R Worship Day 3: Intro to Statistics in R

Drew Allen

Getting Started

- Start a new project in a new directory in R Studio
- Download the files we will be using today into this new directory:
  - `shells.csv`
  - `gala.txt`
  - `mangroves.csv`
  - `rats.csv`
  - **`binary.csv`**
  - **`dioxin.csv`**

Topics Covered

- Statistical Distributions
- Summary Statistics
- T-tests
- Regression (simple linear, multiple linear)
- Analysis of Variance
  - One-way ANOVA
  - Two-way ANOVA
  - ANCOVA
- Generalised linear models

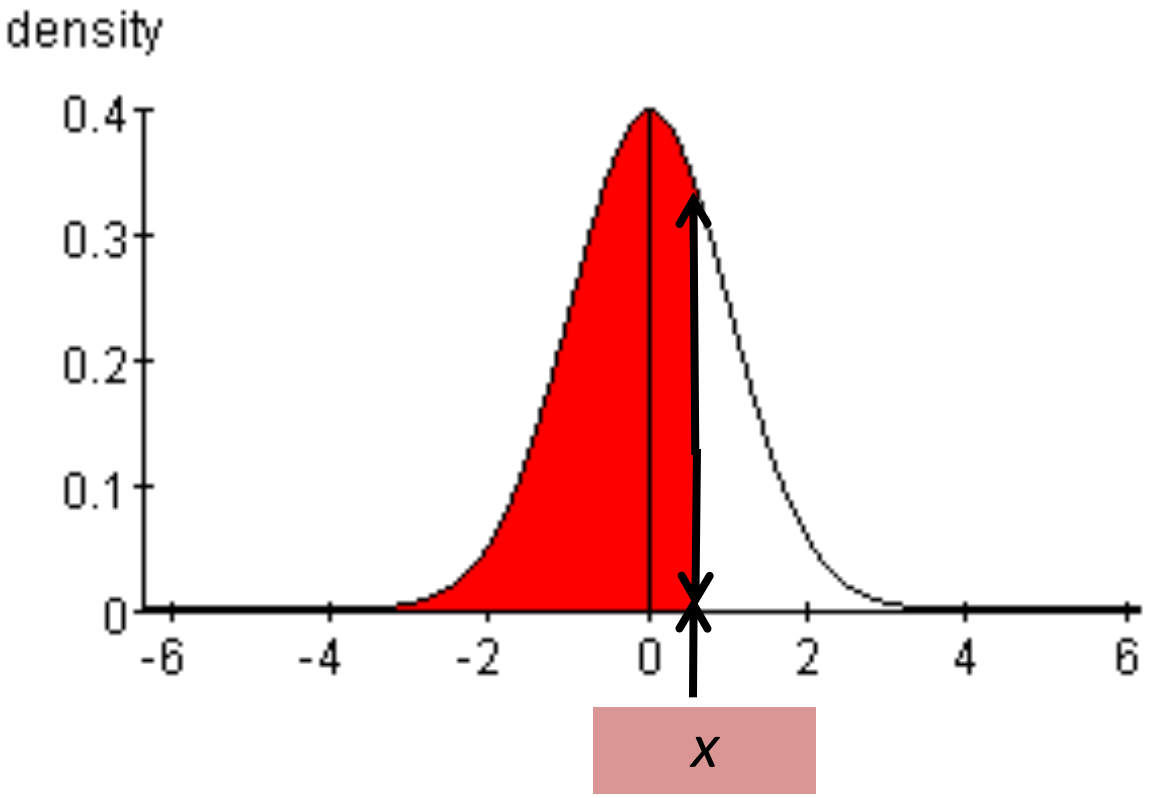
Statistical Distributions

Some Basic Definitions

- **Random Variable** – a variable whose value is not known with certainty, e.g. coin flip
- **Random Variate** – particular outcome of a random variable, e.g. heads
- **Probability** – denotes *relative frequency of occurrence* of particular value, e.g. p(heads) = 0.5
- **Probability distribution** yields the probability of
  - Each value of a random variable (**discrete distribution**)
  - the value of a random falling within a particular interval (**continuous distribution**)

Probability density (i.e. height) at *x*
PDF

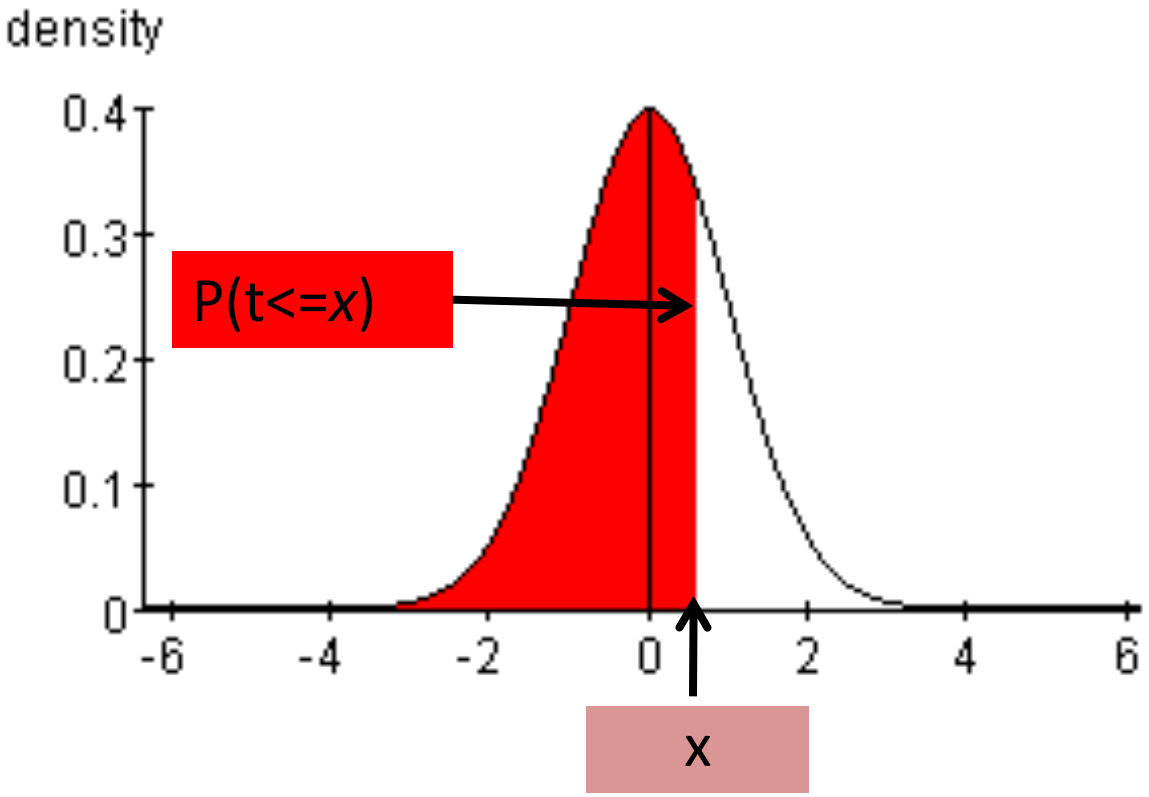
```
dnorm(x,mean=0,sd=1)
```



Probability that variate *t* <= *x*

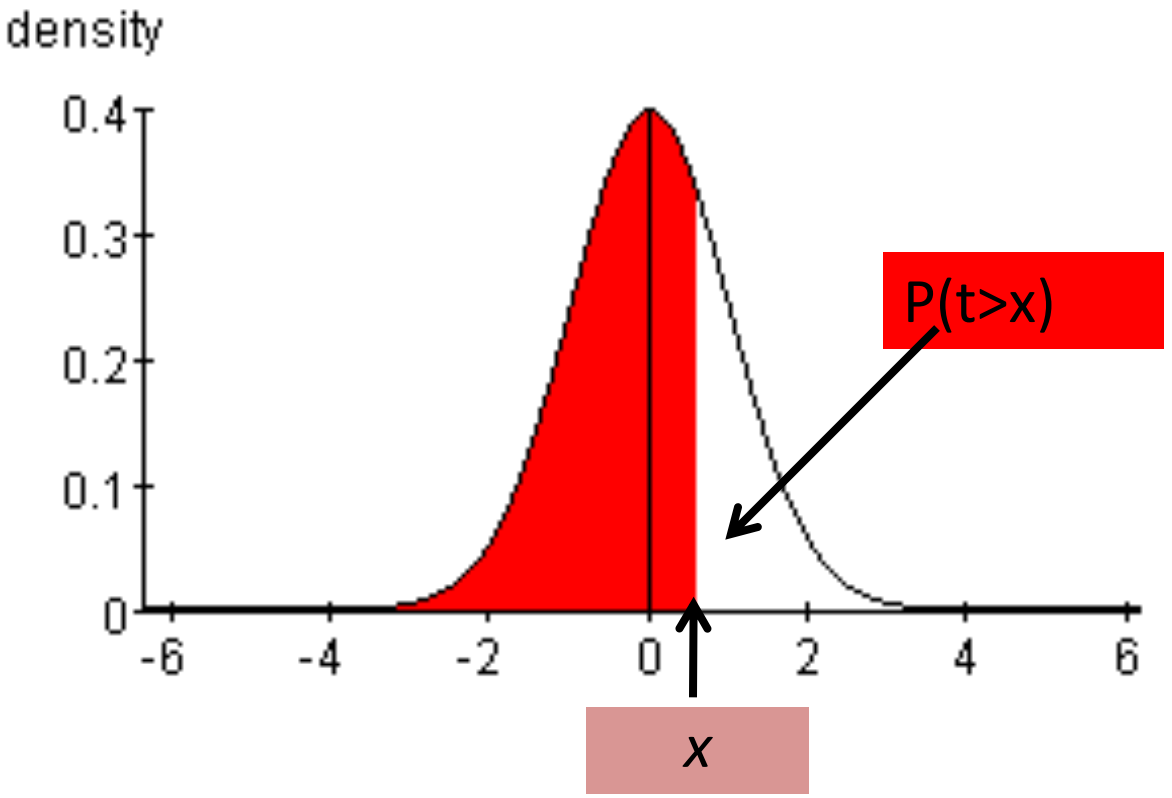
Cumulative Distribution Function, CDF

```
pnorm(x,mean=0,sd=1,lower.tail=TRUE)
```



Probability that variate $t > x$
Complementary CDF

```
pnorm(x,mean=0,sd=1,lower.tail=FALSE)
```

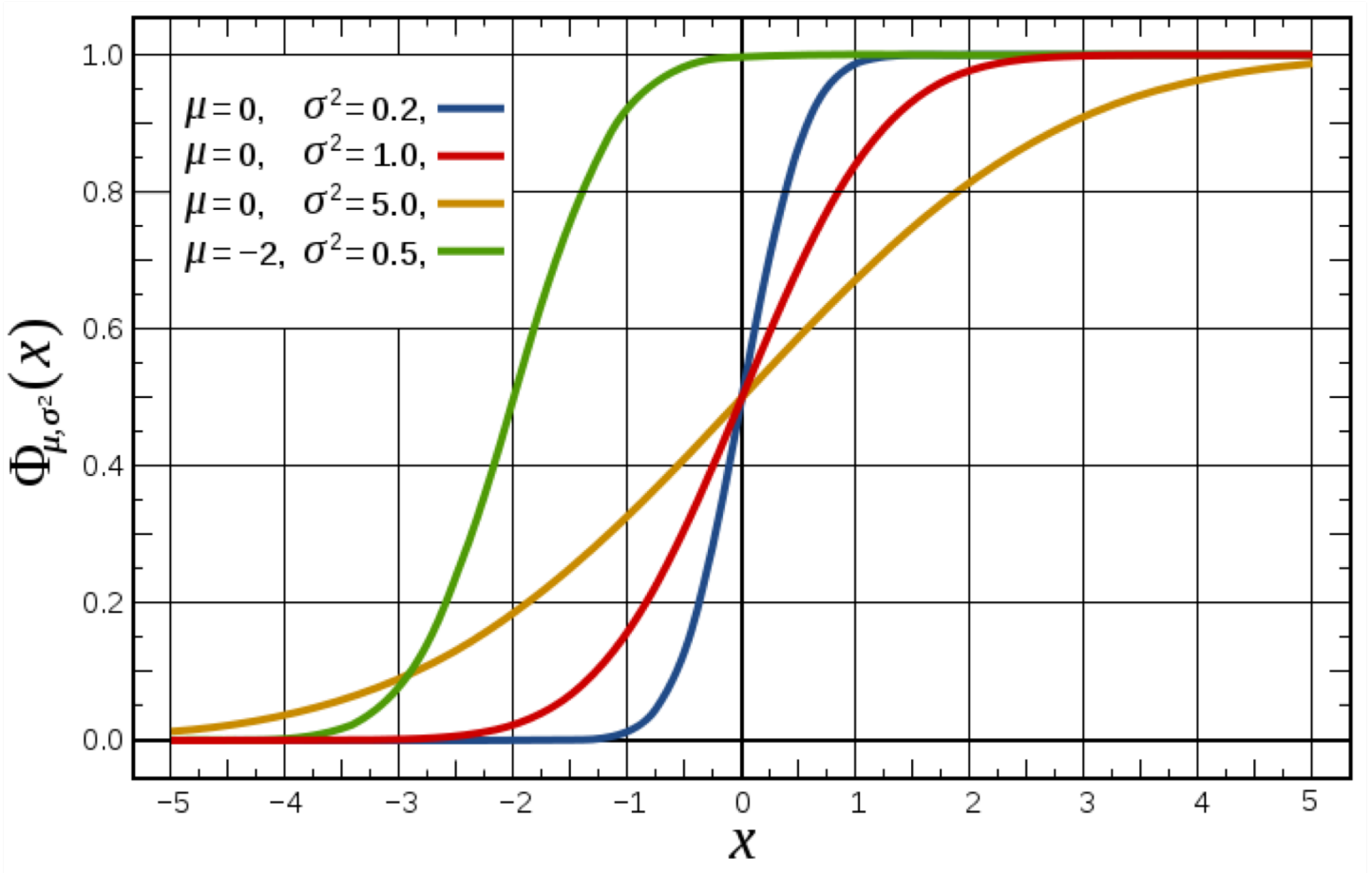


Question: What is this sum?

- **pnorm(x,mean=0,sd=1,lower.tail=TRUE)+**
  pnorm(x,mean=0,sd=1,lower.tail=FALSE)

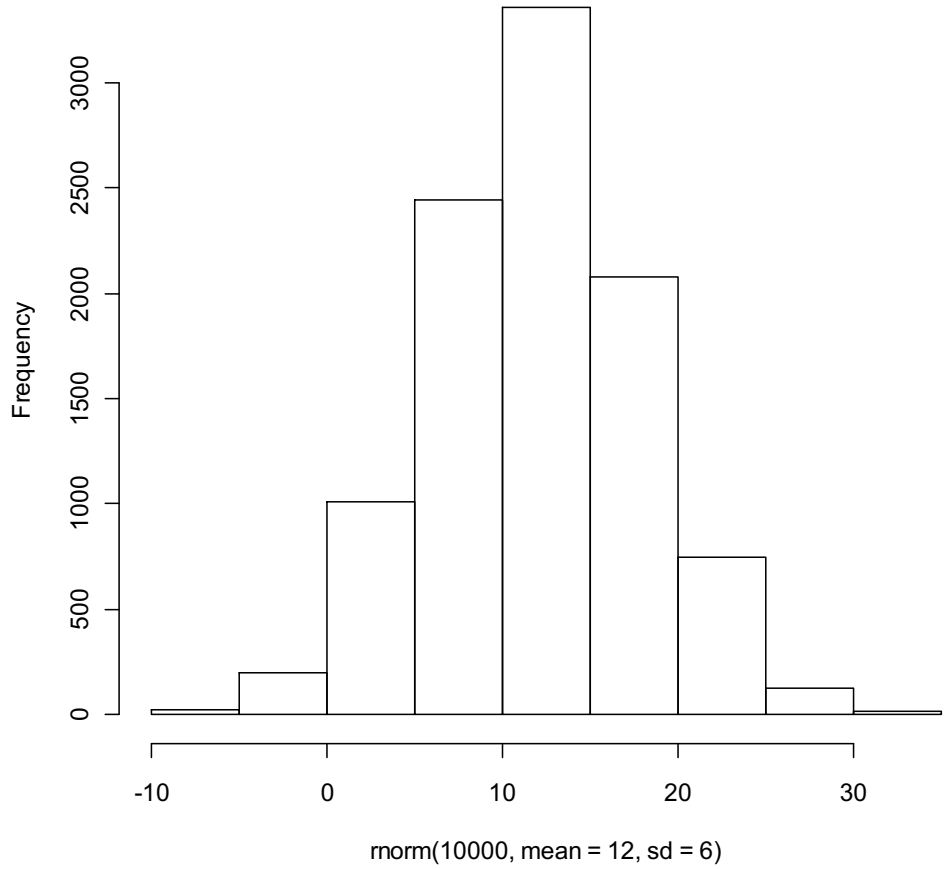
At what value of x is P(*t*<=*x*) = 0.4?

```
qnorm(0.4,mean=-2,sd=sqrt(0.5))
```



Sampling from a distribution

```
hist(rnorm(1000,mean=12,sd=6))
```



Functions have required and optional arguments

- Works fine (no required arguments)
  - `q()#quits R`
- Doesn't work:
  - `rnorm()#missing argument for n, which has no default`
- Does work (caution: computer assigns values for some arguments!)
  - `rnorm(100) #takes default arguments`
- Does work (all arguments specified by user)
  - `rnorm(100,mean=1,sd=4)`
  - `rnorm(mean=1,sd=4,n=100)`

Exercise 1:
Using R as a Statistics Table

- Generate a sample of 1000 variates from a normal distribution of mean 10 and standard deviation 5 using `rnorm`
- For this sample, calculate what fraction of the points take values <5 (hint: subset the vector using `[ ]`, and use `length`)
- Using `pnorm`, calculate the theoretically predicted fraction of points that should take values < 5

Exercise 1: Answer

- `x <- rnorm(1000,mean=10,sd=5)`
- `length(x[x<5])/length(x)`
- `pnorm(5,mean=10,sd=5)`

Built-in Probability Distributions:
for the list, type `?Distributions`

Continuous distributions

- Normal (`dnorm`)
- T (`dt`)
- Chi-squared (`dchisq`)
- F (`df`)
- Exponential (`dexp`)
- Uniform (`dunif`)
- Beta (`dbeta`)
- Cauchy (`dcauchy`)
- Logistic (`dlogis`)
- Lognormal (`dlnorm`)
- Gamma (`dgamma`)
- Weibull (`dweibull`)

Discrete distributions

- Binomial (`dbinom`)
- Poisson (`dpois`)
- Geometric (`dgeom`)
- Hypergeometric (`dhyper`)
- Negative binomial (`dnbinom`)

Other Distributions Use Similar Syntax

NORMAL DISTRIBUTION

- `dnorm(x, mean = 0, sd = 1, log = FALSE)`
- `pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)`
- `qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)`
- `rnorm(n, mean = 0, sd = 1)`

UNIFORM DISTRIBUTION

- `dunif(x, min=0, max=1, log = FALSE)`
- `punif(q, min=0, max=1, lower.tail = TRUE, log.p = FALSE)`
- `qunif(p, min=0, max=1, lower.tail = TRUE, log.p = FALSE)`
- `runif(n, min=0, max=1)`

Exercise 2

Using R as a Statistics Table

- What is the probability that a random variate from a gamma distribution with a shape parameter = 3 and scale parameter = 1 is > 0.68? [use `pgamma`]
- What is the probability that a random variate from an exponential distribution with rate = 0.05 lies between 1 and 10? [use `pexp`]

Exercise 2:
Answers

- pgamma(0.68,shape=3, scale = 1,lower.tail=F)
- 1- pgamma(0.68,shape=3, scale = 1)

- pexp(10,rate=0.05) - pexp(1,rate=0.05)

Exercise 3:
Using R as a Statistics Table

- What is the probability that a random sample of 15 people has 2 people with the same birthday? [Hint: ?pbirthday]

- What is the probability that a random sample of 25 martians includes 2 martians with the same birthday? [Hint: a year on Mars is 687 days]

Exercise 3 Answer:

R functions arguments can be matched positionally or by name

- pbirthday(n = 15, classes = 365, coincident = 2)
- pbirthday(15, 365, 2)
- pbirthday(classes = 365, 15, 2)
- pbirthday(15, coincident = 2)
- pbirthday(25, coincident = 2) #wrong answer for martians
- pbirthday(25,687,2) #right answer for martians

Statistical distributions provide a means to perform simulations

- `#using r for simulation of 1D random walker`
- `steps<-rnorm(n=10000,mean=0,sd=1)`
- `distance.from.origin <- cumsum(steps)`
- `plot(distance.from.origin,type='l')`

Use of `set.seed()` for reproducible random results

- `#using r for simulation of 1D random walker`
- `set.seed(1)`
- `steps<-rnorm(n=10000,mean=0,sd=1)`
- `distance.from.origin <- cumsum(steps)`
- `plot(distance.from.origin,type='l')`

Summary Statistics

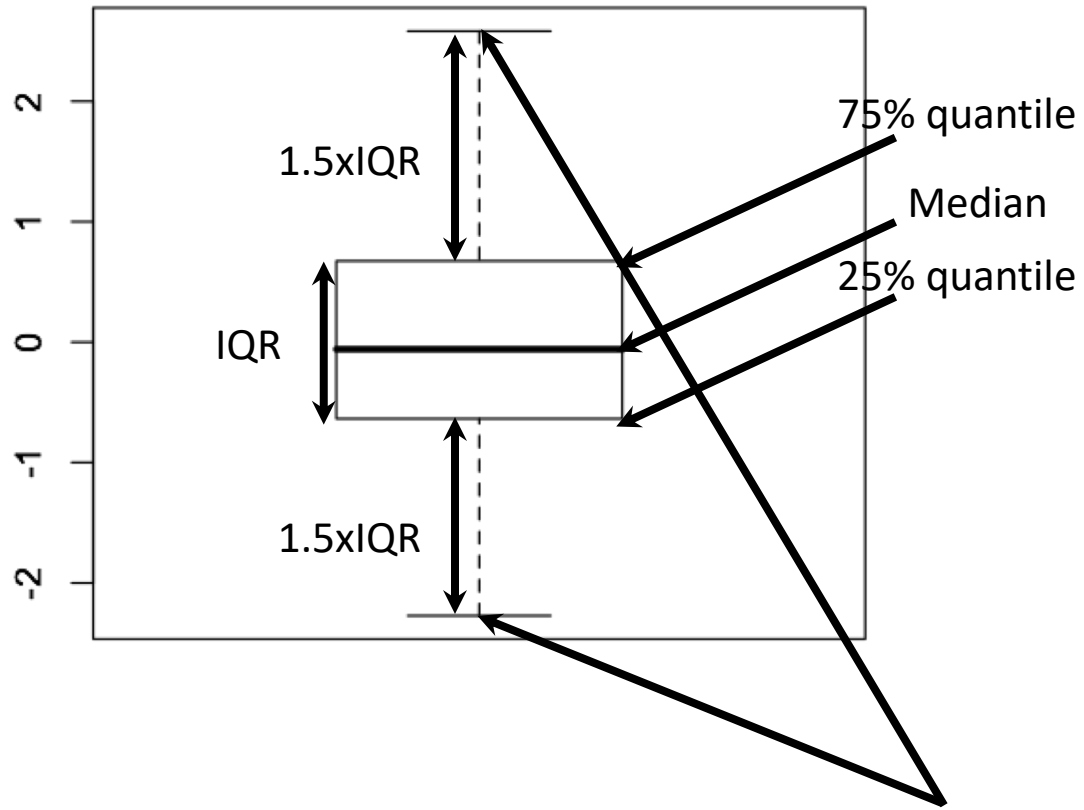
Some Functions for Calculating Summary Statistics

- Minimum: `min()`
- Maximum: `max()`
- Range (Minimum and Maximum): `range()`
- Mean: `mean()`
- Median: `median()`
- Quantiles: `quantile()`
- Interquartile range: `IQR()`
- Variance: `var()`
- Standard Deviation: `sd()`
- Summary: `summary()`
- Stem & Leaf Plot: `stem()`

- Boxplot: `boxplot()`
- QQ Plot: `qqnorm()`, `qqline()`

Functions for Calculating Summary Statistics

```
>x<-rnorm(100)

>boxplot(x)
```



IQR= 75% quantile -25% quantile= Inter Quantile Range

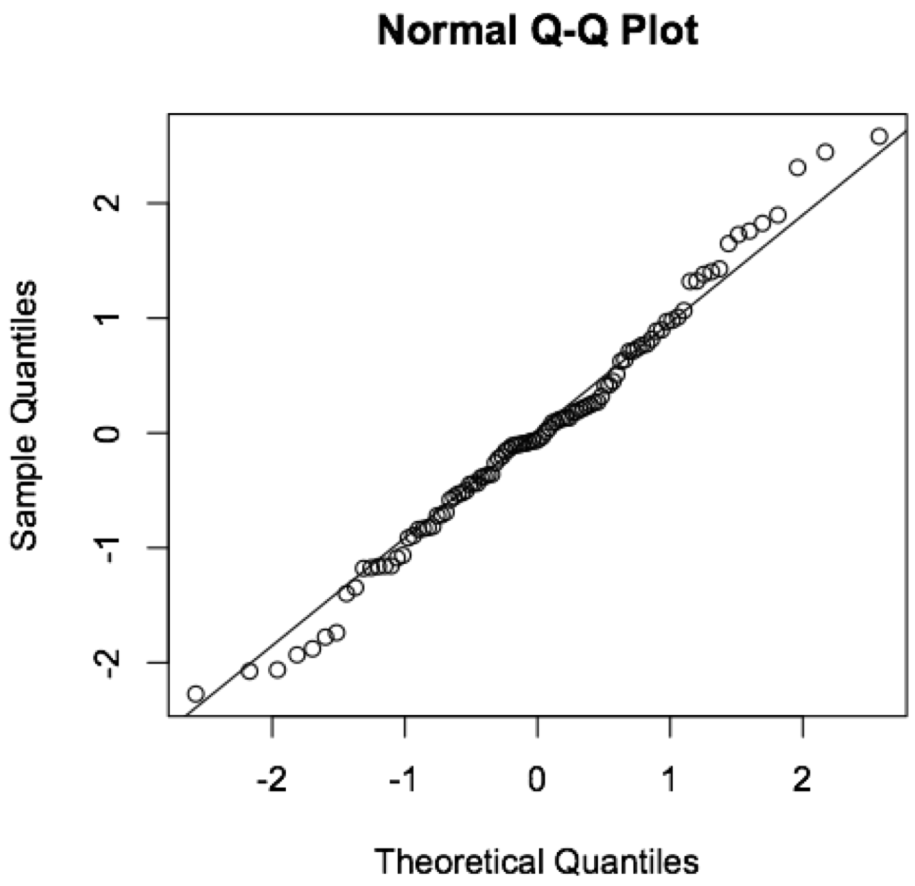
Everything above or below are considered outliers

QQ Plot

- Many statistical methods make some assumption about the distribution of the data (e.g. Normal)
- The quantile-quantile plot provides a way to visually verify such assumptions
- The QQ-plot shows the theoretical quantiles versus the empirical quantiles. If the distribution assumed (theoretical one) is indeed the correct one, we should observe a straight line.

QQ Plot

- `x<-rnorm(100)`
- `qqnorm(x)`
- `qqline(x)`



Functions for Calculating Summary Statistics

- Two functions are extremely useful for calculating summary statistics for subsets of data:
  - `apply()` (calculates function on a column-by – column or row-by-row basis)
  - `tapply()` (groups data in one column based on values in another column)

T test

What does Student's t distribution have to do with Guinness beer?

VOLUME VI MARCH, 1908 No. 1

BIOMETRIKA.

THE PROBABLE ERROR OF A MEAN.

BY STUDENT.

Introduction.

ANY experiment may be regarded as forming an individual of a "population"

T distribution

- The t distribution was introduced by William Gosset, a chemist working for Guinness brewery in Ireland
- He published his work under the pen name “Student” because Guinness regarded the fact that they were using statistics to help with brewing to be a trade secret

T-test Example:
Shell Size Data

- We're on Trunk Reef in the Great Barrier Reef and we have collected random samples of one shell species from two locations, one wave-exposed and the other sheltered.

- We want to determine if shells differ in size between these two environmentally different locations.

- The data are the shell lengths in millimetres for the two locations.

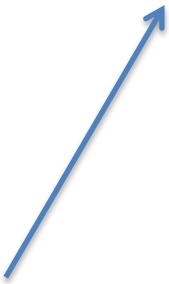
- **Does mean shell size differ between the two locations?**

Specifying Dependent & Independent Variables in R

Formula notation for many functions in R:

```
boxplot(y ~ x,data = my.data)  # boxplot
lm(foot~gender,data = my.data) # one-way ANOVA
t.test(y ~ x,data = my.data)   # t-test
```

t.test(`response~predictor,data=my.table`)



dependent (response)

independent (predictor)

dataframe

Exercise 4:
Shell Size Data

- Conduct a two-sample T test using the function `t.test()`
  - Type `?t.test` for some help
- Answer the following questions:
  - What is the mean difference, *m*, between the treatments?
  - What is the 95% CI for the difference?
  - According to the t test, is the difference significant at the P = 0.05 level for the two-tailed test?
  - According to the non-parametric analogue of the t test (Wilcoxon Rank Sum Test), is the difference significant at the P = 0.05 level for the two-tailed test? **[Use `wilcox.test`]**

Exercise 4 Answers

- `shells <- read.csv('shells.csv')`
- `t.test(length~type,shells)`
- `wilcox.test(length~type,shells)`

More on T tests

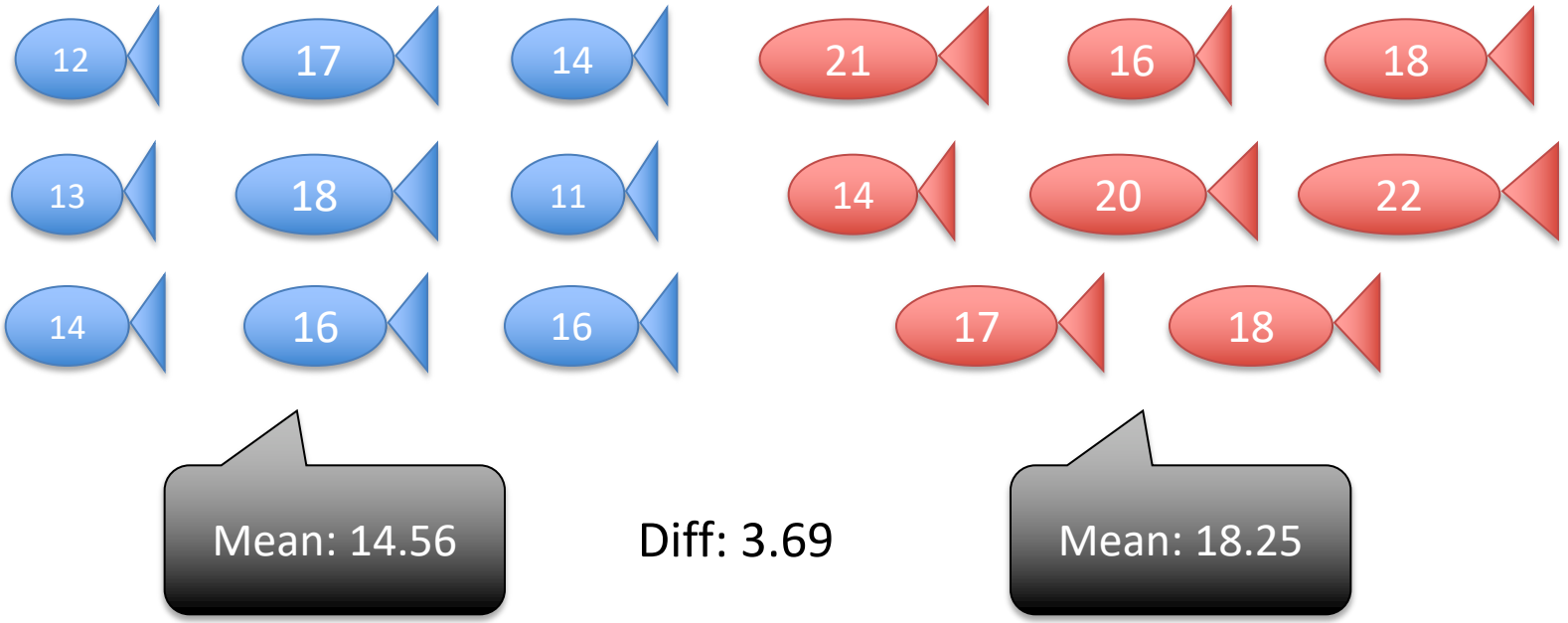
```
# Welch two-sample t-test
t.test(length~type,shells)

# Student two-sample t-test
t.test(length~type,shells,var.equal=TRUE)

# one-sample t-test
# null hypothesis: mean shell size = 14mm
t.test(shells$length,mu=14)
```

Wilcoxon Rank Sum Test

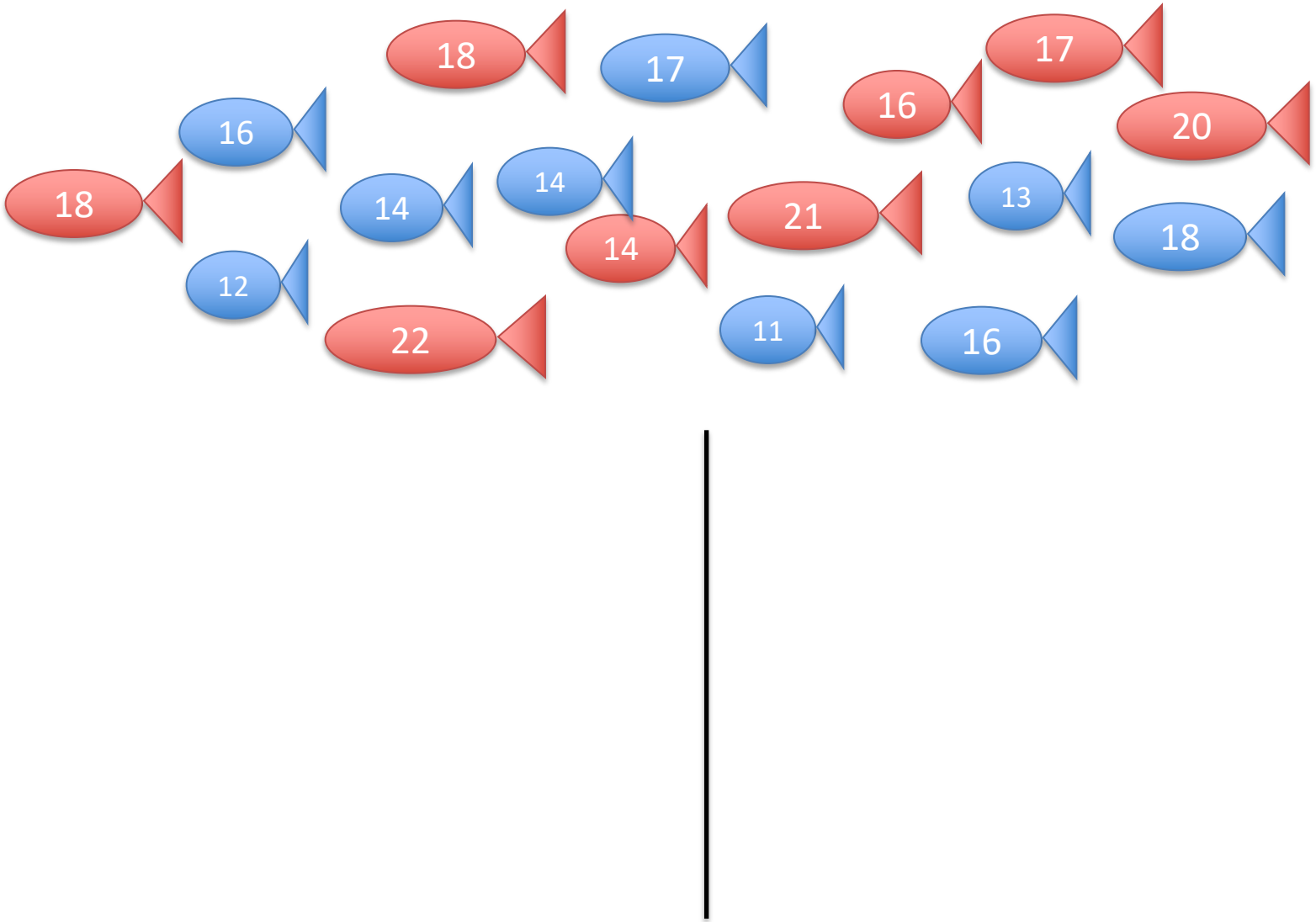
- This technique is non-parametric , meaning that it does not rely on assumptions that the data are drawn from a particular probability distribution.
- Non-parametric methods are particularly suited to data that are not normally distributed.
- Assumptions Wilcoxon Rank Sum Test:
    - random samples from populations
    - independence within samples and mutual independence between samples
    - measurement scale is at least ordinal

Monte Carlo Method

- Monte Carlo (MC) methods – broad class of computational algorithms that rely on random sampling to solve problems
- We can use MC to *sample* permutations



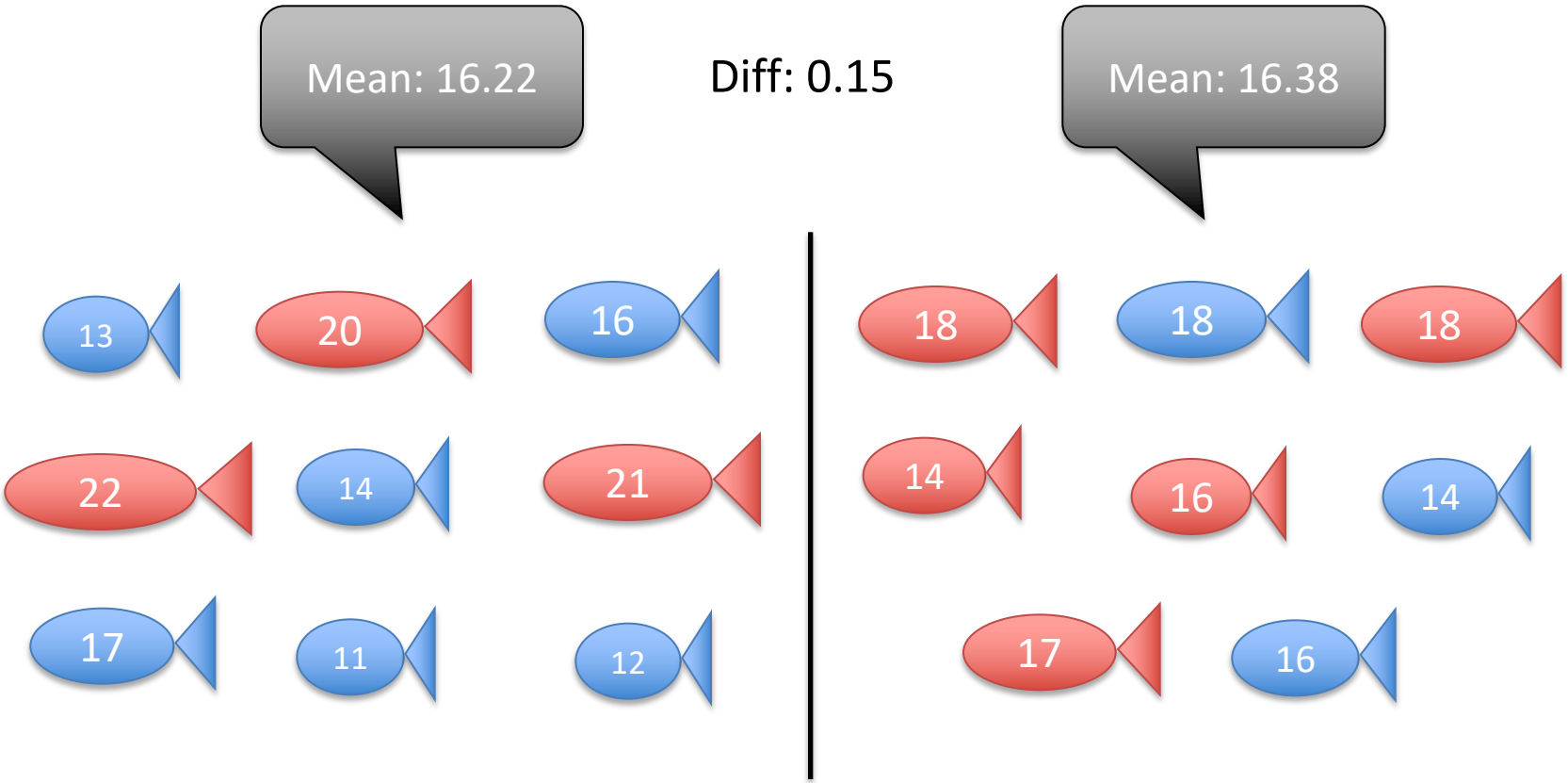
Shuffle together



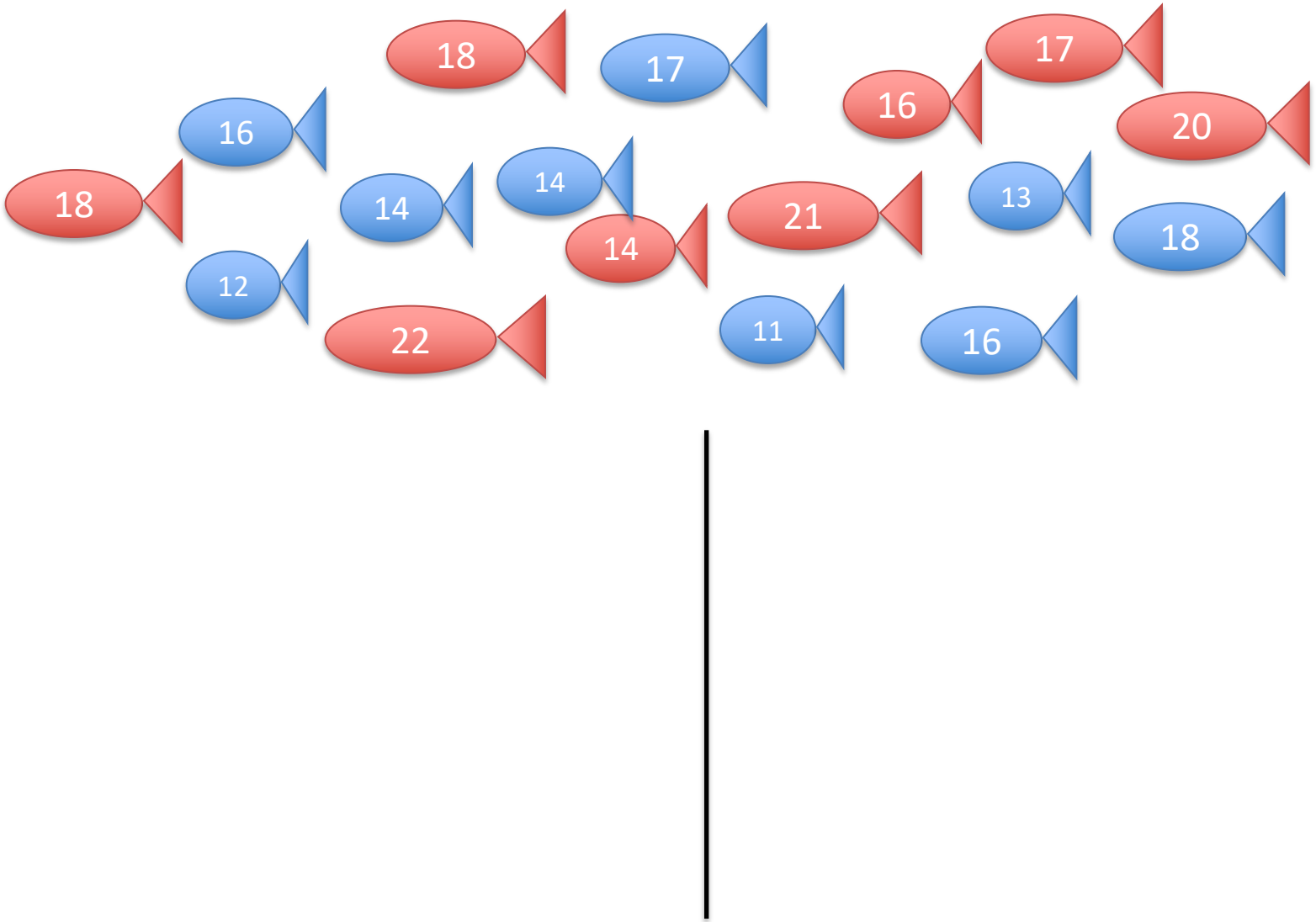
3.69
0.15

Randomly sample

- Split randomly, ensure same number in each group as original treatments

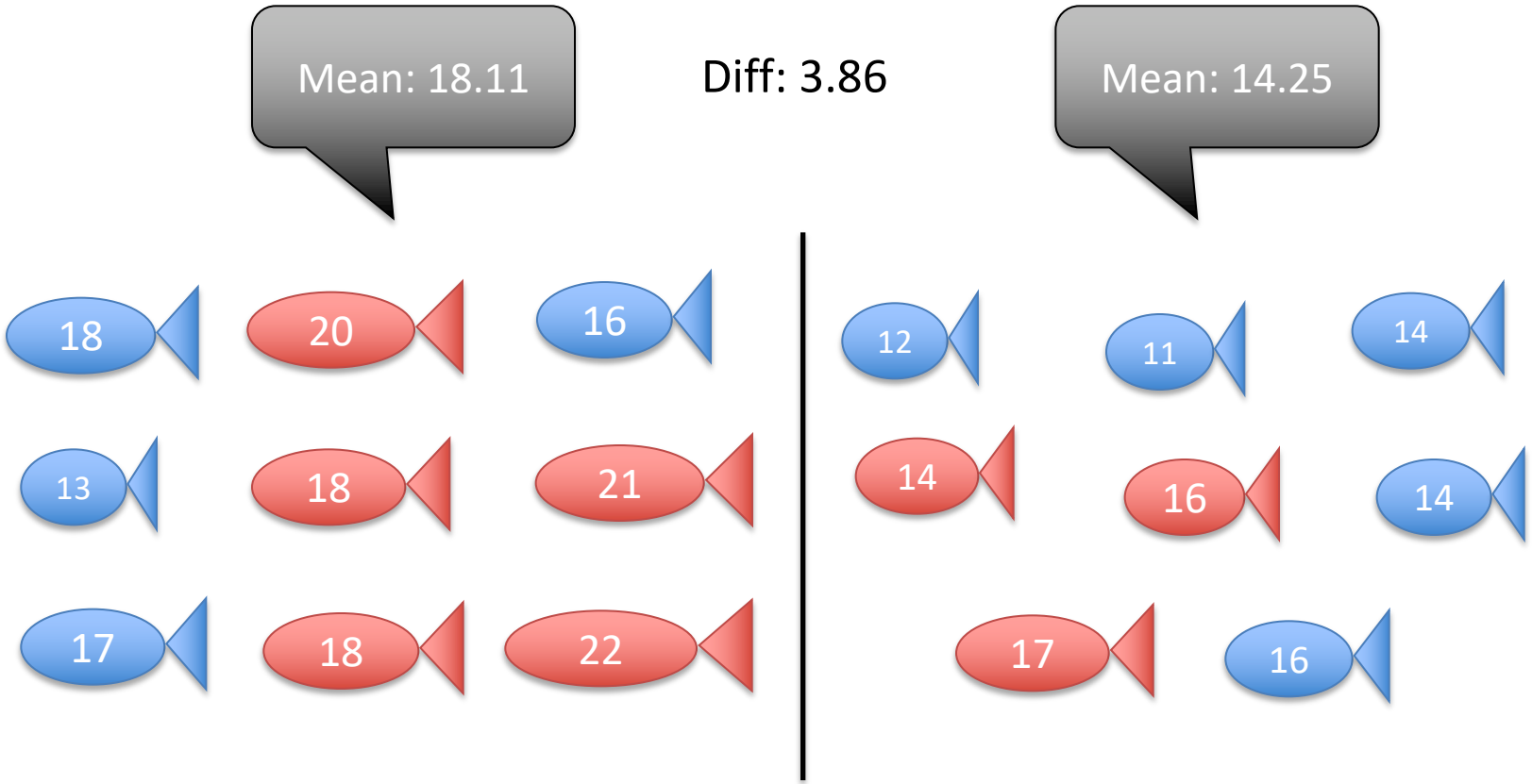


Shuffle together

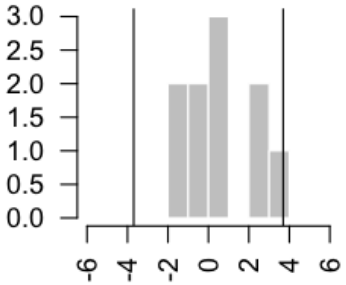


3.69
0.15
-3.86

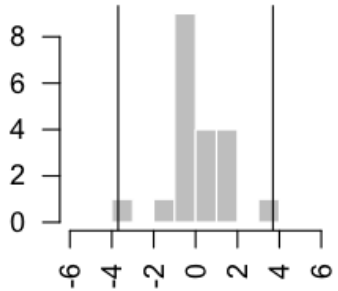
Randomly sample



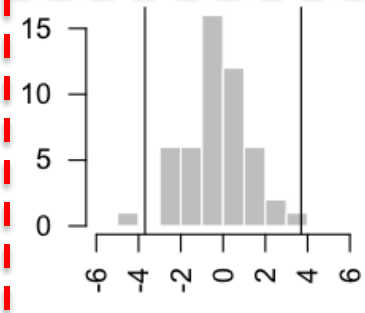
Monte Carlo Method



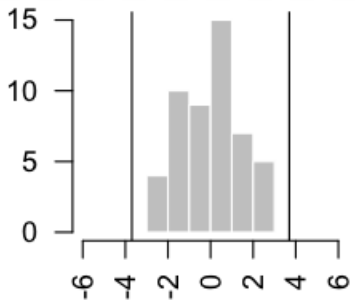
10 samples, 0 >= diff
p = 0



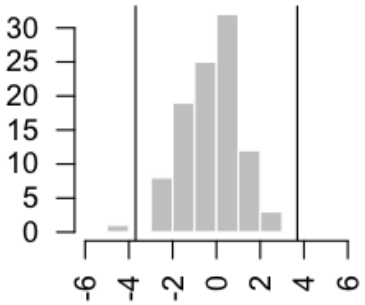
20 samples, 1 >= diff
p = 0.05



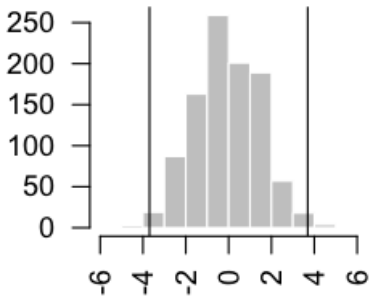
50 samples, 1 >= diff
p = 0.02



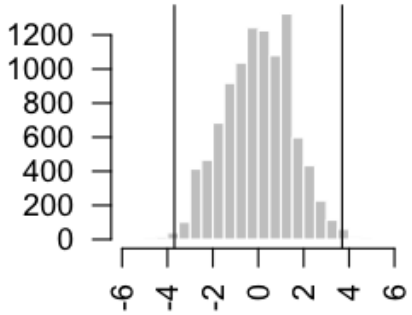
50 samples, 0 >= diff
p = 0



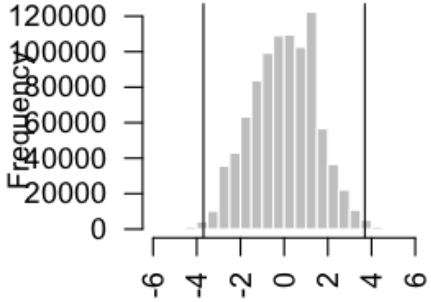
100 samples, 1 >= diff
p = 0.01



1,000 samples, 8 >= diff
p = 0.008



10,000 samples, 65 >= diff
p = 0.0065



1,000,000 samples, 7242 >= diff
p = 0.007242

This took a while!

Power Analysis

- **A very important part of planning research**

- **Power** is the conditional probability of rejecting the null hypothesis given that it is really false

- 1- Power = Type II error

Power Depends on:

- ***α*:** significance level used
- ***ES*:** Effect size of interest
- ***n*:** sample size; a given effect is easier to detect with larger sample sizes
- s^2**:** estimated variance; it is harder detect effects between more variable populations

Exercise 5:
Power Analysis of Shell Data

- In the command window, learn how to conduct a power analysis using `?power.t.test`
- I have calculated `delta` and `sd` for you
- Using this function, calculate the statistical power of the test
- Now use this function to determine how large a sample size would be required to reject the null hypothesis at a significance level of 0.05 with 80% power

Exercise 5 Answers

- `power.t.test(n=51,delta=13.36275-15.56863,sd=sqrt(18.52549))`

- `power.t.test(n=NULL,delta=13.36275-15.56863,sd=sqrt(18.52549),power=0.80)`

Linear Regression

Linear Regression

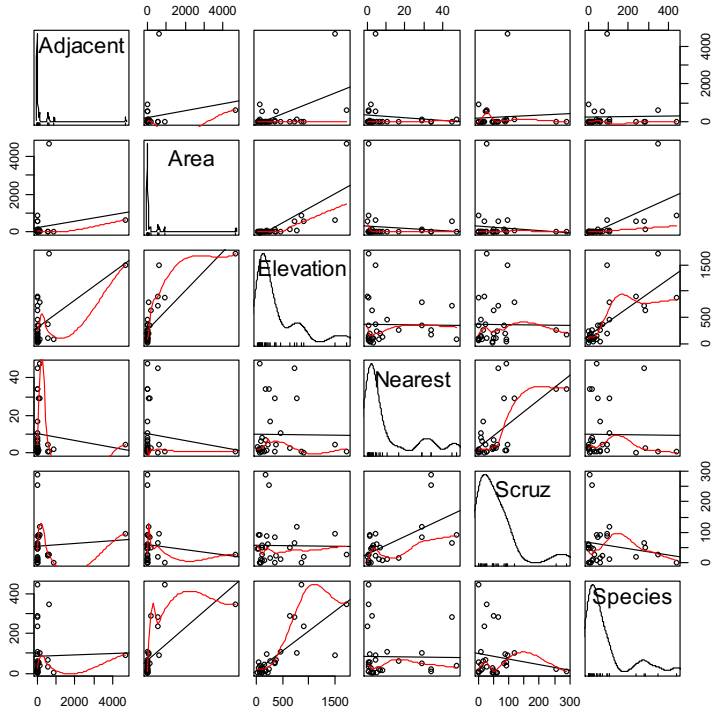
- Use `gala <- read.table(...,header=TRUE,row.names=1)` to import the file `gala.txt` into the dataframe `gala`
- View the dataset using `head(gala)`

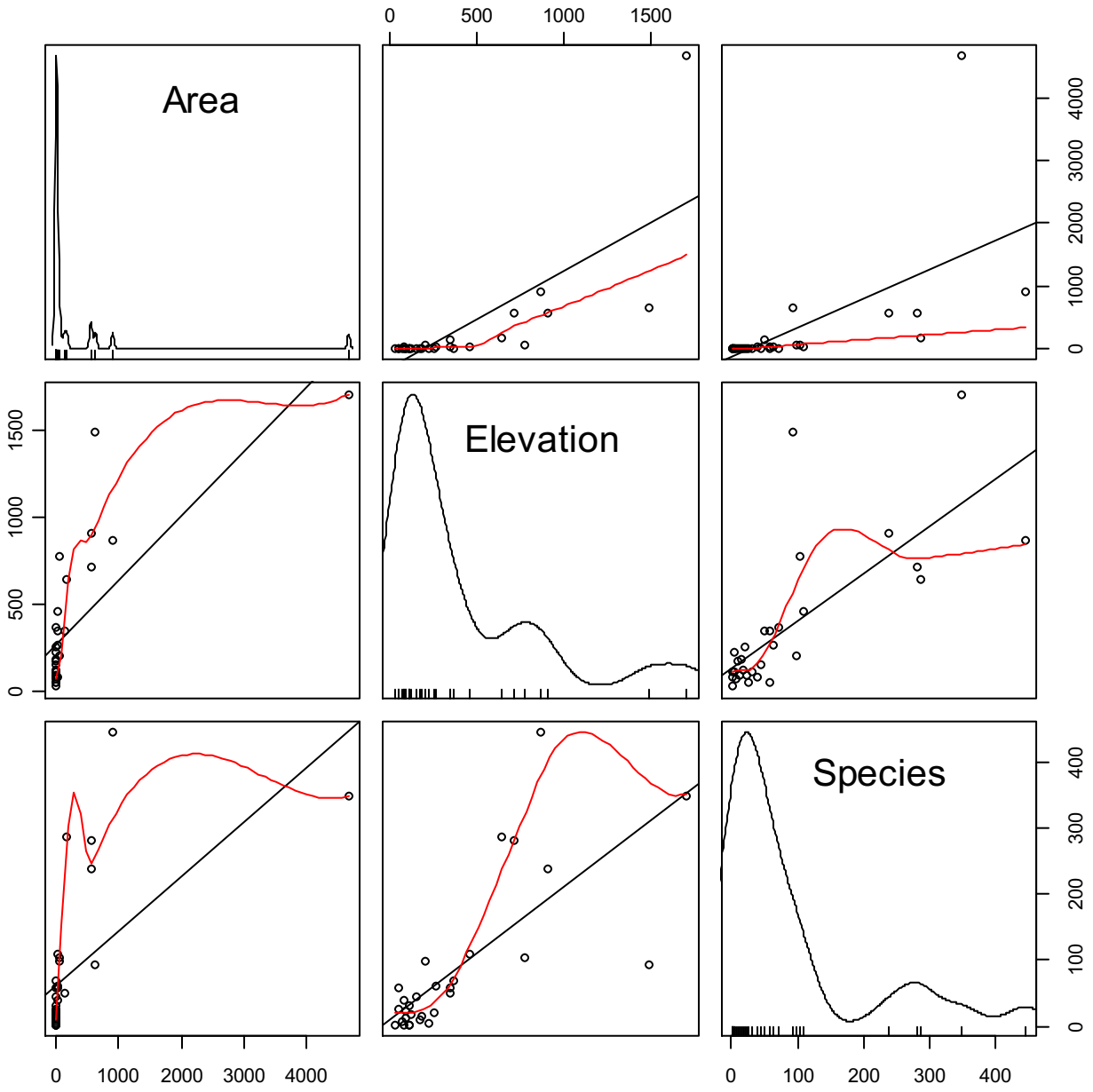
gala

- Source
  - M. P. Johnson and P. H. Raven (1973) "Species number and endemism: The Galapagos Archipelago revisited" Science, 179, 893-895
- Variables
  - **Species** the number of plant species found on the island
  - **Endemics** the number of endemic species
  - **Area** the area of the island (km^2)
  - **Elevation** the highest elevation of the island (m)
  - **Nearest** the distance from the nearest island (km)
  - **Scruz** the distance from Santa Cruz island (km)
  - **Adjacent** the area of the adjacent island (square km)

Investigate Distributions of Variables and Their Relationships

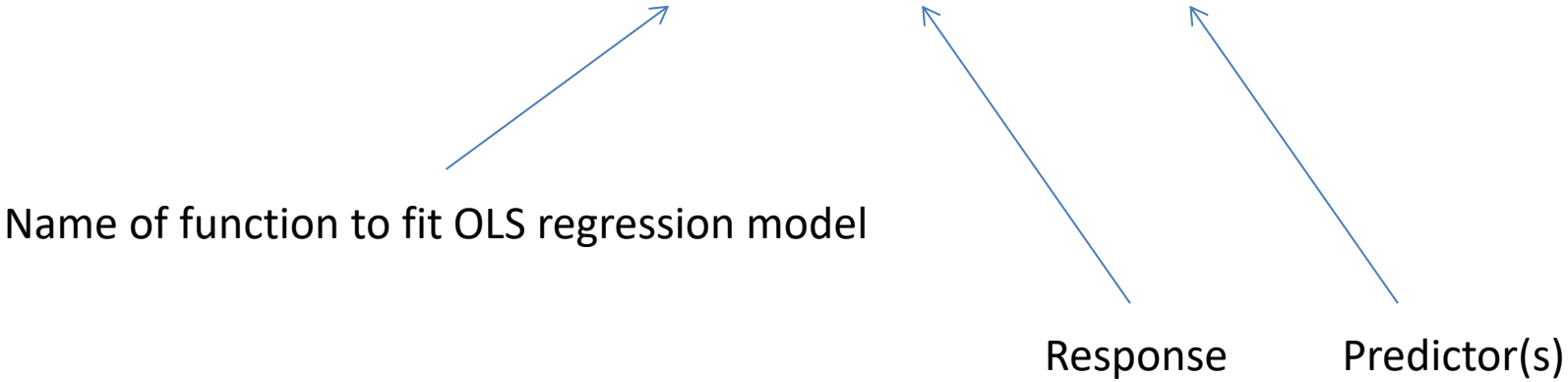
- Generate a plot similar to the one below by typing `plot(gala)`




Area
Elevation
Species
0
500
1000
1500
0
1000
2000
3000
4000
0
100
200
300
400

Ignore these issues and fit a linear model

- Now fit a linear regression model by typing:
  - `gala.model<-lm(Species~Area, data=gala)`



- Let's look at the attributes of this object:
  - `str(gala.model)`

Extractor functions allow you to get information on `lm` objects

- `coef(gala.model)`
- `residuals(gala.model)`
- `fitted.values(gala.model)`
- `cooks.distance(gala.model)`
- `summary(gala.model)`
- `anova(gala.model)`

Assumptions of Linear Regression

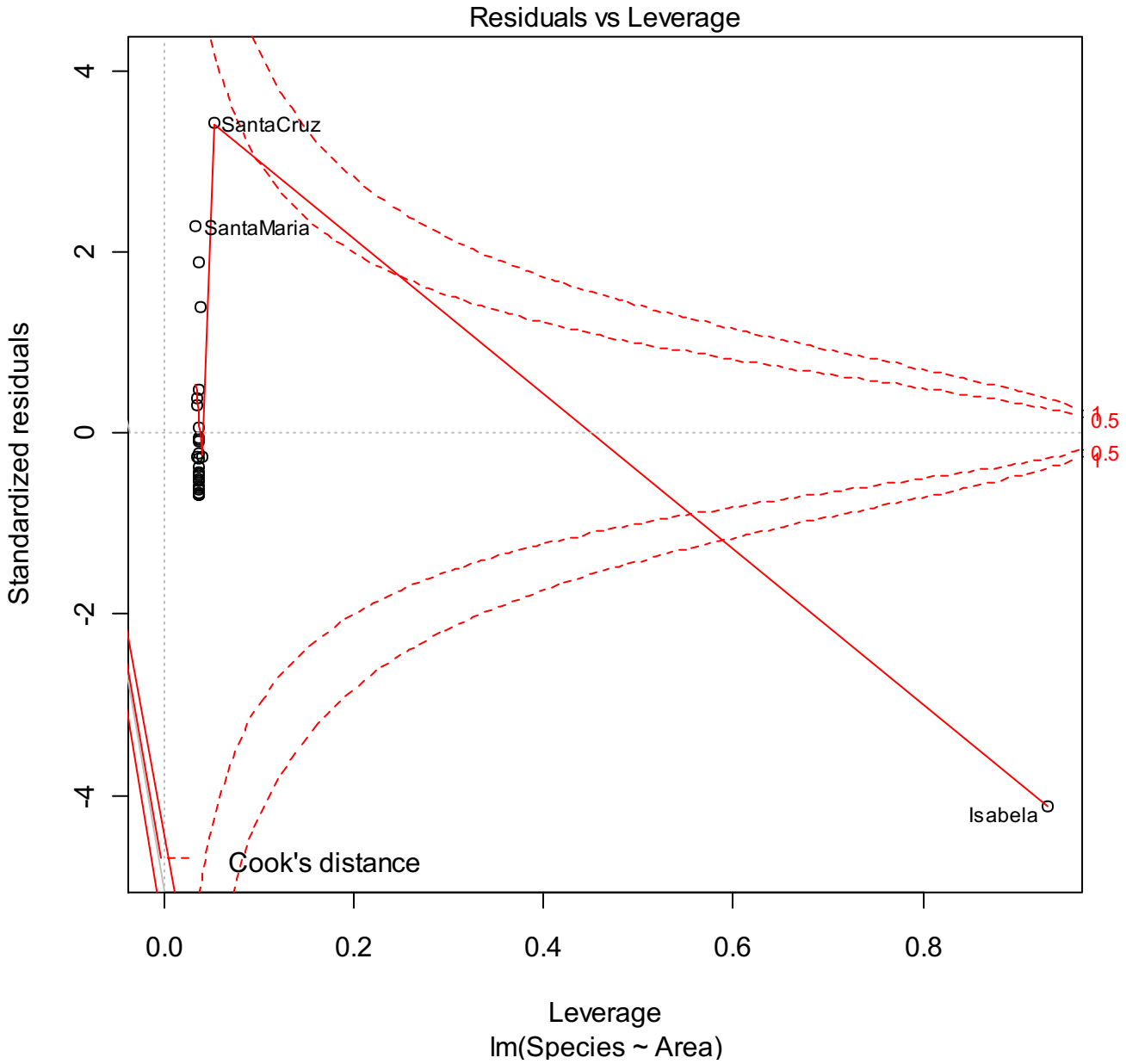
- **Linearity** of the relationship between dependent and independent variables
- **Independence** of the errors (no serial correlation)
- **homoscedasticity** (constant variance) of the errors
- **normality** of the error distribution

Let's evaluate these assumptions

- To evaluate assumptions type:
  - `plot(gala.model)`
- Theory:
  - Leverage is a measure of how far an independent variable deviates from its mean
  - Cook's distance
    - measures the influence of an observation on the overall model:

$$D_i = \frac{\sum_{j=1}^{n} (\hat{Y}_j - \hat{Y}_{j(i)})^2}{p \ \mathrm{MSE}}.$$

    - Y_j is the prediction from the full regression model for observation *j*
    - $Y_{j\,(i)}$ is the prediction for observation *j* from a refitted regression model in which observation *i* has been omitted
  - Frequently proposed rules of thumb include focusing on points with distances $D_i > 1$ or $> 4/n$


Residuals vs Leverage
Standardized residuals
Leverage
lm(Species ~ Area)
SantaCruz
SantaMaria
Isabela
Cook's distance
0.5
0.5
4
2
0
-2
-4
0.0
0.2
0.4
0.6
0.8

Exercise 6:

Independent analysis of `gala` data

- Transform species and area using the log10 transformation, e.g.
- Refit the linear model using the log transformed data and assess whether model assumptions are upheld
- Plot the data and model together using the functions `plot()` and `abline()`
- Inspect the coefficients using `summary()`

Exercise 6: Answer

- gala$log.species<-log10(gala$Species)
- gala$log.area<-log10(gala$Area)
- gala.model<-lm(log.species~log.area, data=gala)
- plot(log.species~log.area,gala)
- abline(gala.model)

Fit of simple linear regression model

- `summary(gala.model)`

```
Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.26106    0.06822  18.484  < 2e-16 ***
log.area     0.38860    0.04160   9.342 4.23e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3406 on 28 degrees of freedom
Multiple R-squared: 0.7571,   Adjusted R-squared: 0.7484
F-statistic: 87.27 on 1 and 28 DF,  p-value: 4.23e-10
```

- 95% confidence interval for fitted slope:
  - lower CI: `0.38860 + qt(.025,28)* 0.04160`
  - Upper CI: `0.38860 + qt(.975,28)* 0.04160`
  - `confint(gala.model)`

Multiple linear regression

- Extending analyses to multiple linear regression is straightforward using `lm()`:
  - lm(y~x1 + x2,data)
- Notation used for formulas (VERY general, applies to many statistical procedures in R):
  - Intercept only
    - `lm(y~1,data)`
  - Force-fit y versus x1 relationship through origin
    - `lm(y~x1-1,data)`
  - Include all variables in data.frame:
    - `lm(y~.,data)`
  - Include all variables in data.frame but x7:
    - `lm(y~.- x7,data)`
  - Include x1, x2 and their interactions:
    - `lm(y~x1*x2,data)`
    - `lm(y~x1+x2+x1:x2)`
    - `Lm(y~x1*x2*x3 – x1:x2:x3) #drop 3-way interaction`

Exercise 7

Formally test for effects of `log.elevation` after accounting for `log.area`

- Fit a new model that includes both `log.elevation` and `log.area`
- Null hypothesis: after account for the effects of area, elevation is not significant
- How do we test this null hypothesis?

- R knows what to do. Just type:
  - `anova(lm1,lm2)`

Exercise 7 Answer

- `gala$log.elevation <- log10(gala$Elevation)`
- `gala.model2 <- lm(log.species~log.area+log.elevation,data=gala)`
- `anova(gala.model,gala.model2)`

Automated Model Selection

- Several methods available:
  - Best subset selection
  - Stepwise selection

- Fit using multiple criteria:
  - Statistical significance [`logLik(lm1)-logLik(lm2)`]
  - AIC [`AIC(lm1) - AIC(lm2)`]
- Key issue: need to first specify a full model

- Controversial among statisticians due to multiple comparisons problem, but still useful for exploration

R Code for BE using `step()`

- Use R function `step`
- Need to define an *initial model* (the full model in this case, as produced by the R function lm) and a *scope* (a formula defining the full model)
- `ffa.lm <- lm(ffa~., data=ffa.df)`
- `step(ffa.lm,direction='backward')`

Forward Selection (FS) using `step()`

- Start with a null model
- Fit all one-variable models in turn. Pick the model with the best (i.e. lowest) AIC
- Then, fit all two variable models that contain the variable selected in 2. Pick the one for which the added variable gives the best AIC
- Continue in this way until adding further variables does not reduce the AIC

R Code for FS using `step()`

- Use R function `step`
- As before, we need to define an *initial model* (the null model in this case and a *scope* (a formula defining the full model)
- **`# R code: first make null model:`**
- **`ffa.lm = lm(ffa~., data=ffa.df)`**
- **`null.lm = lm(ffa~1, data=ffa.df)# then do FS`**
- **`step(null.lm, scope=formula(ffa.lm),`**
- **`direction='forward')`**

R Code Output (1 of 2)

```
> step(null.lm, scope=formula(ffa.lm),
direction="forward")
Start:  AIC=-49.16
ffa ~ 1

           Df Sum of Sq     RSS     AIC
+ weight    1   0.63906 0.91007 -57.799
+ age       1   0.20503 1.34410 -50.000
<none>                  1.54913 -49.161
+ skinfold  1   0.00145 1.54768 -47.179
```

Starts with constant term only

Results of all possible 1 (& 0) variable models. Pick weight (smallest AIC)

R Code Output (2 of 2)

```
Step:  AIC=-57.8
ffa ~ weight

           Df Sum of Sq     RSS     AIC
+ age       1  0.115900 0.79417 -58.524
<none>                  0.91007 -57.799
+ skinfold  1  0.007778 0.90230 -55.971

Step:  AIC= -58.52
 ffa ~ weight + age

           Df Sum of Sq     RSS     AIC
<none>                   0.794 -58.524
+ skinfold  1     0.003   0.791 -56.601
```

Exercise 8:

Choosing the best predictor of richness

- Using BE and function `step()`, determine the "best" model of species richness using the following potential predictors:
  - log.area
  - log.elevation
  - log.nearest
  - log.scruz [note: use log10(x+1) transform]
  - log.adjacent
- Recall:
  - `y.lm <- lm(y~., data=data)`
  - `step(y.lm,direction='backward')`

Exercise 8 Answer

- gala$log.nearest <- log10(gala$Nearest)
- gala$log.scruz <- log10(gala$Scruz+1)
- gala$log.adjacent <- log10(gala$Adjacent)

- gala.full <- lm(log.species~log.area+log.elevation+log.nearest+log.scruz +log.adjacent,gala)
- gala.step <- step(gala.full,direction='backward')

ANOVA and ANCOVA

Factor Variable Type

- `ssize <- sample(0:2,40,replace=TRUE)`
- `ssize`
- `is.factor(ssize)`
- `ssize.f <- factor(ssize,labels=c('s','m', 'l'))`
- `is.factor(ssize.f)`
- `is.ordered(ssize.f)`
- `ssize.f <- factor(ssize,labels=c('s','m', 'l'),ordered=TRUE)`
- `is.ordered(ssize.f)`
- `ssize.f[41] <- 'x'`
- `levels(ssize.f) <- c('s','m','l','x')`
- `ssize.f[41] <- 'x'`

http://www.ats.ucla.edu/stat/r/modules/factor_variables.htm

Example: Mangroves & Sponges

- Mangroves can grow in salt water
- Roots are colonized by sponges, algae, barnacles, etc.
- Are there effects on the plants?

Ellison et al. 1996
Gotelli & Ellison ch 10

Q. Are there effects of sponges on mangrove growth?
E. Measured root growth in each of 4 treatments (*n* = 14):

- Bare roots (Control)
- Roots with artificial foam (Foam)
- Roots with red fire sponge (Tedania)
- Roots with Purple sponge (Haliclona)

Factors & Levels

One Factor: Treatment

Four Levels: 1 = Control
2 = Foam
3 = Tedania
4 = Haliclona

14 replicates in each group

Exercise 9:
One-way ANOVA using `mangroves`

a) Import the data into a dataframe called `mangroves` using `read.csv()`
b) Using `factor()`, create a new variable (`treatment.f`) in the data.frame `mangroves` that converts `treatment` as a factor variable
c) Using `lm()`, fit a linear model that predicts `growth` based on `treatment`. Call it `lm1`.
d) Using `lm()`, fit a linear model that predicts `growth` based on `treatment.f`. Call it `lm2`.
e) Compare the two models using `AIC()` – which is better
f) Run `TukeyHSD(aov(lm2))` – what do you conclude?

Exercise 9 Answer

- mangroves <- read.csv('mangroves.csv')
- mangroves$treatment.f <- factor(mangroves$treatment)

- lm1 <- lm(growth ~ treatment,mangroves)
- summary(lm1) #estimates of coefficients
- anova(lm1) #overall effects of treatment.f

- lm2 <- lm(growth ~ treatment.f,mangroves)
- summary(lm2)
- anova(lm2) #overall effects

- AIC(lm1,lm2)
- TukeyHSD(aov(lm2))

Changing reference level in ANOVA

- contrasts(mangroves$treatment.f)
- mangroves$treatment.f <- relevel(mangroves$treatment.f,ref='4')
- contrasts(mangroves$treatment.f)
- lm2a <- lm(growth ~ treatment.f,mangroves)
- summary(lm2a)

http://www.ats.ucla.edu/stat/r/library/contrast_coding.htm

Other Stuff....

- #formal analysis of variance
- anova(lm1)

- ?aov() #alternative way of fitting anova models, allows for error strata

- #post hoc test
- TukeyHSD(aov(lm1))

- Preplanned contrasts

Mangrove Example

What we want to know:

- Do sponges aid plants by increasing root growth?
- And, how do they do it – is it via physical or chemical mechanisms?

Group the treatments to enable us to answer these questions directly.

(1) If living sponge enhances root growth, then average of two living sponge treatments should > artificial sponge treatment.

Set Up Contrasts I and II

(I) Living vs foam: If living sponge enhances root growth, then average of two living sponge treatments should be > artificial sponge treatment.

Contrast	Control	Foam	Haliclona	Tedania
I	0	-1	1/2	1/2

(II) Control vs others: If physical aspects of sponge enhance root growth, then the control should be < the average of the three sponge treatments.

Contrast	Control	Foam	Haliclona	Tedania
II	1	-1/3	-1/3	-1/3

Check these are **orthogonal:** (0)(1) + (-1)(-1/3) + (1/2)(-1/3) + (1/2)(-1/3) = 0

Coding Contrasts in R

```
> levels(mangrove$treatment)
[1] "Control"   "Foam"      "Haliclona" "Tedania"
> # set first row to constants
> my.contrasts <- rbind(constant=4,
+                       c(0,-1,1/2,1/2),
+                       c(1,-1/3,-1/3,-1/3),
+                       c(0,0,-1,1))
> # drop first column
> my.contrasts.inv <- solve(rbind(my.contrasts))[,-1]
> contrasts(mangrove$treatment) <- my.contrasts.inv
>
> my.contrasts.inv

[1,]  0.0000000  0.75  0.0
[2,] -0.6666667 -0.25  0.0
[3,]  0.3333333 -0.25 -0.5
[4,]  0.3333333 -0.25  0.5
```

ANOVA

```
>mangrove.model2 <-
aov(growth~treatment,data=mangrove)
>anova(mangrove.model2)
Analysis of Variance Table

Response: growth
          Df Sum Sq Mean Sq F value   Pr(>F)
treatment  3 2.6014 0.86713  5.2807 0.002963
**
Residuals 52 8.5388 0.16421
```

ANOVA

- ANOVA yields overall significance of treatment
- Note: overall results will be the same regardless of how contrasts are set up

Evaluating Contrasts

```
>summary.lm(mangrove.model2)
    Coefficients:
                Estimate Std. Error t value Pr(>|t|)
    (Intercept)  0.68000    0.05415  12.558  < 2e-16 ***
    treatment    0.12714    0.13264   0.959 0.342223
    treatment   -0.46762    0.12506  -3.739 0.000461 ***
    treatment    0.14857    0.15316   0.970 0.336519
> mean(my.means)
[1] 0.68
> mean(my.means[c('Tedania','Haliclona')]) - my.means[c('Foam')]
     Foam
0.1271429
> my.means['Control'] - mean(my.means[c('Foam','Haliclona','Tedania')])
  Control
-0.467619
> my.means[c('Tedania')] - my.means[c('Haliclona')]
  Tedania
0.1485714
```

Two-way ANOVA using Rat data

- rats <- read.csv('rats.csv')
- plot(time ~ treat + poison, data=rats)
- interaction.plot(rats$treat,rats$poison,rats$time)
- interaction.plot(rats$poison,rats$treat,rats$time)

Rat Data

- g <- lm(time ~ poison*treat, rats)
- anova(g)
- qqnorm(g$res)
- qqline(g$res)

Exercise 10

- Transform the rat response to `1/time`
- Refit the model using `lm`
- Undertake diagnostic residual plots to assess deviations from normality
- Assess the significance of the interaction term by calling the function `anova`

- Do treatments vary in effectiveness?
- Do poisons vary in toxicity?
- Does the success of treatment vary by poison?

Exercise 10 Answers

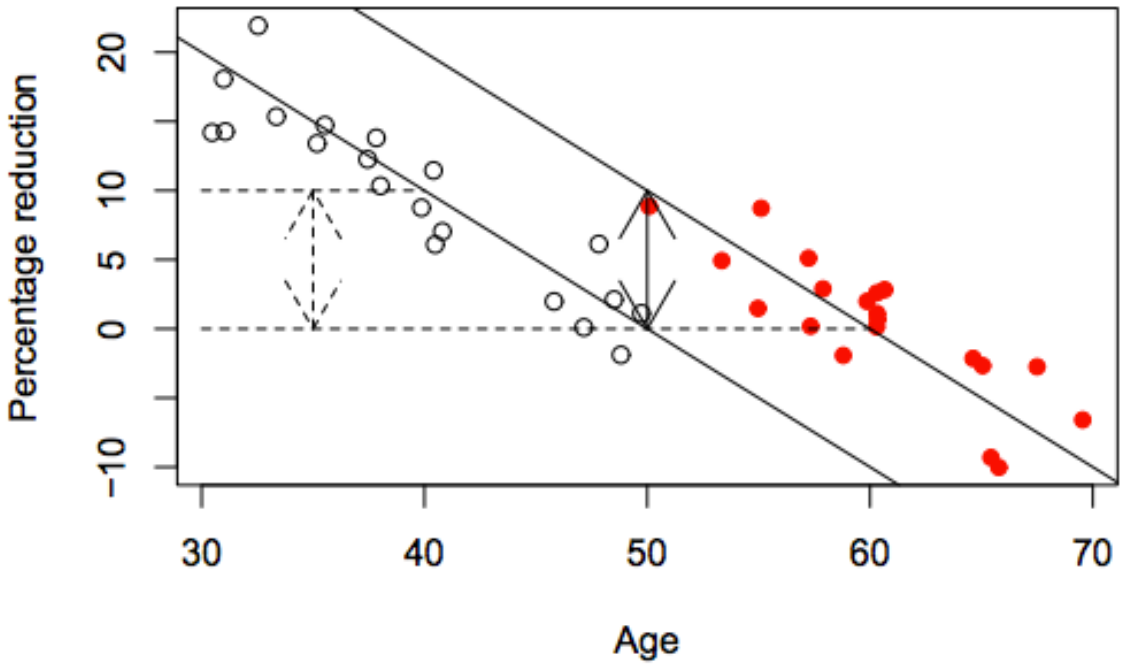
- g <- lm(1/time ~ poison*treat,rats)

- plot(g$fitted,g$res,xlab="Fitted",ylab="Residuals",main="Reciprocal response")
- qqnorm(g$res)
- qqline(g$res)

- anova(g)

ANCOVA

- Refers to regression problems where there is a mixture of quantitative and qualitative predictors



Dioxins in crabs

- Dioxins are a byproduct of pulp-and-paper production
- Carcinogenic
- Persist for many decades in the environment
- Dioxins are now banned in many countries

Worked Example: Dioxins in crabs

- Dioxins can remain in the environment for decades
- The following example is based on a real study
- Government environmental protection agencies take samples of crabs from affected areas each year and measure the amount of dioxins in the tissue.

Methods

- Each year, four crabs are captured from two monitoring stations which are situated quite a distance apart on the same inlet where the pulp mill was located

- The livers from all four crabs are composited together into a single sample

- There are many different forms of dioxin with different toxicities, so a summary measure, Total Equivalent Dose (TEQ), is calculated.

Formulating the Question

- Dioxin levels are given by D = log (TEQ)
- The dioxin level starts at level D_0 and declines linearly with time, t :

$$D = D_0 - r\ t$$

Question: Did the two sites have the same initial concentration of dioxin?

Response Variable: *D*

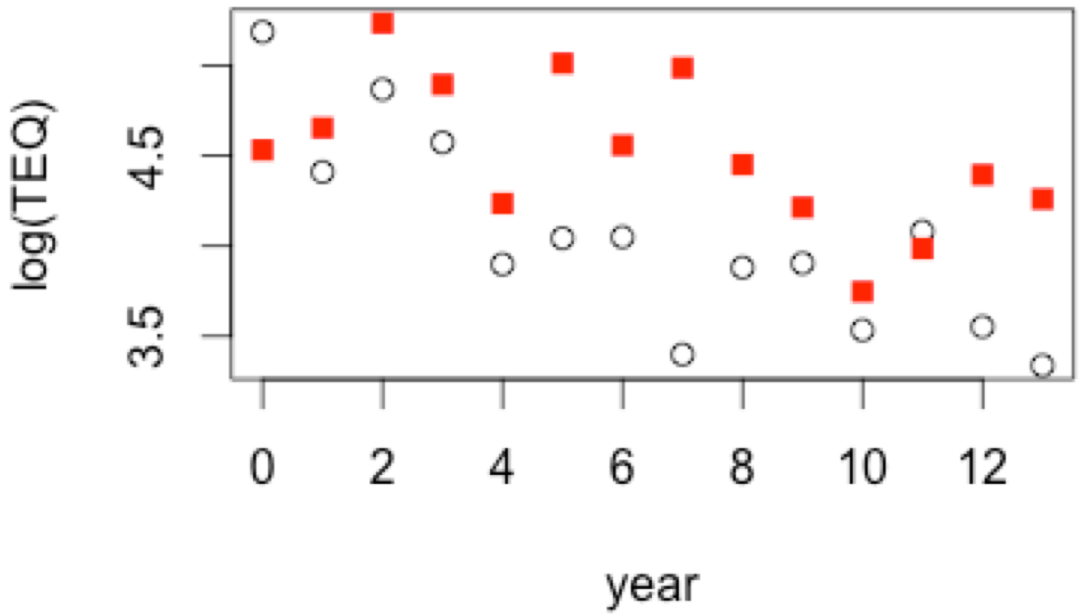
Explanatory Variables:

Site (1 or 2) – categorical

Time (years) - quantitative

How do the data look?

```
> plot(dioxin$Year,dioxin$logTEQ,
      xlab='year',ylab='log(TEQ)',type='n')
> points(dioxin$Year[dioxin$Site=='a'],
      dioxin$logTEQ[dioxin$Site=='a'])
> points(dioxin$Year[dioxin$Site=='b'],
      dioxin$logTEQ[dioxin$Site=='b'],pch=15,col='red')
```



Exercise 11

- Import the dataset `dioxin`
- Perform a homogeneity of slopes test by fitting a model of the form `lm(logTEQ~Year+Site+Year:Site,data=Year:Site)` and evaluating significance of the `length:style` term using the function `summary`
- If the slope difference is not significant, refit the model assuming a constant slope for both groups. Do the idiffer in height after controlling for length?

Further Information on ANOVA

- http://goanna.cs.rmit.edu.au/~fscholer/anova.php

- Provides details on how to partition variance, particularly with unbalanced designs

- My recommendation: if your design is unbalanced, and you have two (or more factors), consider using `Anova()` function in `car` package

GLM

Many response variables are inherently non-normal

- Counts (Integers >= 0; e.g. # of chicks)
- Non-negative continuous variables (>=0; e.g. times between foraging bouts)
- Proportions (0 <= P <= 1; e.g. proportion protein in the diet)
- Binary (integer 0/1 for failure/success; e.g. prey capture during predation event; presence-absence of species)

Modeling counts

- **Poisson regression** – simplest method; there are a number of extensions useful for count models (e.g. quasi-poisson)
- **Negative binomial regression** – for over-dispersed count data, meaning that the conditional variance exceeds the conditional mean

http://cran.r-project.org/web/packages/pscl/vignettes/countreg.pdf

Modeling non-negative continuous variables

- **Exponential regression** – assumes conditional distribution of response variable is exponentially distributed
- **Gamma regression** – assumes conditional distribution of response variable is gamma distributed

Modeling proportions

- **Beta regression** – Assumes conditional distribution of response variable is beta distributed

- Unlike the other types of regression, beta regression can't be conducted using glm()

http://cran.r-project.org/web/packages/betareg/vignettes/betareg.pdf

Modeling binary data

- **Logistic Regression** – standard method, involves modeling binary data using the logit link function

- **Probit Regression** – another frequently used method, involves modeling binary data using the probit link function

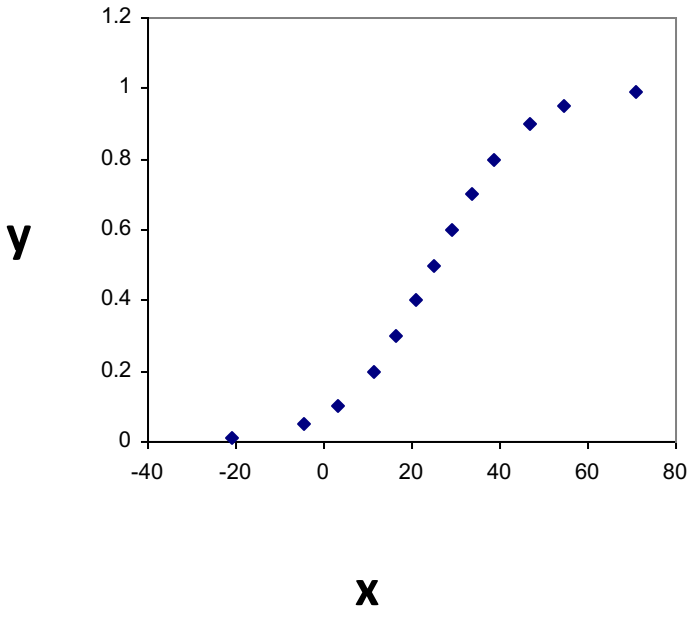
All of these different types of regression are GLM

- Conditional distributions differ:
  - Poisson regression
  - Negative binomial regression
  - Logistic regression
  - Exponential Regression
- Only link functions differ (both assume binomial distribution)
  - Logistic regression
  - Probit regression

Logistic regression

- Old way: arcsine transformation proportion and try OLS regression

- New (better) way: use logit (or probit) link with binomial errors



Source: www.zoology.ubc.ca/~srivast/zool502/Wkshp3-R.ppt

Logistic regression

p = proportion of successes

If $p = e^{ax+b} / (1+ e^{ax+b})$ calculate log(odds):

$$\log_e(p/1-p)$$

Source: www.zoology.ubc.ca/~srivast/zool502/Wkshp3-R.ppt

Logistic regression

Output from logistic regression with logit link:
predicted $\log_e (p/1-p) = a+bx$

To obtain any expected values of p, need to input a and b in original equation:

$p = e^{ax+b} / (1+ e^{ax+b})$

Source: www.zoology.ubc.ca/~srivast/zool502/Wkshp3-R.ppt

Logistic regression analysis

- Import the following file:
  - `binary.csv`
- During import, make sure you specify the separator as comma
- Recode **rank** from numeric to factor
- View the dataset

Logistic regression analysis

- Attributes of data:
  - This dataset has a binary response (outcome, dependent) variable called **admit**.
  - There are three predictor variables: **gre**, **gpa** and **rank**. We will treat the variables **gre** and **gpa** as continuous.
  - The variable **rank** takes on the values 1 through 4. Institutions with a rank of 1 have the highest prestige, while those with a rank of 4 have the lowest.

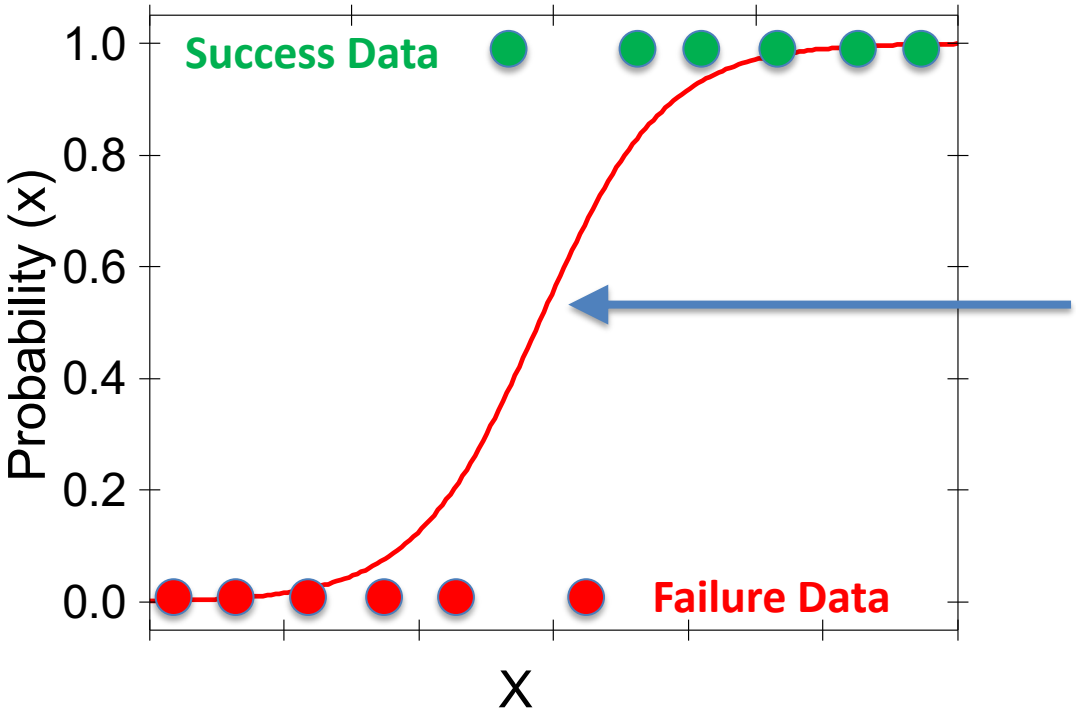
Logistic regression analysis

- Code:
  - `glm(formula = admit ~ gre + gpa + rank, family = binomial(logit), data = admit)`
- Predictors:
  - `gpa + gre + rank`
- Response:
  - `admit`
- Form:
  - Binomial response
  - Logit link

Logistic regression analysis: Summary with Wald Tests

```
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.989979   1.139951  -3.500 0.000465 ***
gpa          0.804038   0.331819   2.423 0.015388 *
gre          0.002264   0.001094   2.070 0.038465 *
rank[T.2]   -0.675443   0.316490  -2.134 0.032829 *
rank[T.3]   -1.340204   0.345306  -3.881 0.000104 ***
rank[T.4]   -1.551464   0.417832  -3.713 0.000205 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 499.98  on 399  degrees of freedom
Residual deviance: 458.52  on 394  degrees of freedom
AIC: 470.52

Number of Fisher Scoring iterations: 4
```

Calculating the Likelihood, *L*, for Logistic Regression



$$\ln\left[\frac{P(x_i)}{1-P(x_i)}\right] = \beta_0 + \beta_1 x_i$$

$$P(x_i) = \frac{\exp[\beta_0 + \beta_1 x_i]}{1 + \exp[\beta_0 + \beta_1 x_i]}$$

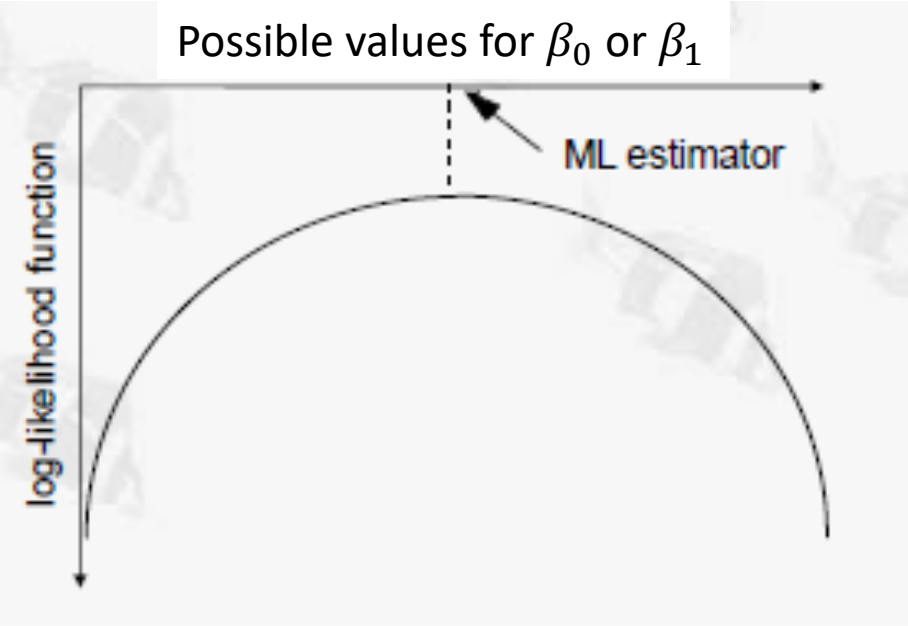
$$1\text{-}P(x_i) = \frac{1}{1+\exp[\beta_0+\beta_1 x_i]}$$

$$L = \prod_{\text{green}} P(x_i) \prod_{\text{red}} (1 - P(x_i)) = \prod_{\text{green}} \frac{\exp[\beta_0 + \beta_1 x_i]}{1 + \exp[\beta_0 + \beta_1 x_i]} \prod_{\text{red}} \frac{1}{1 + \exp[\beta_0 + \beta_1 x_i]}$$

Maximum Likelihood

We can work out which hypothesis (i.e. which values of β_0 and β_1) has the maximum likelihood (ML) – that is, which hypothesis is most likely

(Use logs because it makes the calculation a lot simpler)



Quinn & Keough p 24

Exercise 13

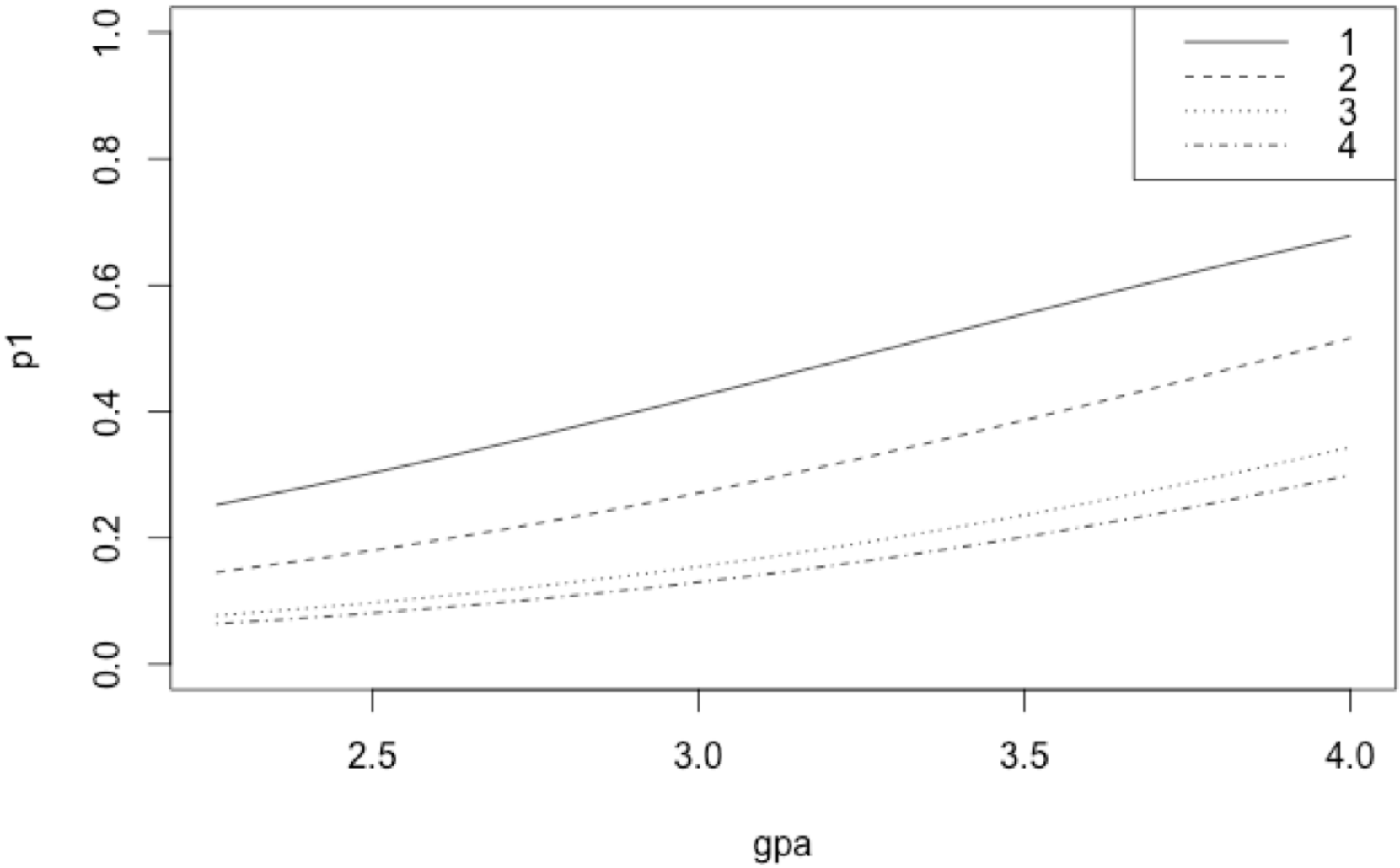
- Fit the full model, including `gpa`, `gre`, and `rank`, using `glm`
- Assess the significance of each term in the model using `drop1(…, ,test='Chisq')`
- Refit the model after dropping the term of lowest significance
- Harder: plot the predicted **P values** of the model for a range of predictor variables

Exercise 13 Answers

- `g <- glm(formula = admit ~ gre + rank + gpa, family = binomial(logit), data = binary)`
- `drop1(g, test='Chisq')`
- `g <- glm(formula = admit ~ gpa + rank, family = binomial(logit), data = binary)`

Plot of Model

- `gpa <- seq(2.26,4,length=100)`
- `p1 <- exp(1.0521*gpa-3.4636)/(1+exp(1.0521*gpa-3.4636))`
- `p2 <- exp(1.0521*gpa-3.4636-0.6810)/(1+exp(1.0521*gpa-3.4636-0.6810))`
- `p3 <- exp(1.0521*gpa-3.4636-1.3919)/(1+exp(1.0521*gpa-3.4636-1.3919))`
- `p4 <- exp(1.0521*gpa-3.4636-1.5943)/(1+exp(1.0521*gpa-3.4636-1.5943))`
- `plot(gpa,p1,ylim=c(0,1),lty=1,type='l')`
- `points(gpa,p2,ylim=c(0,1),lty=2,type='l')`
- `points(gpa,p3,ylim=c(0,1),lty=3,type='l')`
- `points(gpa,p4,ylim=c(0,1),lty=4,type='l')`
- `legend('topright',legend=1:4,lty=1:4)`


p1
0.0
0.2
0.4
0.6
0.8
1.0
2.5
3.0
3.5
4.0
gpa
1
2
3
4