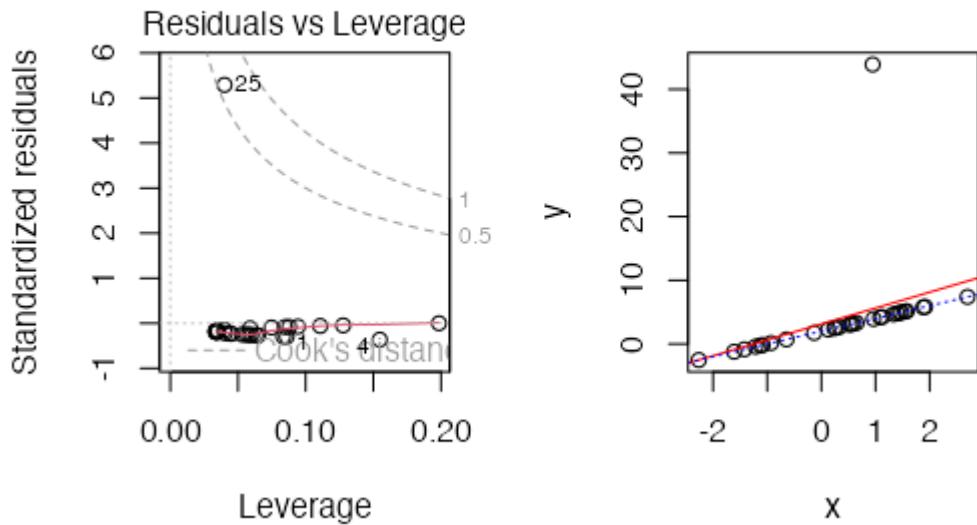
Standardized residuals



Example of an influential outlier

```
set.seed(1028)
x ← rnorm(30)
y ← 2 + 2 * x
```

```
y[25] ← y[25] + 40 # Add an outlier  
  
fit_eg ← lm(y ~ x)  
  
par(mfrow=c(1,2))  
plot(fit_eg, which = 5)  
  
plot(x, y)  
abline(fit_eg, col = "red")  
  
fit_eg2 ← lm(y[-25] ~ x[-25])  
abline(fit_eg2, col = "blue", lty = 3)
```



Points that exceed the dashed line (which appears once they approach the Cook's distance), are likely to influence the model. These outliers should be removed.

e.g. this is of a perfect line with one extreme outlier – the line of best fit deviates because of a single point!

What can we do if the assumptions aren't met?

It depends...

...which assumption is not met and the type of data i.e. circumstances.

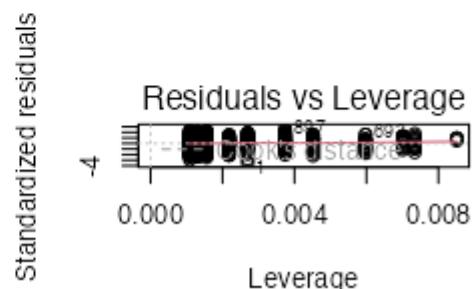
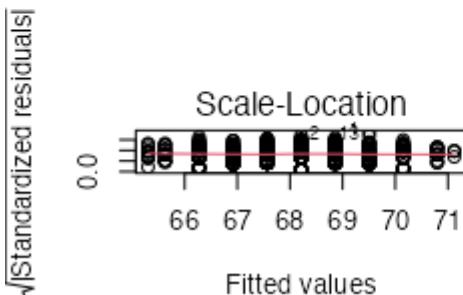
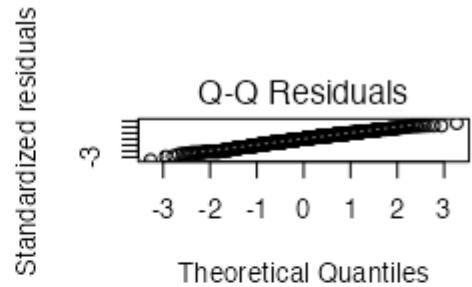
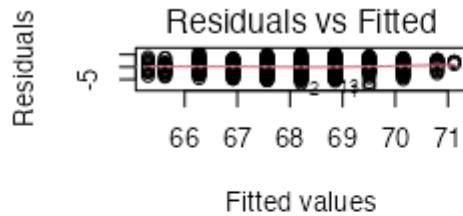
- If data is **non-linear**, try a transformation of the response variable y , from light to extreme:
 - ▶ root: \sqrt{y} or $\sqrt{y + 1}$ if y contains zeros
 - ▶ log: $\log(y)$ or $\log(y + 1)$ if y contains zeros
 - ▶ inverse: $\frac{1}{y}$ or $\frac{1}{y+1}$ if y contains zeros
- If residuals are **not normally distributed**, try a transformation of the response variable y first, otherwise transform the predictor variable x . Both can be done at the same time.
- If **equal variances** assumption is not met, same as above.
- If **outliers** are present, try removing them, or transforming the response variable y .

What if transformation doesn't work?

If the assumptions are still not met after trying the above, you can try:

- Using a different type of regression e.g. logistic regression, non-linear regression
- Using a different model e.g. machine learning.
- Using a non-parametric test.

Back to Galton - model assumptions are met



Now what?

Model Assessment and Interpretation

| Hypothesis? How good is the model? What can we understand about the relationship between `child` and `parent`?

Interpreting the output

```
Call:  
lm(formula = child ~ parent, data = Galton)  
  
Residuals:  
    Min      1Q  Median      3Q     Max  
-7.8050 -1.3661  0.0487  1.6339  5.9264  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept) 23.94153   2.81088   8.517 <2e-16 ***  
parent       0.64629   0.04114  15.711 <2e-16 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 2.239 on 926 degrees of freedom  
Multiple R-squared:  0.2105,    Adjusted R-squared:  0.2096  
F-statistic: 246.8 on 1 and 926 DF,  p-value: < 2.2e-16
```

- Call: the model formula

- **Residuals**: distribution of the residuals

Interpreting the output

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Multiple R-squared:  0.2105,    Adjusted R-squared:  0.2096  
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```

- **Coefficients**: a summary table of the coefficients, their standard errors, t-values, and p-values.

- (Intercept)/Estimate : the **y-intercept**, or the mean response when all predictors are 0.
- parent/Estimate : the **slope** coefficient - i.e. the change in the **mean** of the response for a **one-unit increase in the predictor**.

Interpreting the output

```
Call:  
lm(formula = child ~ parent, data = Galton)  
  
Residuals:  
    Min      1Q  Median      3Q     Max  
-7.8050 -1.3661  0.0487  1.6339  5.9264  
  
Coefficients:  
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Multiple R-squared:  0.2105,    Adjusted R-squared:  0.2096  
F-statistic: 246.8 on 1 and 926 DF,  p-value: < 2.2e-16
```

- `Pr`: the p-value

- ▶ `(Intercept)/Pr`: the p-value of the y-intercept is not meaningful.
- ▶ `parent/Pr`: is `parent` a significant predictor to the model?

Interpreting the output

```
Call:  
lm(formula = child ~ parent, data = Galton)  
  
Residuals:  
    Min      1Q  Median      3Q     Max  
-7.8050 -1.3661  0.0487  1.6339  5.9264  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept) 23.94153   2.81088   8.517 <2e-16 ***  
parent       0.64629   0.04114  15.711 <2e-16 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 2.239 on 926 degrees of freedom  
Multiple R-squared:  0.2105,    Adjusted R-squared:  0.2096  
F-statistic: 246.8 on 1 and 926 DF,  p-value: < 2.2e-16
```

- We can also use the **Estimate** values to write the equation of the regression line:

$$\widehat{child} = 23.94153 + 0.64629 \cdot parent$$

- For every one-inch increase in the parent height, the child height is predicted to increase by 0.64629 inches.
- e.g. if a parent is 70 inches, how tall will the child be? $23.94153 + 0.64629 \cdot 70 = 68.5$ inches (174 cm).

Interpreting the output

```
Call:  
lm(formula = child ~ parent, data = Galton)  
  
Residuals:  
    Min      1Q  Median      3Q     Max  
-7.8050 -1.3661  0.0487  1.6339  5.9264  
  
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Multiple R-squared:  0.2105,    Adjusted R-squared:  0.2096  
F-statistic: 246.8 on 1 and 926 DF,  p-value: < 2.2e-16
```

- **Residual standard error**: the standard deviation of the residuals.

- ▶ Interpretation: the average amount that the response will *deviate* from the true regression line.
- **degrees of freedom**: the number of observations minus the number of parameters being estimated. Used in hypothesis testing and calculating the standard error of the regression coefficients.

Interpreting the output

```
Call:  
lm(formula = child ~ parent, data = Galton)  
  
Residuals:  
    Min      1Q  Median      3Q     Max  
-7.8050 -1.3661  0.0487  1.6339  5.9264  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept) 23.94153   2.81088   8.517 <2e-16 ***  
parent       0.64629   0.04114  15.711 <2e-16 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 2.239 on 926 degrees of freedom  
Multiple R-squared:  0.2105,    Adjusted R-squared:  0.2096  
F-statistic: 246.8 on 1 and 926 DF,  p-value: < 2.2e-16
```

- **Multiple R-squared**: the proportion of variance (0-1) explained by the model (for simple linear regression).

- **Adjusted R-squared**: the proportion of variance (0-1) explained by the model, adjusted for the number of predictors (for multiple linear regression).
- Ranges from 0 to 1; $R^2 = 1$ is a perfect fit.
- “The proportion of variance in the response that is explained by **parent** : 21.05%.”

Interpreting the output

```
Call:  
lm(formula = child ~ parent, data = Galton)  
  
Residuals:  
    Min      1Q  Median      3Q     Max  
-7.8050 -1.3661  0.0487  1.6339  5.9264  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept) 23.94153   2.81088   8.517 <2e-16 ***  
parent       0.64629   0.04114  15.711 <2e-16 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 2.239 on 926 degrees of freedom  
Multiple R-squared:  0.2105,    Adjusted R-squared:  0.2096  
F-statistic: 246.8 on 1 and 926 DF,  p-value: < 2.2e-16
```

- **F-statistic**: the ratio of the variance explained by predictors, and the residual variance (variance not explained by predictors).
 - ▶ Also known as the partial F-test between the full model and the intercept-only (null) model.
- **p-value**: the probability that the F-statistic is greater than the observed value under the null hypothesis.
 - ▶ In a simple linear regression, the p-value for the slope coefficient is the same as the p-value for the F-statistic.

Hypothesis testing

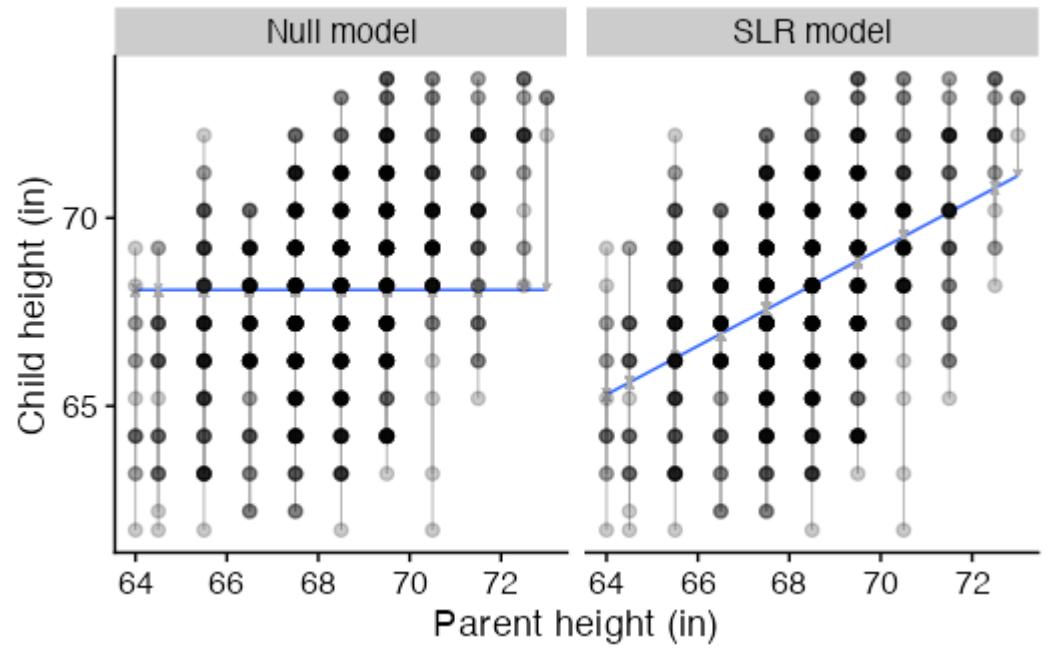
How does our null ($H_0 : \beta_1 = 0$) model compare to the linear ($H_0 : \beta_1 \neq 0$) model?

- In simple linear regression, the p-value for the slope coefficient is the same as the p-value for the F-statistic.

```
null_model ← Galton %>%
  lm(child ~ 1, data = .) %>%
  augment(Galton)
lin_model ← Galton %>%
  lm(child ~ parent, data = .) %>%
  augment(Galton)
models ← bind_rows(null_model, lin_model) %>%
  mutate(model = rep(c("Null model", "SLR model"), each = nrow(Galton)))

ggplot(data = models, aes(x = parent, y = child)) +
  geom_smooth(
    data = filter(models, model == "Null model"),
    method = "lm", se = FALSE, formula = y ~ 1, size = 0.5
  ) +
```

```
geom_smooth(  
  data = filter(models, model == "SLR model"),  
  method = "lm", se = FALSE, formula = y ~ x, size = 0.5  
) +  
geom_segment(  
  aes(xend = parent, yend = .fitted),  
  arrow = arrow(length = unit(0.1, "cm")),  
  size = 0.3, color = "darkgray"  
) +  
geom_point(alpha = .2) +  
facet_wrap(~model) +  
xlab("Parent height (in)") +  
ylab("Child height (in)")
```



What are we testing?

- The **null model** is a model with no predictors, i.e. $y = \beta_0 + \epsilon$
- The **alternative model** is a linear model with one predictor, i.e. $y = \beta_0 + \beta_1 x + \epsilon$
- We use the t-test to compare the two models:

$$t = \frac{\text{estimate} - 0}{\text{Standard error}} = \frac{\hat{\beta}_1 - 0}{SE(\hat{\beta}_1)}$$

where $SE(\hat{\beta}_1)$ is the standard error of the slope estimate:

$$SE(\hat{\beta}_1) = \frac{\hat{\sigma}}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2}}$$

i Note

If the model is **not significant**, then the null model (i.e. mean) is better. If the model **is significant**, then the linear model is better.

Reporting

Refresher on earlier steps

Galton collected data on the average height of both parents and their children. There was a moderate, positive, linear relationship ($r = 0.46$) between parent and child height.

Can we rely on our model results? Assumptions and hypothesis?

We fitted a linear model to predict child height from parent height, and model assumptions were met. The model was statistically significant ($R^2 = 0.21$, $F(1, 926) = 246.84$, $p < .001$), hence the null hypothesis was rejected in favour of the linear model. The effect of parent height is statistically significant and positive ($\beta = 0.65$, $t(926) = 15.71$, $p < .001$).

Equation? Inference?

For every one-inch increase in parent height, child height is predicted to increase by 0.65 inches ($\$ = 23.94 + 0.65 \text{ parent\$}$). The average height of both parents explains 21.05% of the variance in child height – there is an effect but there are clearly more factors at play.

Fun fact

- Galton's key finding was that children of tall parents are not as tall, children of short parents are not as short.

$$\widehat{\text{child}} = 23.94153 + 0.64629 \cdot \text{parent}$$

- e.g. if average parent height is 60 inches (152 cm), how tall will the child be? $23.94153 + 0.64629 \cdot 60 = 62.7$ inches (159 cm).
- e.g. if average parent height is 75 inches (191 cm), how tall will the child be? $23.94153 + 0.64629 \cdot 75 = 72.4$ inches (184 cm).
- The height of children appeared to **regress** towards the population mean, i.e. the concept of **regression to the mean**
- Hence the **Galton** is credited with coining the term **regression** (and also correlation, percentile, median, etc.)

Let's practice

Can we predict the weight of an alligator from its length? [Download data](#) 



Photo by Shelly Collins

Explore

Read the data:

```
library(readxl) # load the readxl package  
  
alligator ← read_excel(path = "data/ENVX1002_Lecture_wk10_data.xlsx",  
sheet = "Alligator") # read in the data
```

What does the data look like?

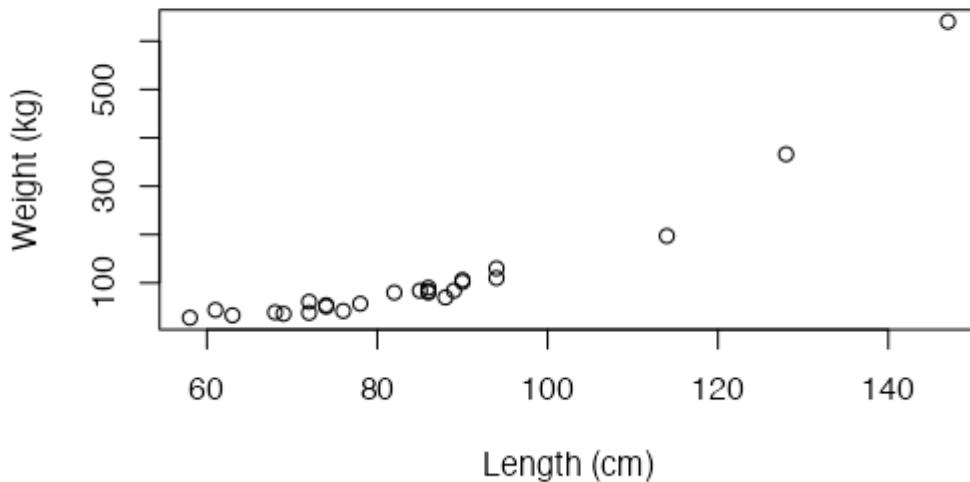
```
str(alligator)
```

```
tibble [25 × 2] (S3: tbl_df/tbl/data.frame)  
$ Length: num [1:25] 58 61 63 68 69 72 72 74 74 76 ...  
$ Weight: num [1:25] 28 44 33 39 36 38 61 54 51 42 ...
```

Plot

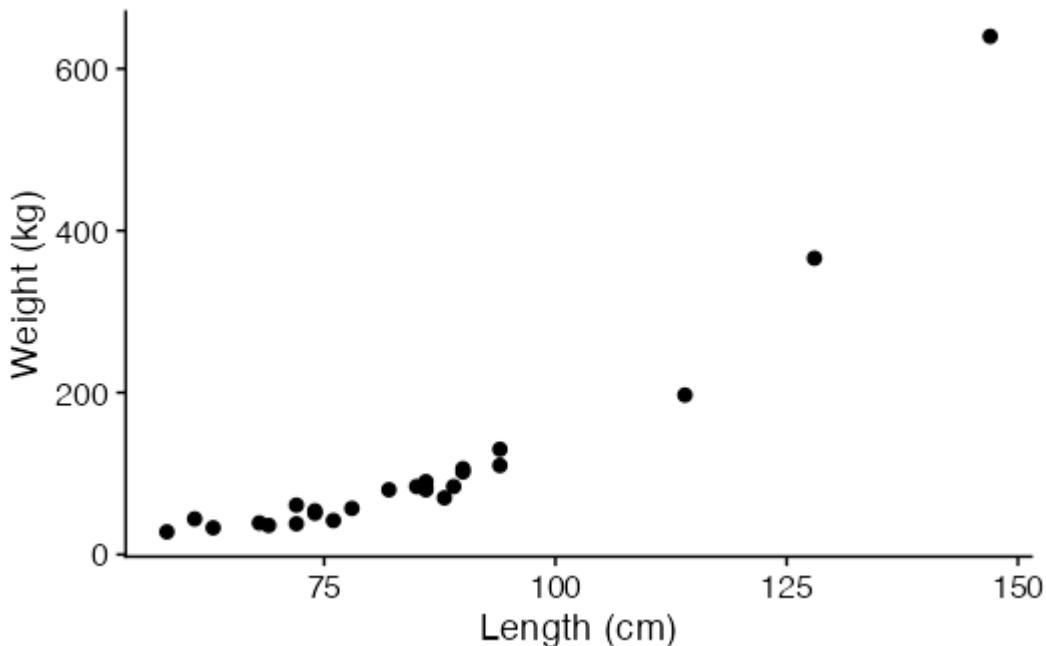
Using base R

```
plot(x = alligator$Length, y = alligator$Weight,  
     xlab = "Length (cm)", ylab = "Weight (kg)")
```



Using ggplot2

```
library(ggplot2) # load the ggplot2 package
ggplot(data = alligator, aes(x = Length, y = Weight)) +
  geom_point() +
  labs(x = "Length (cm)", y = "Weight (kg)")
```

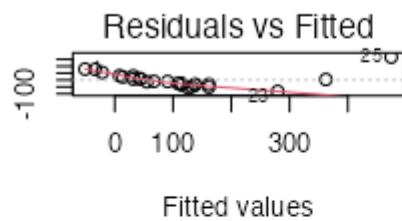


Plot residual diagnostics

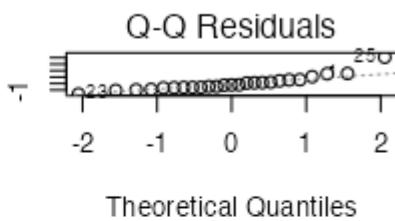
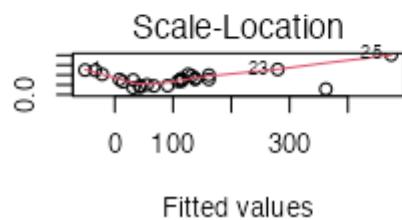
To check assumptions, we need to fit the model first, then plot the model.

```
fit ← lm(formula = Weight ~ Length, data = alligator)
par(mfrow = c(2, 2)) # set up a 2 x 2 grid for plots
plot(fit)
```

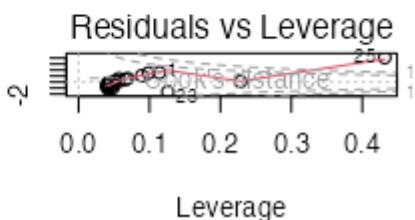
Residuals



Standardized residuals

 $\sqrt{|\text{Standardized residuals}|}$ 

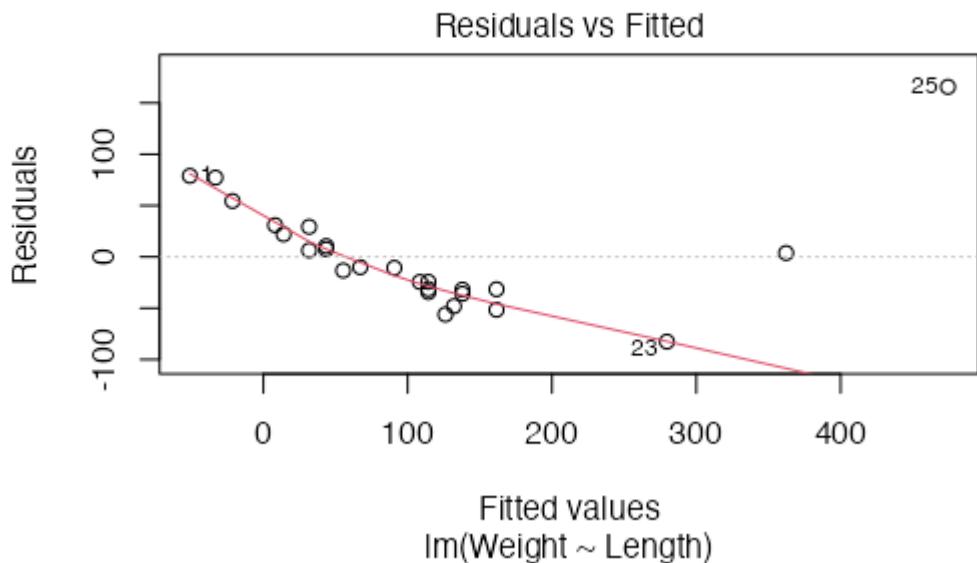
Standardized residuals



Check assumptions

Is the relationship linear?

```
plot(fit, which = 1)
```



If the linearity assumption is not met, there is no reason to validate the model since it is no longer suitable for the data.

Dealing with non-linearity: transform the data

```
library(patchwork)

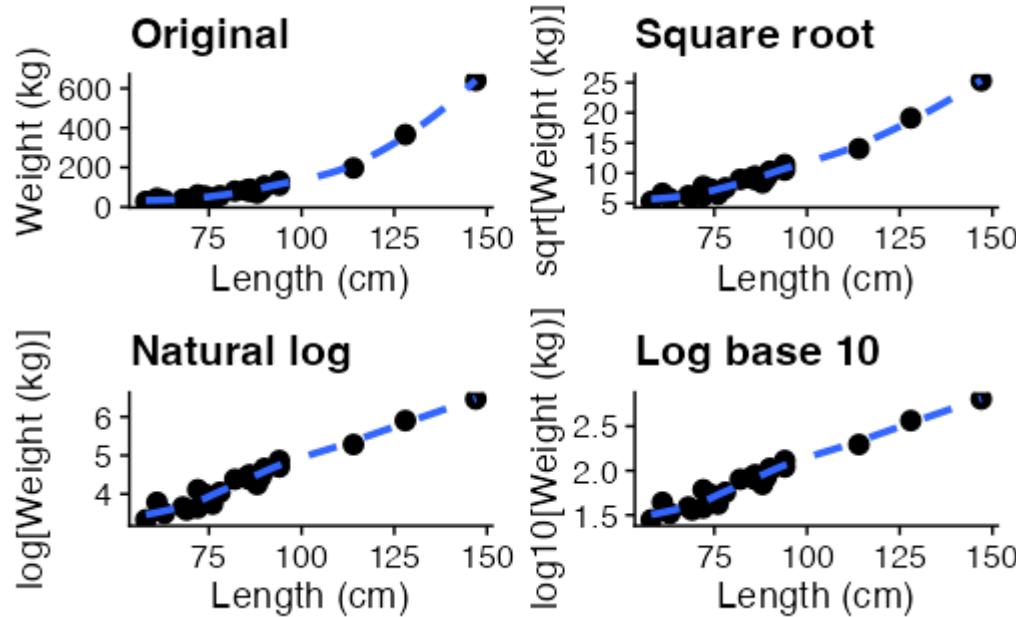
p1 ← ggplot(data = alligator, aes(x = Length, y = Weight)) +
  geom_point(size = 3) +
  labs(x = "Length (cm)", y = "Weight (kg)", title = "Original") +
  geom_smooth(se = FALSE, linetype = 2)

p2 ← ggplot(data = alligator, aes(x = Length, y = sqrt(Weight))) +
  geom_point(size = 3) +
  labs(x = "Length (cm)", y = "sqrt[Weight (kg)]", title = "Square root") +
  geom_smooth(se = FALSE, linetype = 2)

p3 ← ggplot(data = alligator, aes(x = Length, y = log(Weight))) +
  geom_point(size = 3) +
  labs(x = "Length (cm)", y = "log[Weight (kg)]", title = "Natural log") +
  geom_smooth(se = FALSE, linetype = 2)

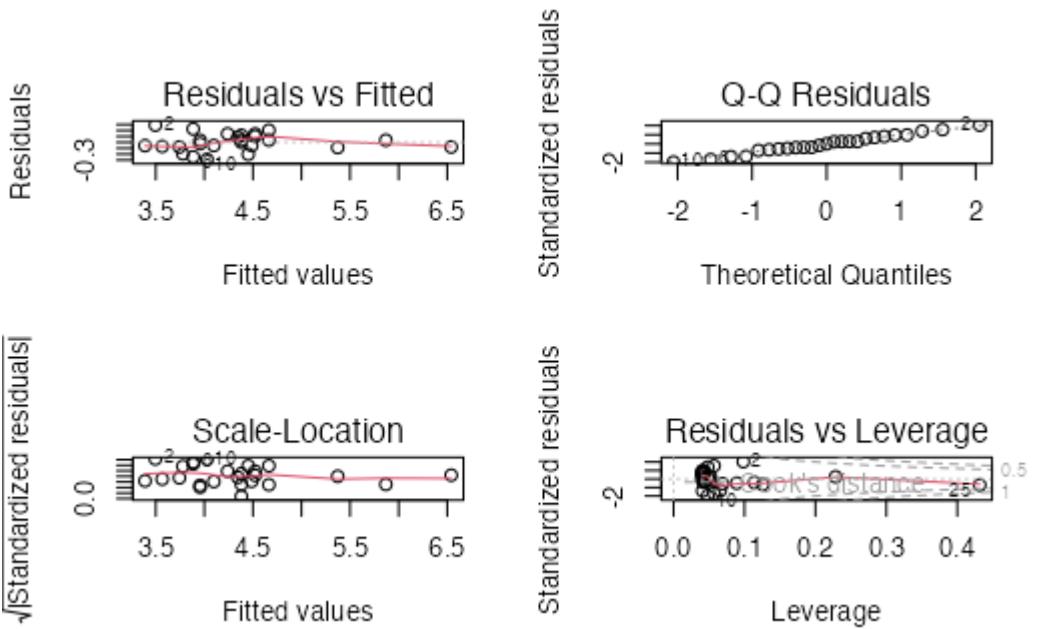
p4 ← ggplot(data = alligator, aes(x = Length, y = log10(Weight))) +
  geom_point(size = 3) +
```

```
labs(x = "Length (cm)", y = "log10[Weight (kg)]", title = "Log base 10") +  
geom_smooth(se = FALSE, linetype = 2)  
  
p1 + p2 + p3 + p4
```



Natural log transformation – Check assumptions again

```
fit <- lm(formula = log(Weight) ~ Length, data = alligator)
par(mfrow = c(2, 2)) # set up a 2 x 2 grid for plots
plot(fit)
```



Interpretation

```
summary(fit)
```

Call:

```
lm(formula = log(Weight) ~ Length, data = alligator)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.289266	-0.079989	0.000933	0.102216	0.288491

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)							
(Intercept)	1.335335	0.131394	10.16	5.63e-10 ***							
Length	0.035416	0.001506	23.52	< 2e-16 ***							

Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1

Residual standard error: 0.1493 on 23 degrees of freedom

```
Multiple R-squared:  0.9601,    Adjusted R-squared:  0.9583
F-statistic:  553 on 1 and 23 DF,  p-value: < 2.2e-16
```

- `Length` is a statistically significant predictor of `log(Weight)` ($p < .001$)
- The model explains a statistically significant and large proportion (96%) of variance ($R^2 = 0.96$, $F(1, 23) = 553$, $p < .001$)
- For every 1 cm increase in `Length`, `log(Weight)` increases by a value of 0.0354, `Weight` increases by $e^{0.0354}$ **times** and `Weight` increases by *approximately* 3.54%

Percent change with \ln transformation

Interpreting as a percent change can be more meaningful - it can be done with any log transformation (substitute e below for 10 or any other base), but the **quick approximation only works with natural log transformations**.

If y has been transformed with a natural log ($\log(y)$), for a one-unit increase in x the **percent change in y** (not $\log(y)$) is calculated with:

$$\Delta y\% = 100 \cdot (e^{\beta_1} - 1)$$

If β_1 is small (i.e. $-0.25 < \beta_1 < 0.25$), then: $e^{\beta_1} \approx 1 + \beta_1$. So $\Delta y\% \approx 100 \cdot \beta_1$.

β	Exact $(e^\beta - 1)\%$	Approximate $100 \cdot \beta$
-0.25	-22.13	-25
-0.1	-9.52	-10
0.01	1.01	1
0.1	10.52	10
0.25	28.41	25
0.5	64.87	50
2	638.91	200

- **y transformed:** a one-unit increase in x is *approximately* a $\beta_1\%$ change in y .
- **x transformed:** a 1% increase in x is *approximately* a $0.01 \cdot \beta_1$ change in y .
- **Both x and y transformed:** a 1% increase in x is *approximately* a $\beta_1\%$ change in y .

Summary

Workflow

1. **Understand the variables:** Which is the response variable? Is there a reason to believe a causal relationship?
2. **Explore data:** How many observations? Summary statistics? Scatterplot and correlation?
3. **Fit model**
4. **Check assumptions:** Remember - it's about the residuals! If assumptions fail, try transforming and return to Step 3. If assumptions *still* fail, consider another model and return to Step 3.
5. **Assess model fit:** Hypothesis test, significance, F-statistic, p-value. R^2 , how much model variation was explained by the model.
6. **Interpret output:** 'For every one-unit increase in x , y increases by β_1 units...' and any additional research/insight.

Thanks!

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