

REGRESSIONS

Correlations for the Advanced?



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1 The Basics

- Correlation Tests
- Regression Models
- Least Squares vs. Maximum Likelihood

2 Methods & Models

- Single Linear Regression
- Mixed Effect Models
- Generalised Linear Models

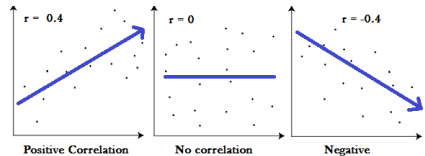
3 Choosing the Right Method

Terminology

Correlation is **not** necessarily **causation** (spurious correlations).

Correlation tests yield two measurements:

- r value (measure of correlation)
 - $r \approx 1$ (strong, positive correlation)
 - $r \approx 0$ (no correlation)
 - $r \approx -1$ (strong, negative correlation)
- p value (measure of statistical significance)



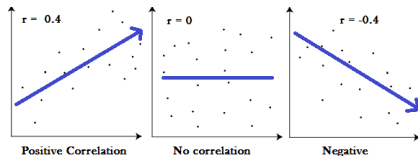
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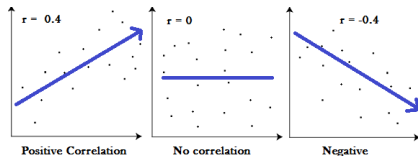
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Types of Correlations

These approaches are extremely useful in data exploration and for preliminary analyses!

Prominent correlation tests include:

- Contingency Coefficient
- Kendall's Tau
- Spearman Correlation
- Pearson Correlation
- Cramer's V
- ANalysis Of VAriance (ANOVA)
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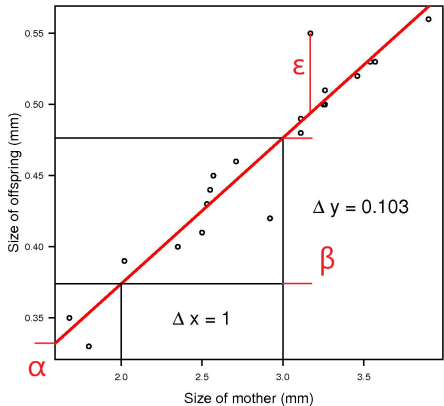
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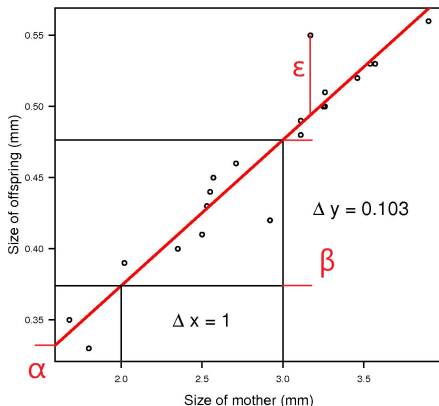
- α - The **Intercept**. The value of y when $x = 0$ (also referred to as β_0).
- β_i - The **Correlation Coefficient**. The increase in y for a one-unit increase in dependent variable i (usually, x if only one dependent variable).
- ϵ - The **Random Error**. The deviation of data points from the regression line. Usually assumed to follow $\epsilon \sim N(0, \sigma^2)$



Modified after Knut Helge Jensen.

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Assumptions in Theory

Linear regression models need to be inspected for violations of assumptions after regressing:

- **Residuals vs. Fitted values**

Non-linear patterns identify a non-linear relationship between dependent and independent variables.

- **Normal Q-Q plot**

Non-normal distribution of residuals shows that the assumption of $\epsilon \sim N(0, \sigma^2)$ is violated.

- **Scale Location**

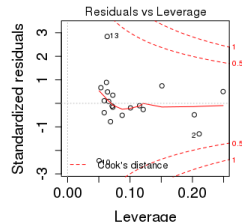
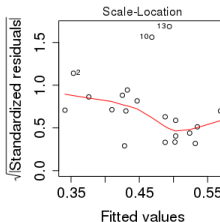
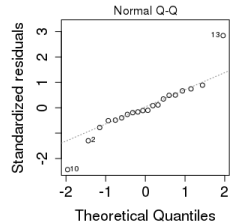
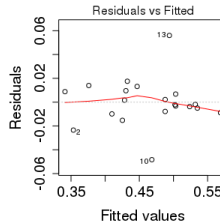
Non-constant variance identifies show that the assumption of homoscedasticity (invoked by least squares fitting).

- **Residuals vs. Leverage**

A non-zero trend identifies the presence of influential outliers.

Assumptions in R

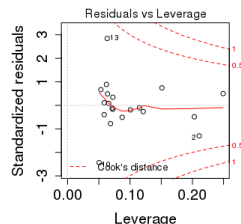
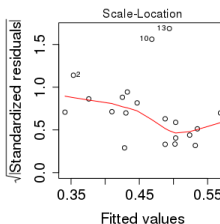
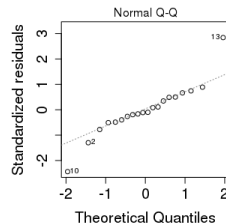
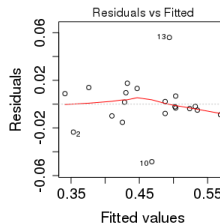
- Simply type `plot(...)` with `'...'` denoting your regression model.
- You can also target individual plots by writing:
 - `'plot(..., 1)'` for Residuals vs. Fitted values
 - `'plot(..., 2)'` for Normal Q-Q plot
 - `'plot(..., 3)'` for Scale Location
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By Knut Helge Jensen.

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Types of Regressions

Less model variables result in a more interpretable model!

Prominent regression approaches include the following:

- **Single Linear Regression**
- Multiple Linear Regression
- **Linear Mixed Effect Models**
- **Generalized Linear Models**
- Polynomial Regressions
- Generalized Additive Models
- Regression Splines
- Smoothing Splines
- Local Regressions
- ...

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Least Squares vs. Maximum Likelihood

These methods refer to **parameter estimation**.

Ordinary Least Squares (OSL):

- Used for most basic linear regressions
- obtain coefficient estimates $\hat{\beta}_0$ and $\hat{\beta}_1$ such that the linear model fits the available data well — that is, so that $\hat{y}_i \approx \hat{\beta}_0 + \hat{\beta}_1 x_i$ for $i = 1, \dots, n$.

Minimize:

$$RSS = \sum_{i=1}^n (y_i - \hat{y}_i)^2 \quad (1)$$

with $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$

Maximum Likelihood Estimation (MLE):

- Used in logistic regressions and generalized linear models
- estimates for β_0 and β_1 such that the predicted probability $\hat{Pr}(x_j)$ corresponds to the observed response variable status.

Maximize:

$$\ell(\beta_0, \beta_1) = \prod_{i: y_i=1} Pr(x_i) \prod_{i': y_{i'}=0} (1 - Pr(x_{i'})) \quad (2)$$

Purpose & Assumptions

Single linear regression

`lm()` in base R

Purpose: Identify whether and how two variables are related.

■ Down to *Study-Design*:

- Predictor variable is continuous (ratio or interval scale)
- Response variable is continuous (ratio or interval scale)
- Variable values are **independent** (not paired)

Assumptions:

■ Need for *Post-Hoc Tests*:

- Variable values follow **homoscedasticity** (equal variance across entire data range)
- Residuals follow normal distribution (**normality**)
- Absence of **influential outliers**
- Response and Predictor are related in a **linear** fashion

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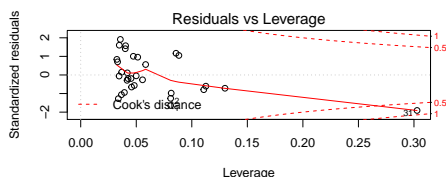
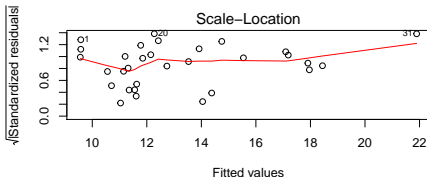
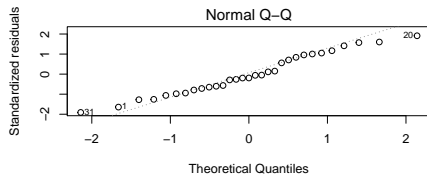
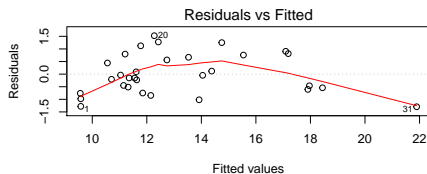
```
# measures of Diameter (labelled as Girth), Height, and Volume of Timber  
data("trees")  
head(trees)
```

##	Girth	Height	Volume
## 1	8.3	70	10.3
## 2	8.6	65	10.3
## 3	8.8	63	10.2
## 4	10.5	72	16.4
## 5	10.7	81	18.8
## 6	10.8	83	19.7

→ Let's see if there is a good regression to be had between *Girth* and *Volume*.

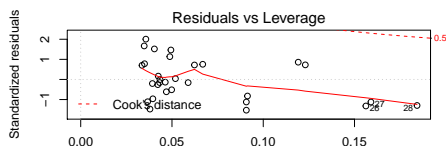
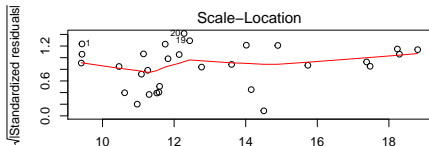
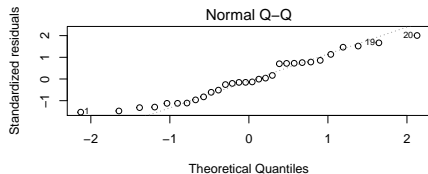
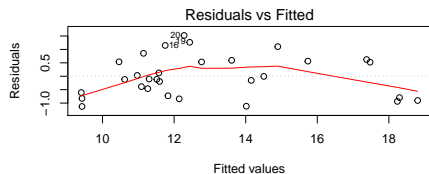
Example - The Model

```
SingleLin_Mod <- with(trees, lm(Girth ~ Volume))
par(mfrow=c(2,2))
plot(SingleLin_Mod)
```



Example - Refining The Model

```
trees <- trees[-31,] # removing the influential outlier in row 31
SingleLin_Mod <- with(trees, lm(Girth ~ Volume))
par(mfrow=c(2,2))
plot(SingleLin_Mod)
```



Example - Model Output

```
summary(SingleLin_Mod)
```

```
##
## Call:
## lm(formula = Girth ~ Volume)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.126 -0.699 -0.109  0.557  1.521
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   7.4141     0.3217    23.0  <2e-16 ***
## Volume        0.1954     0.0101    19.3  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.772 on 28 degrees of freedom
## Multiple R-squared:  0.93,    Adjusted R-squared:  0.928
## F-statistic: 374 on 1 and 28 DF,  p-value: <2e-16
```

At a Volume of 0, Girth is predicted to be 7.4141 (of course that doesn't make sense, not only is a volume of 0 biological nonsense, height also plays a part here for sure). For a one-unit increase in Volume, Girth is predicted to go up by 0.1954 inches (yes, they recorded in inches). Both estimates are statistically significant.

Purpose & Assumptions

Linear mixed effect model

`lme()` in base `nlme` package

Purpose: Identify whether and how variables are related.

- Down to *Study-Design*:

- Predictor variable is continuous (ratio or interval scale)
- Response variables are continuous (ratio or interval scale) and/or categorical (metric or ordinal scale)

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Fixed vs. Random Effects

Fixed effects and random effects are also referred to as fixed effect factors and random effect factors.

Fixed Effects:

- Informative factor levels regarding hypothesis.
- Want to study these levels and their effects.
- Factor levels are deliberate part of the study-design.
- Higher sample size \neq higher number of levels.

Random Effects:

- Uninformative factor levels regarding hypothesis.
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Example - The Data

```
# measures of Weight, Diet, Time, and Chicks  
data("ChickWeight")  
head(ChickWeight)
```

```
##      weight  Time  Chick  Diet  
## 1         42     0      1     1  
## 2         51     2      1     1  
## 3         59     4      1     1  
## 4         64     6      1     1  
## 5         76     8      1     1  
## 6         93    10      1     1
```

→ Let's see if there is a good regression to be had between *weight* and *Time* while accounting for random effects belonging to *Chick*, and fixed effects of *Diet*.

Example - The Model

```
library(nlme)
MultiLin_Base <- lme(weight ~ Time*Diet, # weight as an interaction of time and diet
  random = ~+1|Chick, # random effect of Chick
  data = ChickWeight)
```

We now have our model. However, we know that time is a component and we likely have repeated samples here. In these cases, we need to account for auto-correlation by defining a correlation structure.

```
MultiLin_Mod <- lme(weight ~ Time*Diet, random = ~+1|Chick,
  cor=corAR1(), # adding autocorrelation structure since we have repeated measures
  data = ChickWeight)
```

Let's see which model (basic or the one with auto-correlative structure) performs better:

```
anova(MultiLin_Base, MultiLin_Mod) # second model is better
```

##	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
##	MultiLin_Base	1 10	5487	5530	-2734			
##	MultiLin_Mod	2 11	4457	4505	-2217	1 vs 2	1032	<.0001

We clearly prefer the more sophisticated, auto-correlative model and want to see which of its parameters are informative:

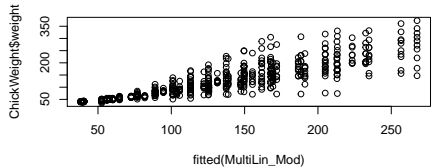
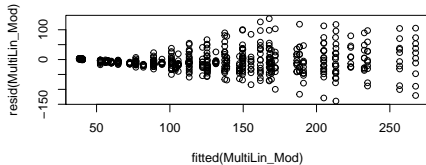
```
anova(MultiLin_Mod) # all parameters should be kept
```

##		numDF	denDF	F-value	p-value
##	(Intercept)	1	524	485.8	<.0001
##	Time	1	524	1436.8	<.0001
##	Diet	3	46	3.5	0.0219
##	Time:Diet	3	524	24.9	<.0001

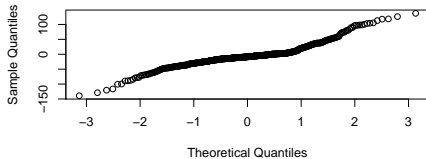
We keep all parameters. Although the inclusion of `Diet` is not significant, the interaction of `Diet` and `Time` is, therefore, both `Time` and `Diet` need to stay irrespective of their significance.

Example - Assessing the Model

```
par(mfrow=c(2,2))
plot(fitted(MultiLin_Mod), resid(MultiLin_Mod)) # values around 0 -> good
plot(fitted(MultiLin_Mod), ChickWeight$weight) # pattern fuzzy, but linear -> good
qqnorm(resid(MultiLin_Mod)) # residuals are not normal distributed -> bad
```



Normal Q-Q Plot



Example - Model Output

```
summary(MultiLin_Mod)
```

```
## Linear mixed-effects model fit by REML
## Data: ChickWeight
##      AIC   BIC logLik
##  4457 4505  -2217
##
## Random effects:
## Formula: ~+1 | Chick
##      (Intercept) Residual
## StdDev:    0.006581    42.46
##
## Correlation Structure: AR(1)
## Formula: ~1 | Chick
## Parameter estimate(s):
##      Phi
## 0.9706
## Fixed effects: weight ~ Time * Diet
##              Value Std.Error DF t-value p-value
## (Intercept) 40.42      9.487 524   4.260 0.0000
## Time         6.06      0.350 524  17.347 0.0000
## Diet2        -0.88     16.430  46  -0.054 0.9575
## Diet3        -2.19     16.430  46  -0.133 0.8944
## Diet4        -1.01     16.431  46  -0.062 0.9512
## Time:Diet2    2.21      0.589 524   3.749 0.0002
## Time:Diet3    4.86      0.589 524   8.250 0.0000
## Time:Diet4    3.13      0.592 524   5.297 0.0000
## Correlation:
##      (Intr) Time    Diet2  Diet3  Diet4  Tm:Dt2 Tm:Dt3
## Time      -0.358
```

Example - Model Output Explained

Variance between chicks (0.006581) than residual variance (42.46). This is good!

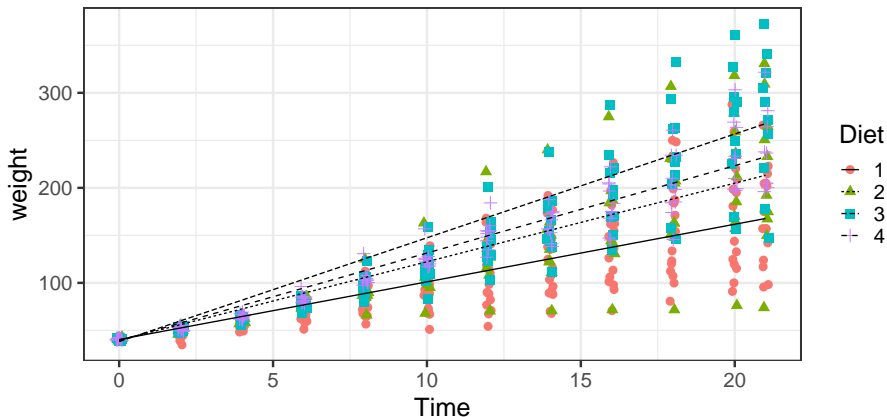
A chick is expected to have a `weight` of 40.4165 at `Time = 0` and `Diet = 1`. Per time-step, `weight` is expected to increase by 6.0637.

Mean chick `weight` is different to (read: “Diet1 weights are smaller by”) `Diet = 1` by -0.8794, -2.1932, and -1.0109 for `Diet = 2`, `Diet = 3`, and `Diet = 4` respectively (take note that these differences aren’t statistically significant).

`weight` of chicks increases, on average, increases by 2.2077 units more per one-unit increase in time when compared to `Diet = 1`. The same logic applies to `Diet = 3`, and `Diet = 4`.

Example - Model Output Visualised

```
library(ggplot2)
ChickWeight$fit <- predict(MultiLin_Mod, level=0)
ggplot(ChickWeight, aes(Time, weight)) +
  geom_jitter(aes(colour=Diet, shape=Diet), width=0.1, size=3) +
  theme_bw(base_size=20) +
  geom_line(aes(y=fit, lty=Diet))
```



Purpose & Assumptions

Generalized Linear Models

`glm()` in base R

Purpose: Identify whether and how variables are related.

■ Down to *Study-Design*:

■ Variable values are **independent** (not paired)

Assumptions: ■ Need for *Post-Hoc Tests*:

■ Absence of **influential outliers**

■ Response and Predictor are related in a **linear** fashion

→ Allow for **non-normal** distributions and **heteroscedasticity**

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Linear Predictor, Link Function, and Variance Function

Components of a Generalized Linear Model:

1 Linear predictor e.g.: $y_i = \alpha + \beta_1 + x_i$

2 Link function $g(\hat{y}_i) = y_i$

Relationship between predictor value and estimated value.

3 Variance function $var(y_i) = \phi V_i(\bar{x})$

Variance depends on predictor mean, dispersion parameter ϕ is a constant

Which **combinations** of components do I use?

Error	Link function	Variance function	Typical type of data
normal	identity	1 (constant)	Textbook examples
Poisson	\log	$var = \bar{x}$	Count data
binomial	$\text{logit}, \log(\bar{x}/(1 - \bar{x}))$	$var = \bar{x}(1 - \bar{x})/n$	Binary data

Linear Predictor, Link Function, and Variance Function

Components of a Generalized Linear Model:

1 Linear predictor e.g.: $y_i = \alpha + \beta_1 + x_i$

2 Link function $g(\hat{y}_i) = y_i$

Relationship between predictor value and estimated value.

3 Variance function $var(y_i) = \phi V_i(\bar{x})$

Variance depends on predictor mean, dispersion parameter ϕ is a constant

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Example - The Data

```
data("ChickWeight")
```

```
head(ChickWeight)
```

```
## Grouped Data: weight ~ Time | Chick
```

```
##   weight Time Chick Diet
```

```
## 1      42    0     1    1
```

```
## 2      51    2     1    1
```

```
## 3      59    4     1    1
```

```
## 4      64    6     1    1
```

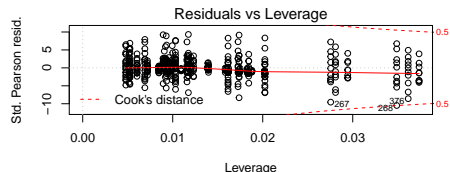
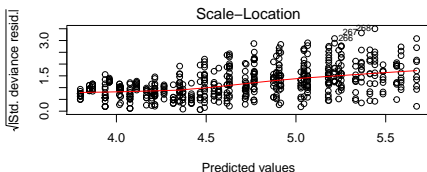
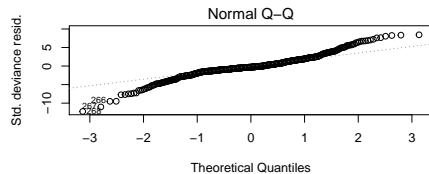
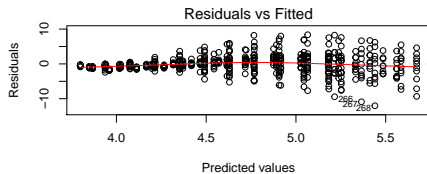
```
## 5      76    8     1    1
```

```
## 6      93   10     1    1
```

→ Let's reassess our earlier analysis of chick **weight** as a function of **time** and **diet**. This time, we will forego the random effect of chicks since that would create a generalized linear mixed effect model.

Example - The Model

```
GeneralLin_Mod <- glm(weight ~ Time*Diet, family = poisson, data = ChickW)
par(mfrow=c(2,2))
plot(GeneralLin_Mod)
```



Example - Model Output

```
summary (GeneralLin_Mod)

##
## Call:
## glm(formula = vs ~ wt + disp, family = binomial, data = mtcars)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.675   -0.284   -0.084    0.573    2.082
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.6086     2.4390   0.66   0.510
## wt            1.6264     1.4907   1.09   0.275
## disp         -0.0344     0.0154  -2.24   0.025 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 43.86  on 31  degrees of freedom
## Residual deviance: 21.40  on 29  degrees of freedom
## AIC: 27.4
##
## Number of Fisher Scoring iterations: 6
```

As you can see, the estimates to earlier have changed drastically.

Example - Model Output Explained

A chick is now expected to have a `weight` of 3.7988 at `Time = 0` and `Diet = 1`. Per time-step, `weight` is expected to increase by 0.0692.

Mean chick `weight` of `Diet = 1` is smaller by 0.0686, 0.0506, and 0.1616 for `Diet = 2`, `Diet = 3`, and `Diet = 4` respectively (these differences are now significant).

`weight` of chicks increases, on average, increases by 0.0056 units more per one-unit increase in time when compared to `Diet = 1`. The same logic applies to `Diet = 3`, and `Diet = 4`.

Choices, Choices, Choices...

- **Linear Model** `lm`. When all **assumptions are met** (i.e.: homoscedasticity, normality, independence).
- **Linear Mixed Effect Model** `lme`. When the assumption of **independence is violated**.
- **Generalized Linear Model** `glm`. When the assumptions of **homoscedasticity** and **homoscedasticity** are **violated**.
- **Generalized Linear Mixed Effect Model** `glmmPQL` from MASS, or `glmer` from `lme4`. When the assumptions of **homoscedasticity**, **homoscedasticity**, and **independence** are **violated**.