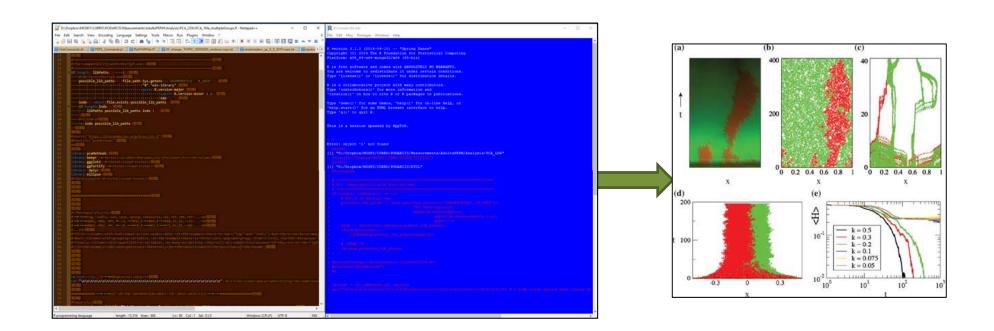


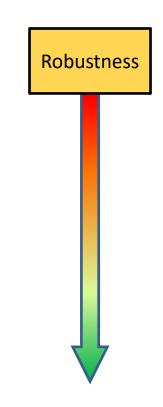
# Use of R environment in **Evolutionary Ecology**



### Remember this?

### **ANOVA**

Continuous (numerical)
Samples are chosen randomly
Normal distribution for each group
Homoscedasticity
Degrees of freedom =  $n-1 \ge 2$ 



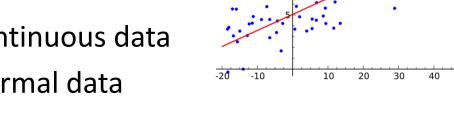
- Preferred because more powerful finding differences
- Data needs to be Normal to fit the predicted distribution
- One of many analysis based on the general linear model

### GENERAL LINEAR MODELS

Simple analysis based on linear regression



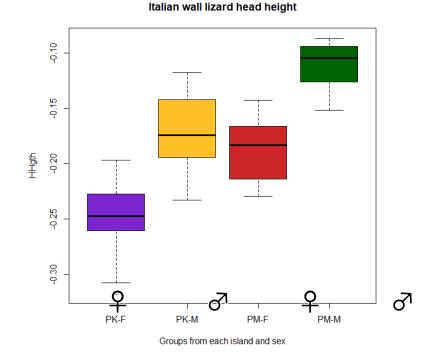
- can **not** handle **not** Normal data
- Can only handle a few variables at the same time



ANOVA, ANCOVA, MANOVA, MANCOVA, t-test, F-test...

Categorical variable = **explanatory variable**: Group (Sex+Population) Continuous variable = **response variable**: Head Height

Are there significant differences in the response variable between groups?





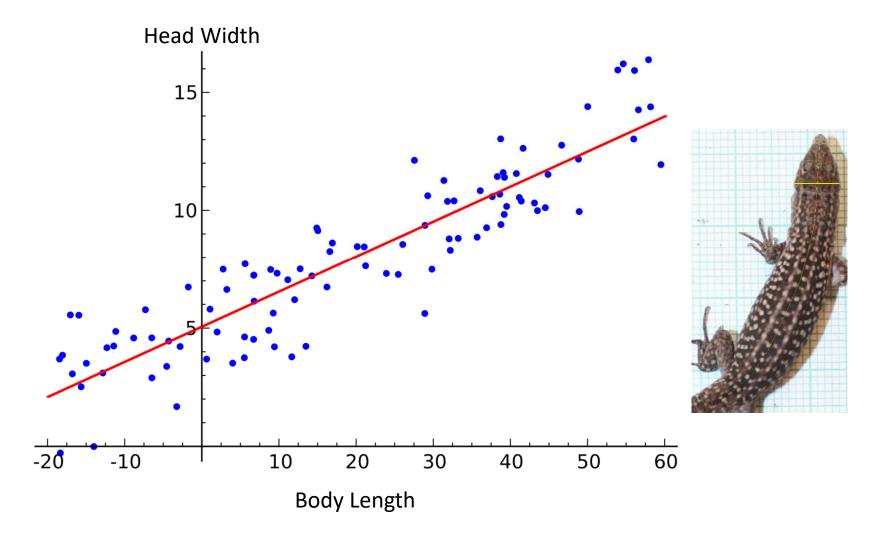
Until now the question was:

Are there significant differences in the response variable (Head Height) between groups?

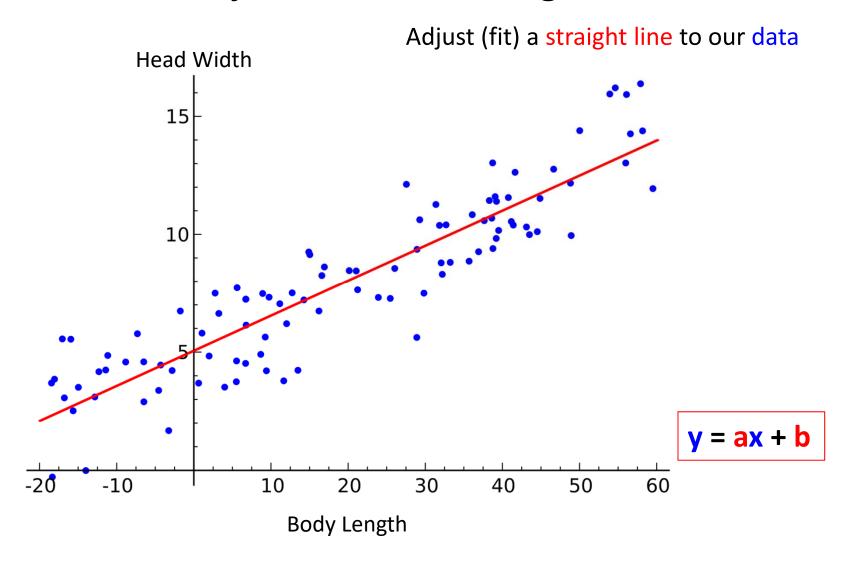
How linear models work:

- 1.- Our data is adjusted to a linear model
- y = ax + b
- 2.- The model **PREDICTS** the expected values of Head Width acording to another variable (Group, Body Length, etc.)
- 3.- Then compares expected values with real values

How do linear models make predictions?



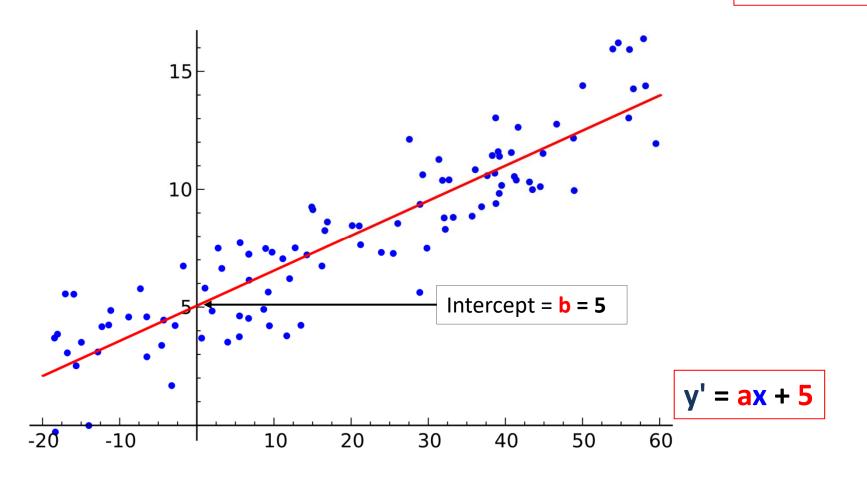
### 1. Data is adjusted to linear regression model:



### 2. Calculate expected values:

Predict value of y from x (we need a and b)

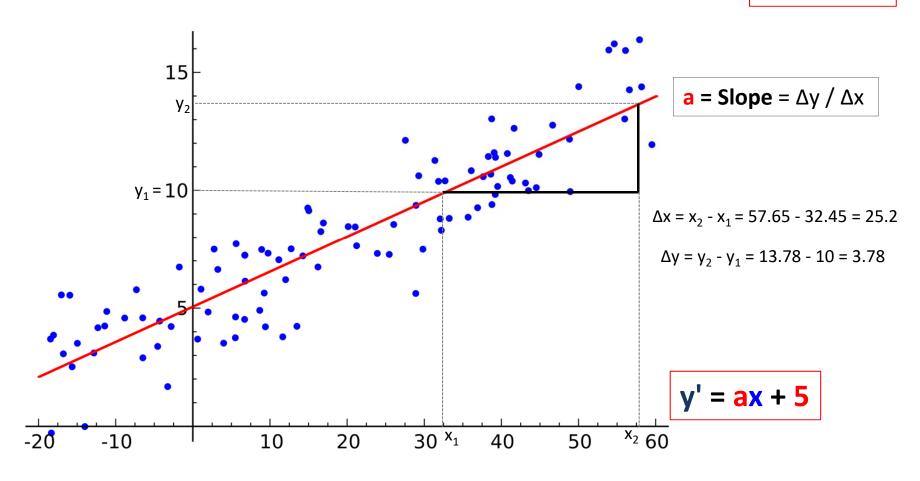
$$y = ax + b$$



### 2. Calculate expected values:

Predict value of y from x (we have b, still need a)

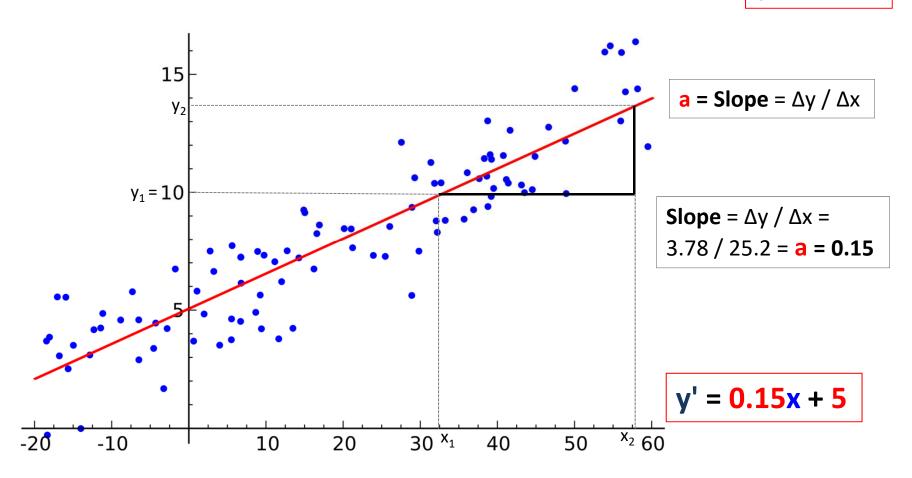
$$y = ax + b$$



### 2. Calculate expected values:

Predict value of y from x (we have b, still need a)

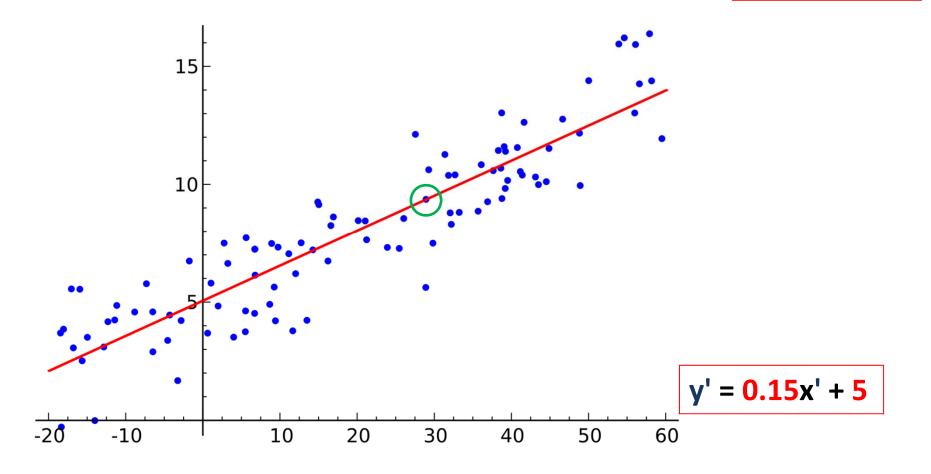
$$y = ax + b$$



### 2. Calculate expected values:

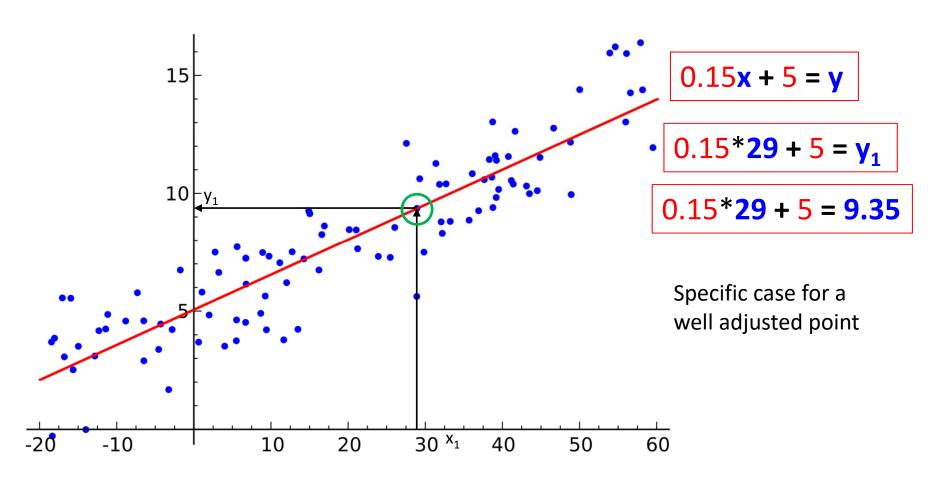
**Now** we can predict value of **y** from **x** 

$$y = 0.15x + 5$$



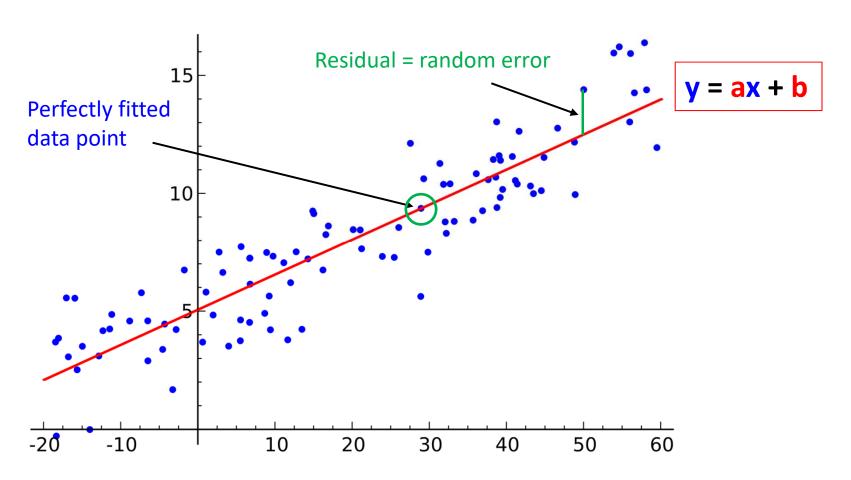
### 2. Calculate expected values:

**Now** we can predict value of **y** from **x** 

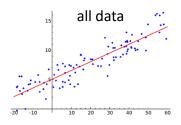


### 3. Compare expected values with real values:

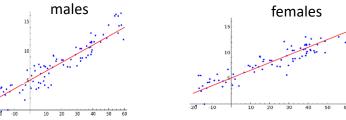
difference (expected – observed) = error



Linear models first adjust all data and predict values



Then adjust again the data but **for each group independently** and predict values again.

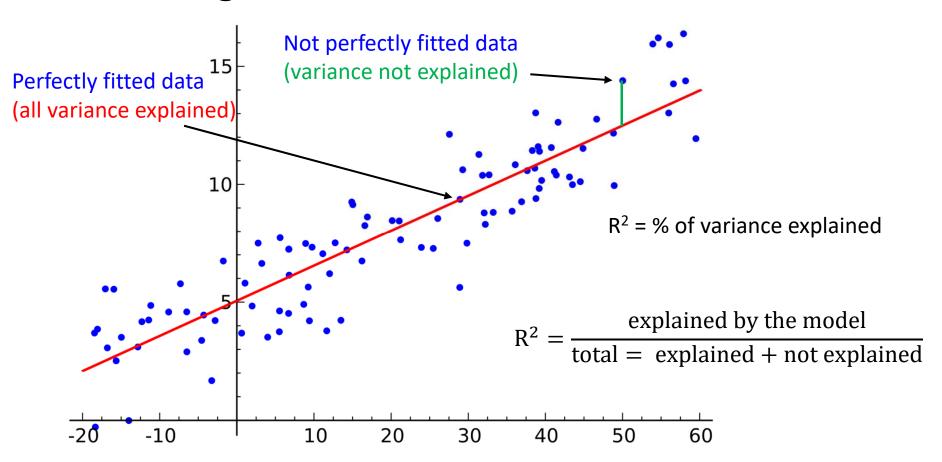


Then compares:

Which prediction is better the one from the model with all data or from the model adjusted separately for each group?

Better = smaller "error"

Linear regression model: Goodness of fit



### General Linear Models

We already know how to run one **linear model** in **R**: ANOVA aov (response~explanatory, data) aov (Head Height ~ Group, data=dataset)

We could tell **R** to run a **general linear model**Linear model -> **lm()** 

- Will assume **normality**
- Will choose the analysis according to our data
  - Response is continuous; Explanatory is categorical/discrete -> **ANOVA**
  - Response is continuous; Explanatory is continuous -> linear regression

### General Linear Models

#### Im ()

- Needs to be normal distributed
- Only one continuous response variable
- One or more (few) explanatory variables (categorical or continuous)

Data Distribution	Response variable	Explanatory variable	# Predictors	Test
Normal	continuous	discrete	one	One-way ANOVA
Normal	continuous	discrete	multiple	Multi-way ANOVA
Normal	continuous	continuous	one	Linear regression
Normal	continuous	continuous	multiple	Multiple regression
Normal	continuous	discrete & continuous	multiple	ANCOVA

# General Linear Models

```
Im ( response ~ explanatory, data=dataset )
Im (Head Width~ Group)
                                                      One-way ANOVA
                                             ->
Im (Head Width ~ Pop*Sex)
                                                      Multi-way ANOVA
                                             ->
Im (Head Width ~ Body Length)
                                                      Linear Regression
                                             ->
Im (Head Width ~ Jaw Length*Body Length)
                                                      Multiple Regression
                                             ->
Im (Head Width ~ Body Length *Group )
                                                      ANCOVA
                                             ->
```

Data Distribution	Response variable	Explanatory variable	# Predictors	Test
Normal	continuous	discrete	one	One-way ANOVA
Normal	continuous	discrete	multiple	Multi-way ANOVA
Normal	continuous	continuous	one	Linear regression
Normal	continuous	continuous	multiple	Multiple regression
Normal	continuous	discrete & continuous	multiple	ANCOVA

### GENERAL LINEAR MODELS

### Agrupation of Linear Models

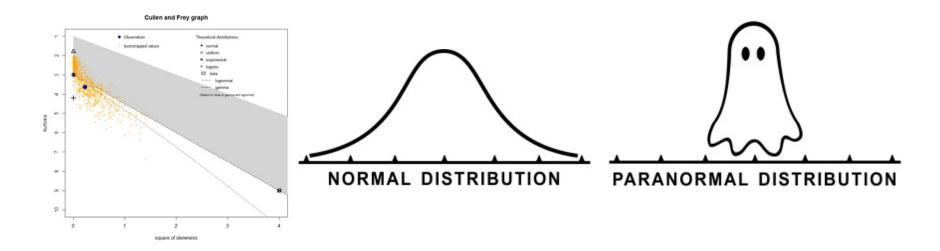
- Handle only continuous response variables
- Handle only data with Normal distributions
- Only one type of regression (linear)
- Only one response variable
- Handle a few explanatory variables
- Significance checked by maximum likelihood (p-value)

### OTHER DISTRIBUTIONS?

If distribution does not fit the Normal distribution:

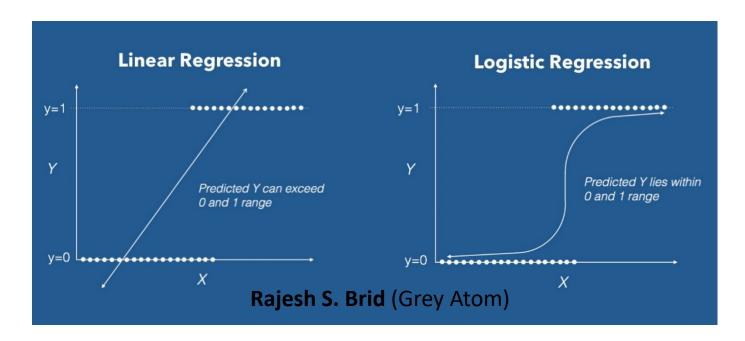
transformation of dataset (log?)
 OR

use of low-power non parametric tests (Kruskal-Wallis)



### OTHER REGRESSIONS?

- Logistic regression (1/0; yes/no; male/female)
- Poisson regression (discrete and ordinal data)



### GENERAL LINEAR MODELS

### Agrupation of Linear Models

- Handle only continuous response variables
- Handle only data with Normal distributions
- Only one type of regression (linear)
- Only one response variable
- Handle a few explanatory variables
- Significance checked by maximum likelihood (p-value)

### GENERALIZED LINEAR MODELS

#### **Generalization** of **General** Linear Models

- Response variable can be from continuous to categorical
- Handle data with Normal or other distributions
- Adjust model to linear and other regressions
- Handle many variables at the same time and their interactions (N/10)

# GENERALIZED LINEAR MODELS

#### Regressions:

Linear, multivariate, logistic, Poisson's

#### Distributions:

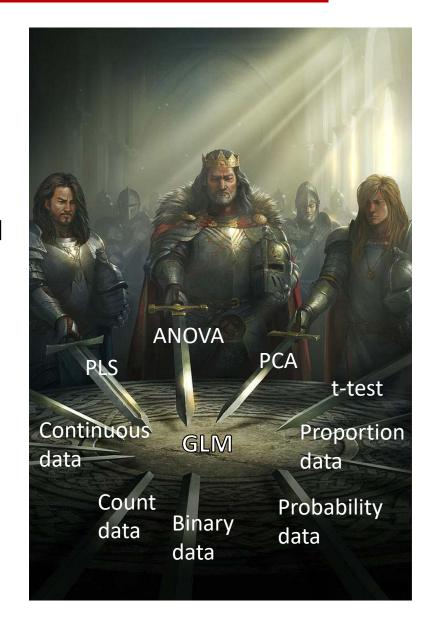
Normal, Poisson, Binomial, Multinomial

#### Significance:

Maximum likelihood, Bayesian, and least squares

#### Data:

Continuous, Count, Probability, Frequency, Binary, etc.



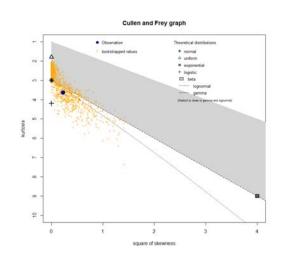
### **GLM** LINK FUNCTIONS

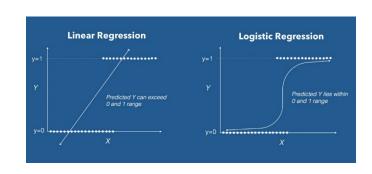
#### Link function links the explanatory variables

Link function for linear regression

$$y = ax + b$$

GLM handles many types of data, regressions, and models We need to tell R which kind of link function will need to apply





### **GLM** LINK FUNCTIONS

#### Don't need to transform data to fit it in a distribution

You tell GLM to which **family** (type of data) belongs your data and it will choose the right link function to process it!

### Which Link function?

Tell GLM to which FAMILY belongs our data:



**Family** is a combination of data characteristics and distributions: Continuous / categorical, includes zeros (0), does not include zeros, has negative values, only positive, type of distribution, etc.

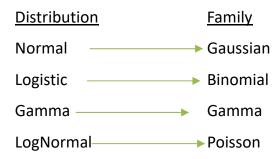
# Rules of thumb to choose "family"

DATA	FAMILY
Normal Distribution	Gaussian
Positive continuous data, no zeros	→ Gamma
Gamma distribution	Gamma
Binary data (y/n)	→ Binomial
Proportions (3:1)	→ Binomial
Logistic distribution	→ Binomial
Counts	→ Poisson
Categorical (SD= ȳ)	→ Poisson
Poisson distribution ————————————————————————————————————	Poisson
Log Normal distribution	Poisson
Other categorical ————————————	Negative binomial

# If we doubt which family fits better

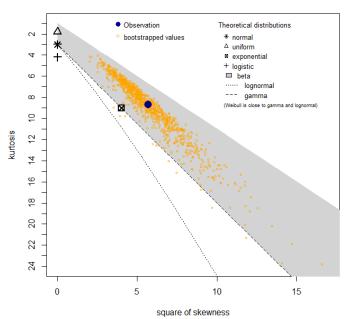
#### fitdistrplus()

Check the fit of some typical distributions with **descdist()** plot



Check other specific distributions with fitdist()

#### **Cullen and Frey graph**



# Running GLMs

- 1. Choose variables, choose a family
- 2. If not sure, or want to be extra sure: fitdistr()
  - descdist()
- 3. run the analysis and check if model is well fitted

```
glm ( response(s)~predictor(s), family, data )
```



Understanding

# **OUTPUTS**

**GENERALIZED LINEAR MODELS (open RStudio)** 

```
> summary(glm1)
Call:
glm(formula = Sex ~ Pop, family = "binomial", data = morelizards)
Deviance Residuals:
    Min 10 Median 30
                                   Max
 -1.317 -1.317 1.044 1.044 1.127
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) 3.228e-01 2.026e-01 1.593 0.111
         7.837e-16 2.865e-01 0.000 1.000
  PK
  PM -2.026e-01 2.849e-01 -0.711 0.477
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 411.06 on 299 degrees of freedom
Residual deviance: 410.39 on 297 degrees of freedom
AIC: 416.39
Number of Fisher Scoring iterations: 4
```

```
> summary(glm1)
Call:
glm(formula = Sex ~ Pop, family = "binomial", data = morelizards)
Deviance Residuals:
           10 Median
     Min
                              30
                                       Max
  -1.317 -1.317 1.044 1.044
                                      1.127
      HOW WELL ADJUSTED IS THE MODEL?
Coeff
      AIC can be used to compare with other models, but is not an absolute
 (Intercept) 3.228e-01 2.026e-01 1.593
                                            0.111
           7.837e-16 2.865e-01 0.000 1.000
   PK
   PM
            -2.026e-01 2.849e-01 -0.711 0.477
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  -1.317 -1.317 1.044 1.044 1.127
       HOW WELL ADJUSTED IS THE MODEL?
Coeff
       AIC can be used to compare with other models, but is not an absolute
 (Inter
       Compare how well our data fits each distribution with:
   PK
        Akaike Information Criterion (AIC)
   PM
       The lower the value the better.
 (Dispe
    Null deviance: 411.06 on 299 degrees of freedom
Residual deviance: 410.39 on 297 degrees of freedom
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Number of Fisher Scoring iterations: 4
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              10 Median
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                               30
                                       Max
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                                      1.127
      HOW WELL ADJUSTED IS THE MODEL?
Coeff.
      There is no R<sup>2</sup> we need to calculate ourselves
(Intercept) 3.228e-01 2.026e-01 1.593
                                            0.111
           7.837e-16 2.865e-01 0.000 1.000
   PK
   PM
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(Dispersion parameter for binomial family taken to be 1)
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Call:
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Deviance Residuals:
      Min 10 Median 30
                                               Max
  -1.317 -1.317 1.044 1.044 1.127
       HOW WELL ADJUSTED IS THE MODEL?
Coeff
       There is no R<sup>2</sup> we need to calculate ourselves
(Inter
          R^2 = \frac{\text{Null deviance - Residual deviance}}{\text{Null deviance - Residual deviance}} = \frac{411.06 - 410.39}{\text{Null deviance - Residual deviance}}
   PK
                                                                     - = 0.0016
                         Null deviance
                                                            411.06
   PM
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 411.06 on 299 degrees of freedom
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Call:
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Deviance Residuals:
                 10 Median
     Min
                                     30
                                              Max
  -1.317 -1.317 1.044
                                 1.044
                                            1.127
       HOW WELL ADJUSTED IS THE MODEL?
Coeff
       Rule of Thumb:
(Inter
       If: degrees of freedom*2 < Residual deviance \longrightarrow Data are overdispersed
   PM
                                       Fit is not great, but
                297*2 = 594 \ge 410.39 \longrightarrow
                                       data are not overdispersed 🗸
(Dispe
    Null deviance: 411.06 on 299 degrees of freedom
Residual deviance: 410.39 on 297 degrees of freedom
AIC: 416.39
Number of Fisher Scoring iterations: 4
```

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Deviance Residuals:
          10 Median
    Min
                            30
                                     Max
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Number of Fisher Scoring iterations: 4
```

```
> summary(glm1)
Call:
glm(formula = Sex ~ Pop, family = "binomial", data = morelizards)
Deviance Residuals:
                                             Each "free" group/covariable
           10 Median
     Min
                              30
                                        Max
                                             comparison against the
  -1.317 -1.317 1.044 1.044
                                       1.127
                                             intercept. Interesting, but not
                                             super useful
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) 3.228e-01 2.026e-01 1.598
                                             0.111
             7.837e-16 2.865e-01 0.000
                                             1.000
   PK
   PM
            -2.026e-01 /2.849e-01 -0.711
                                             0.477
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 411.06 on 299 degrees of freedom
Residual deviance: 410.39 on 297 degrees of freedom
AIC: 416.39
Number of Fisher Scoring iterations: 4
```



#### https://tinyurl.com/evolecopract

--> morelizards.csv and fifth\_linear\_models.R

**GLM** Libraries: fitdistrplus, car, boot

- 1. Choose variables (discrete or continuous, all allowed)
- 2. Plot the distribution: descdist(variable)
- 3. Fit your data to distributions that make sense for your type of data and compare how well they fit

fit1<-fitdistr(na.omit(variable), "negative binomial")

AIC (fit1, fit2, ...) #The lowest the better

- Choose the families that better adjust to your data: gaussian, poisson, poisson, Gamma, binomial, negative.binomial
- 5. Perform glm()

glm(response~explanatory, family=negative.binomial, data=dataset)

- 6. Check AIC, calculate R<sup>2</sup> and "degrees of freedom vs variance"
- 7. Perform an ANOVA with the output: aov(glm\_output)
- 8. Are there significant effects for the chosen variables?
- 9. Plot

