Statistical inference and linear models

December 6, 2018

1 Statistical inference

2 Little R-Studio tricks

3 t-test, ANOVA, regression: all is one, one is all

4 Linear models in details

General approach

1. Scientific question

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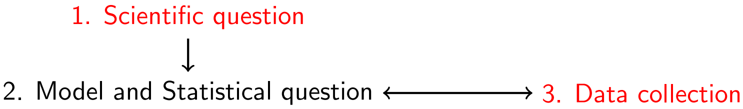
↓

2. Model and Statistical question

General approach



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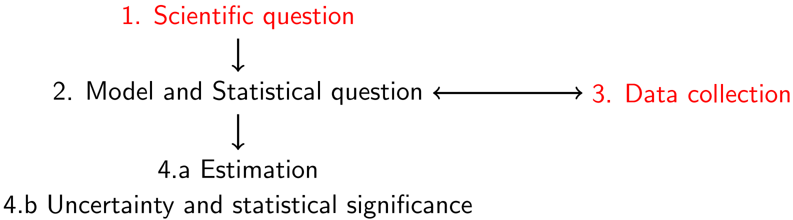

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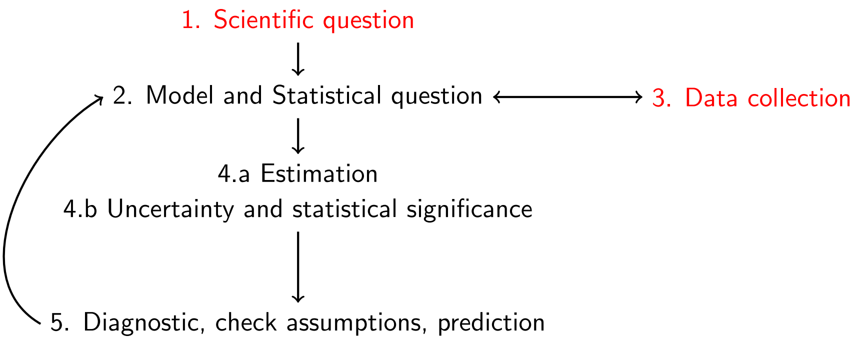
4.a Estimation

4.b Uncertainty and statistical significance

General approach



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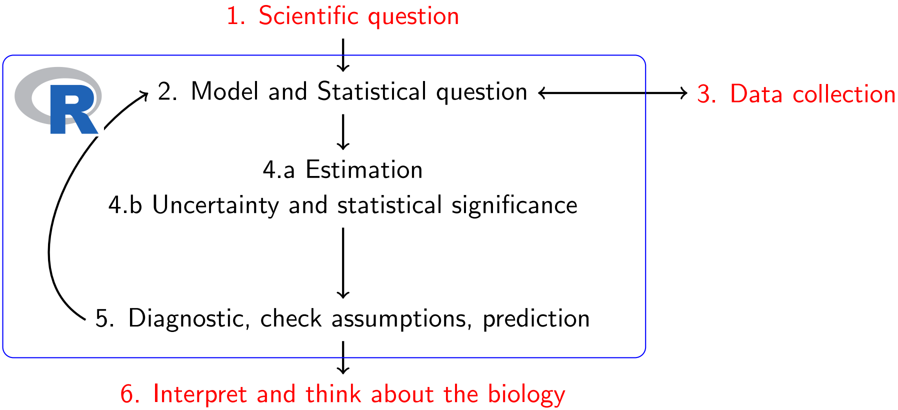

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Iris t.test

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str(iris)
plot(iris)
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   - Model:
     - There is an intrinsic/expected sepal length value for a species; an individual value is the sum of this expectation and a random Gaussian deviation.
     - $y_i = \mu_{species_i} + \epsilon_i$ with $\epsilon \sim N(0, \sigma^2)$
     - t-test

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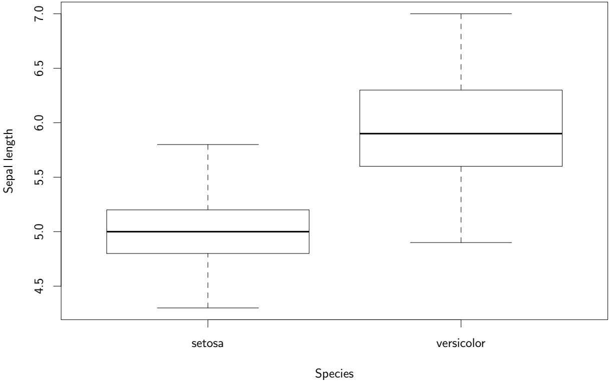
    - Statistical question:
        - Does sepal length **differ significantly** between the two taxa **in our sample**?
        - Is the observed difference between taxa likely if both taxa have the same intrinsic/expected value?
3. Data collection

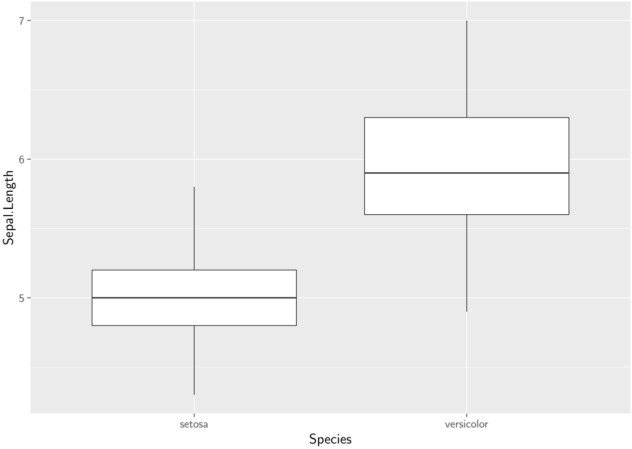
Iris t.test, visualization

```
boxplot(Sepal.Length ~ Species,
        data = iris[iris$Species %in% c("setosa","versicolor"),],
        drop = TRUE, ylab="Sepal length", xlab="Species")
```



Iris t.test, visualization

```
library(ggplot2)
  ggplot( iris[iris$Species %in% c("setosa","versicolor"),],
          aes(x=Species, y=Sepal.Length)) + geom_boxplot()
```



Iris t.test

One t-test for sepal length between *setosa* and *versicolor*:

```
  t.test(x = iris$Sepal.Length[iris$Species == "setosa"],
        y = iris$Sepal.Length[iris$Species == "versicolor"])


Welch Two Sample t-test

data:  iris$Sepal.Length[iris$Species == "setosa"] and iris$Sepal.Le
t = -10.521, df = 86.538, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.1057074 -0.7542926
sample estimates:
mean of x mean of y
    5.006     5.936
```

When do we know it is different?

4. Statistical estimation
   - a Estimation
     - Cannot know true difference $\mu_{species_1} - \mu_{species_2}$
     - Estimated difference $=$ $\text{Mean}_1 - \text{Mean}_2$
     - Estimated difference contains random variation
   - b Quantify uncertainty / Statistical significance
     - $t = \frac{\text{Mean}_1 - \text{Mean}_2}{\text{Variation}} \frac{\sqrt{\text{Sample Size}}}{\sqrt{2}}$
     - We know exactly how t is distributed when $\mu_{species_1} - \mu_{species_2} = 0$
     - Hence we know probability of $\geq t$ if $\mu_{species_1} - \mu_{species_2} = 0$ (p-value)
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Less uncertainty with

- Larger absolute difference
- Smaller variability
- Larger sample size

When do we know it is different? Simulations

Simulations in R

- Pseudo-random generator
- Deterministic chain starting from a number calculated from computer time and R processus ID (the ”seed”)
- Hence reproducible using `set.seed()`
- Default algorithm: Mersenne-Twister

```r
rnorm(n = , mean = , sd = )
```

When do we know it is different? Simulations

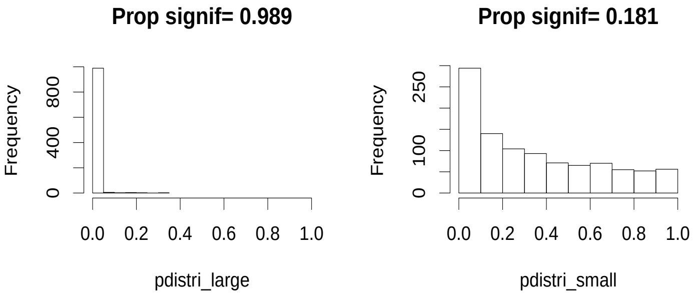
When do we know it is different? Simulations

1. Larger absolute difference

```r
nbsim <- 1000
pdistri_large <- vector(length = nbsim)
pdistri_small <- vector(length = nbsim)
for (i in 1:nbsim)
  {
  x1 <- rnorm(n = 10, mean = 2, sd = 1)
  x2 <- rnorm(n = 10, mean = 4, sd = 1) #large diff
  x3 <- rnorm(n = 10, mean = 2.5, sd = 1) #small diff
  out_large <- t.test(x1, x2)
  out_small <- t.test(x1, x3)
  pdistri_large[i]<-out_large$p.value
  pdistri_small[i]<-out_small$p.value
}
```

When do we know it is different?

```
par(mfrow=c(1,2), cex=2)
hist(pdistri_large, xlim=c(0,1),
     main=paste("Prop signif=",mean(pdistri_large<0.05)))
hist(pdistri_small, xlim=c(0,1),
     main=paste("Prop signif=",mean(pdistri_small<0.05)))
```



```
par(mfrow=c(1,1))
```

When do we know it is different? Try it!

Exercise

Check the effect of smaller variability and/or larger sample size.

By the way, what are these p-values?

Probability for a summary statistic to be greater or equal to the observed summary statistic, **when the null-hypothesis of a given statistical model is true.**

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Properties

- Depends on the null-hypothesis (H_0) of a given model with assumptions
- Uniform distribution under H_0 . . .
- . . . hence proportion(significance under H_0) = significance threshold

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- Uniform distribution under H_0 …
- … hence proportion(significance under H_0) $=$ significance threshold

NB: Focus on *p*-value criticized, but common and they are no more evil than other misused statistics!

Playing with loops and p-values

```
set.seed(1234)
x <- rnorm(100)
y <- rnorm(100)
summary(lm(y~x))



Call:
lm(formula = y ~ x)

Residuals:
     Min       1Q   Median       3Q      Max
-2.88626 -0.61401  0.00236  0.58645  2.98774

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.03715    0.10498   0.354    0.724
x           -0.02608    0.10378  -0.251    0.802

Residual standard error: 1.037 on 98 degrees of freedom
```

Playing with loops and p-values

While-loop

Are we every going to find a significant p-value with two sets of random numbers? Write a while loop to find out. How many iterations until you find a p-value below 0.05?

For-loop

How often do you observe a significant test with randomly drawn numbers?

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Column selection

```r
lm1   <- lm(y ~ x1 + x2)
lm2   <- lm(y ~ 1)
lm3   <- lm(y ~ x1*x2)
lm3   <- lm(y ~ x2)
lm4   <- lm(y ~ x1)
...

plot(lm1)
plot(lm2)
...
```

Column selection

You changed the name to be more explicit

```
lmadd  <- lm(y ~ x1 + x2)
lmnull <- lm(y ~ 1)
lmff   <- lm(y ~ x1*x2)
lmx2   <- lm(y ~ x2)
lmx1   <- lm(y ~ x1)
...

plot(lm1)
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What a pain to repeat the changes in `plot()`!

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`Alt + click`

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What if my code was not well aligned??

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```

`Ctrl + Alt + clicks` creates multiple cursors
then `Shift + Home` and `Ctrl + C`

Shortcuts

`Alt + Shift + K`

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A small example

Animal behavior in response to weather
Load data:

```
getwd()
setwd()
```

```
dat.behav <- read.csv(file = "Data/datbehav.csv") # path to file
```

A small example

Animal behavior in response to weather
Load data:

```r
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setwd()
```

```r
dat.behav <- read.csv(file = "Data/datbehav.csv") # path to file
```

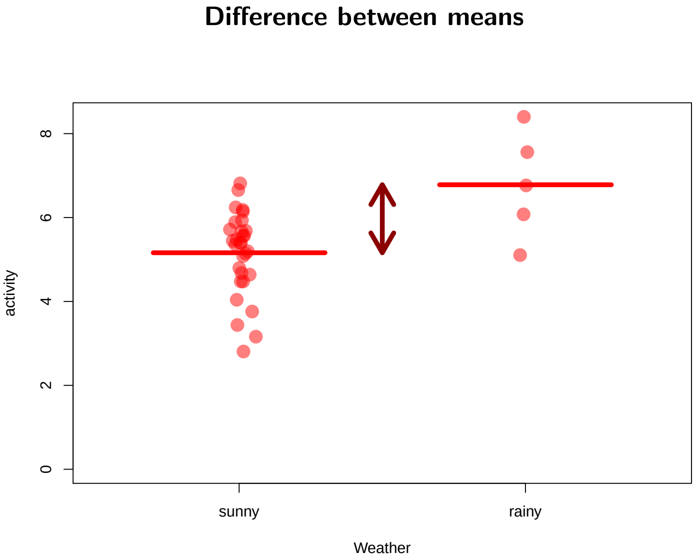
STEP 1: have a look at your data

```r
str(dat.behav)
summary(dat.behav)
plot(dat.behav)
```

t-test

```
fitstudent <- t.test(x = dat.behav$activity[dat.behav$weather==
                                              "rainy"],
                     y = dat.behav$activity[dat.behav$weather==
                                              "sunny"],
                     var.equal = TRUE)
print(fitstudent)


Two Sample t-test

data:  dat.behav$activity[dat.behav$weather == "rainy"] and dat.beha
t = 3.2752, df = 33, p-value = 0.002485
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.6138373 2.6270325
sample estimates:
mean of x mean of y
 6.781476  5.161041
```

t-test, graphically

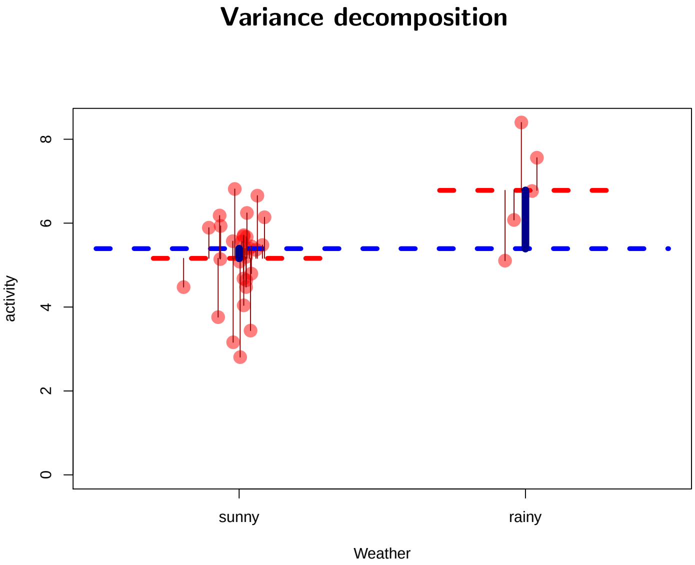


ANOVA

1. What is the fastest way to get row averages in a data-frame?
2. Create a function called colVars, like colMeans but for variance
3. Create nice plots to visualize iris data (ideally journal-quality)

```
fitanova <- aov(data = dat.behav, formula = activity ~ weather)
summary(fitanova)

            Df Sum Sq Mean Sq F value  Pr(>F)
weather      1  11.25  11.253   10.73 0.00248 **
Residuals   33  34.62   1.049
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

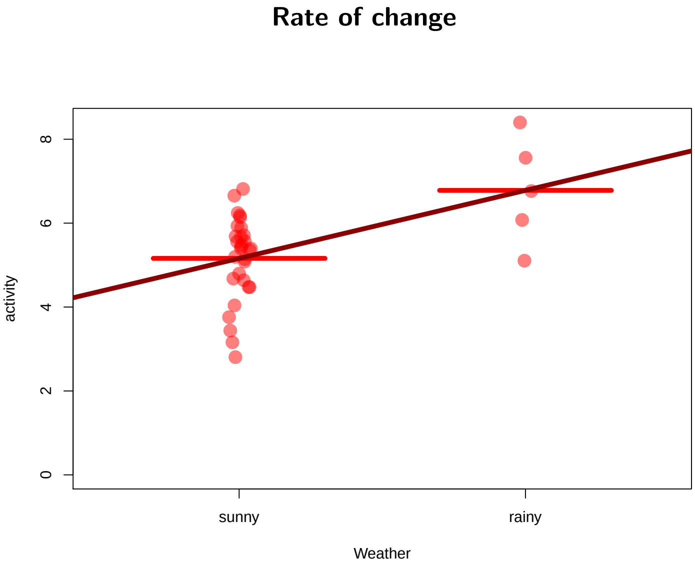
ANOVA, graphically



Linear regression

```
fitlm <- lm(data = dat.behav, formula = activity ~ weather)
summary(fitlm)


Call:
lm(formula = activity ~ weather, data = dat.behav)

Residuals:
    Min      1Q  Median      3Q     Max
-2.3547 -0.6028  0.2346  0.6419  1.6534

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)    6.7815     0.4581  14.805 3.94e-16 ***
weathersunny  -1.6204     0.4948  -3.275  0.00248 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.024 on 33 degrees of freedom
```

Regression, graphically



NB: aov() vs. anova()

```r
aov(data = dat.behav, formula = activity ~ weather)
anova(fitlm)
```

All is one. . .

All is one. . .

. . . but `lm()` rules!

- t-test, ANOVA, regression and others can be mathematically equivalent
- In R, `lm()` and related functions can do them all. . .
- . . . and much more!

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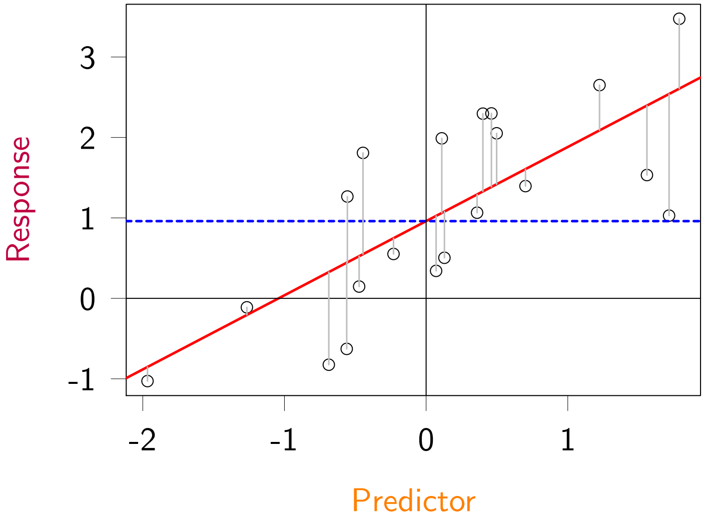
A simple linear model

Response = **Intercept** + **Slope** × **Predictor** + **Error**



A simple linear model

Response = **Intercept** + **Slope** × **Predictor** + **Error**

In R:

```
lm(response ~ 1 + predictor1 + predictor2, data=data)
  # equivalent to
lm(response ~ predictor1 + predictor2, data=data)
```

- Intercept can be explicit or implicit
- Can remove intercept with `...`$\sim$ `0 + ...`
- Error is implicit
- Feed the option `data=` to keep code short, reliable and flexible
- Order of predictors do not matter

Interpretation

```r
Ans <- read.csv(file = "Data/Anscombe.csv")
```

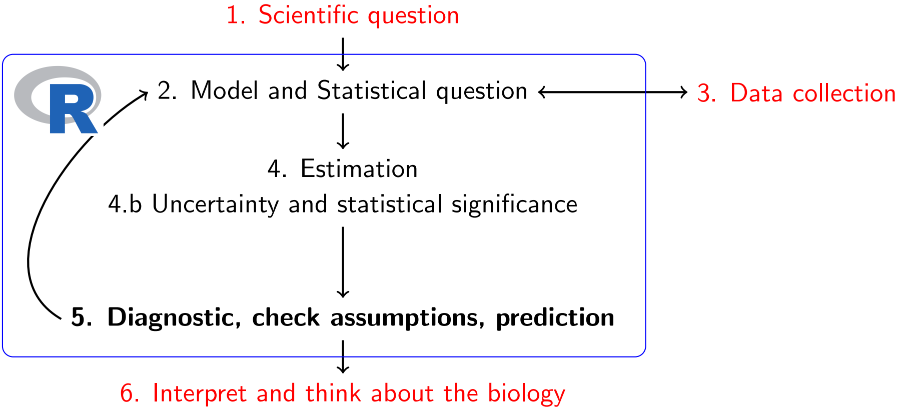
```r
lm1 <- lm(y ~ x , data=Ans[Ans$distri==1,])
summary(lm1)
plot(Ans$x[Ans$distri==1], Ans$y[Ans$distri==1],
     xlim=c(0,15), ylim=c(0,12))
abline(lm1)
```

Interpretation

lm vs. plot

- Fit a linear model $y \sim x$for each of the four “distri”
- Plot the relationship $y \sim x$ for each of the four “distri”
- Can we trust these models? For what?

General approach



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Not necessarily wrong, but typical interpretation assumes:

- Linear combination of parameters (including transformation, polynoms, interactions. . .)
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  Risk: Poor predictions
- Homoscedasticity (constant error variance)
  Risk: Over-optimistic uncertainty, unreliable predictions
- Independence of error
  Risk: Bias and over-optimistic uncertainty

Diagnostic: summary and plot

```
lm1 <- lm(y ~ x , data=Ans[Ans$distri==1,])
lm2 <- lm(y ~ x , data=Ans[Ans$distri==2,])
```

```
summary(lm1)
par(mfrow=c(2,2))
plot(lm1)
```

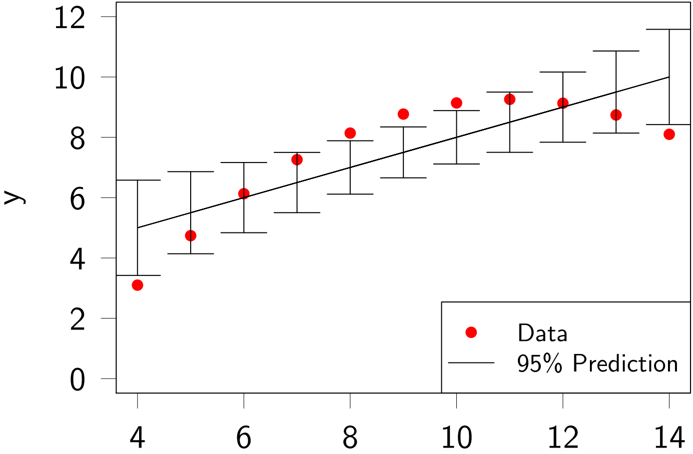
```
 summary(lm2)
plot(lm2)
 par(mfrow=c(1,1))
```

Diagnostic: prediction

```r
pred2 <- predict(lm2, se.fit = TRUE, interval = "confidence")
pred2 <- cbind(Ans[Ans$distri==2,], pred2)
```

Diagnostic: prediction

```
pred2 <- predict(lm2, se.fit = TRUE, interval = "confidence")
pred2 <- cbind(Ans[Ans$distri==2,], pred2)
```



Practice lm() with parasites

What explains variation in parasitic load?

You collected ecto-parasites on some furry large mammals at three locations. Parasites break easily when we collect them and are impossible to count, so we decide to measure parasitic load as their mass. **Why do some mammals have larger parasitic load?**

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- Load the `Para.csv` data (don't forget: str(), summary(), plot()...)
- Model `Parasite_Mass` using `lm()`
- Find what variables predict `Parasite_Mass`
- How good are your models? Assumptions? Prediction?
- What biological interpretation can you imagine?