

What on earth is going on with my linear models??!

March 8, 2018

1 Linear model, reminder

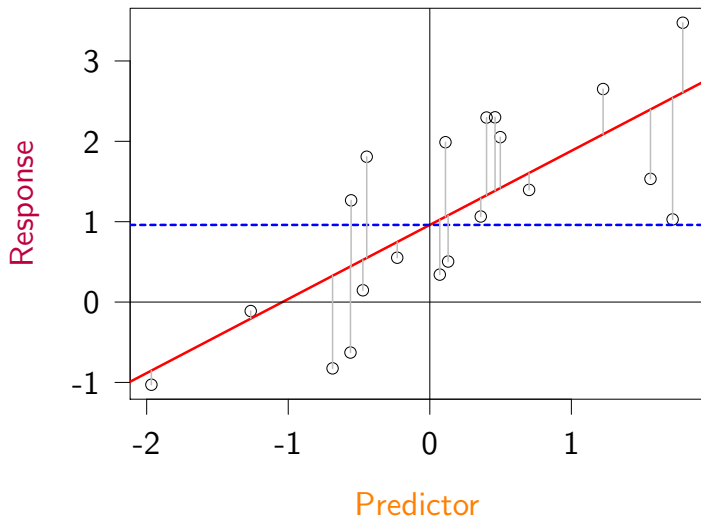
2 Checks and prediction

3 Cures

4 Bonus fun

# A simple linear model

$$\text{Response} = \text{Intercept} + \text{Slope} \times \text{Predictor} + \text{Error}$$



# A simple linear model

$$\text{Response} = \text{Intercept} + \text{Slope} \times \text{Predictor} + \text{Error}$$

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  $\dots \sim 0 + \dots$
- Error is implicit
- Feed the option `data=` to keep code short, reliable and flexible
- Order of predictors do not matter

1 Linear model, reminder

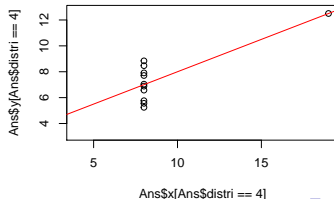
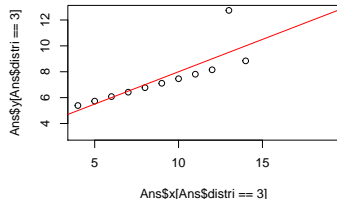
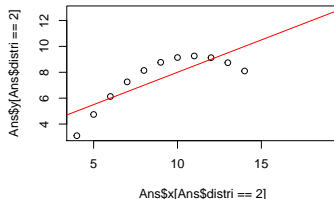
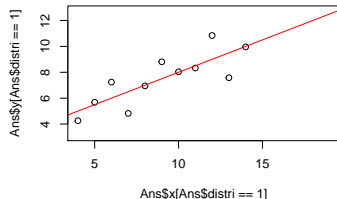
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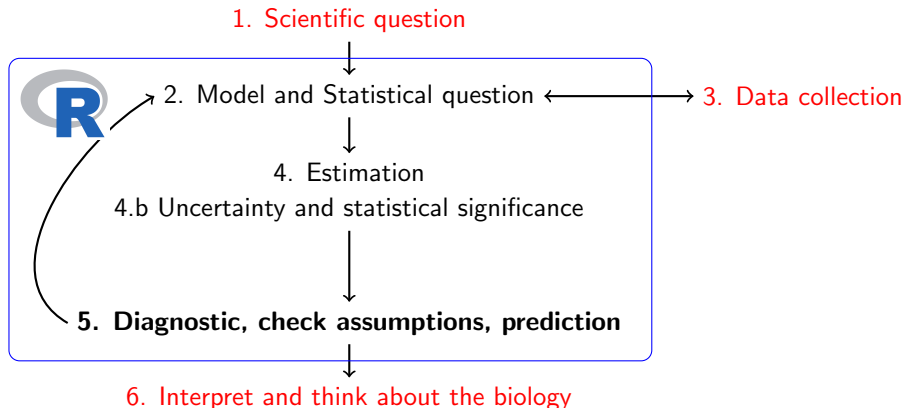
4 Bonus fun

# Why we need checks: summary(lm) isn't enough

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



# General approach



# Why we need checks: missing a relationship

```
forprediction <- read.csv(file = "forprediction.csv")
```

Does "predictor" predict "obs"?



# Why we need checks: missing a relationship

```
forprediction <- read.csv(file = "forprediction.csv")
```

Does "predictor" predict "obs"?

```
summary(lm(obs ~ 1 + predictor, data=forprediction) )
```

# Why we need checks: missing a relationship

Does "predictor" predict "obs"? Apparently not:

```
summary(lm(obs ~ 1 + predictor, data=forprediction) )
```

Call:

```
lm(formula = obs ~ 1 + predictor, data = forprediction)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.1962	-0.5326	0.1378	0.5785	1.8664

Coefficients:

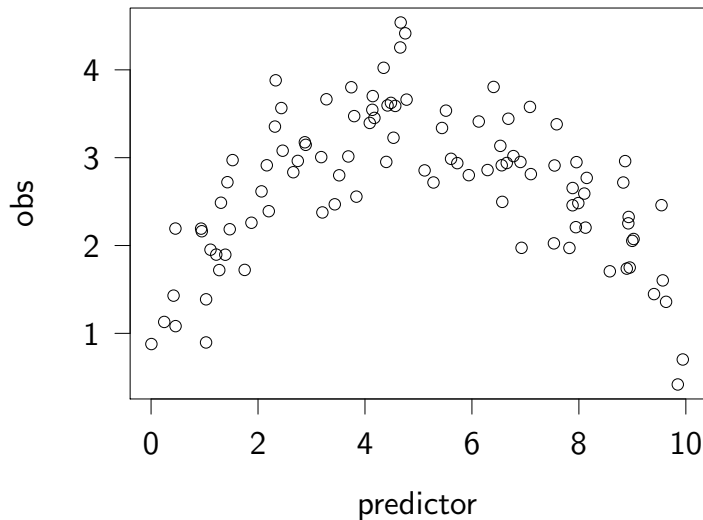
	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.72530	0.16953	16.076	<2e-16 ***
predictor	-0.01129	0.02956	-0.382	0.703

---

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

Residual standard error: 0.8382 on 98 degrees of freedom

# Why we need checks: missing a relationship



# How to check?

```
m0 <- lm(obs ~ 1 + predictor, data=forprediction)
summary(m0)
```

Call:

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lm(formula = obs ~ 1 + predictor, data = forprediction)
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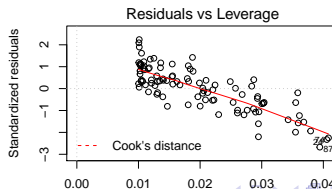
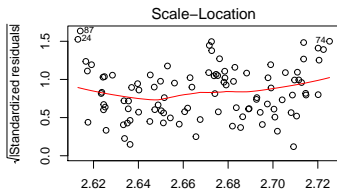
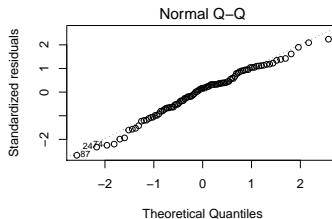
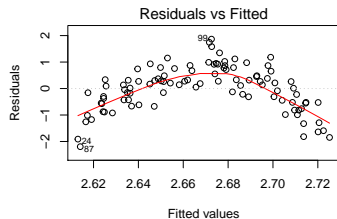
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# How to check?

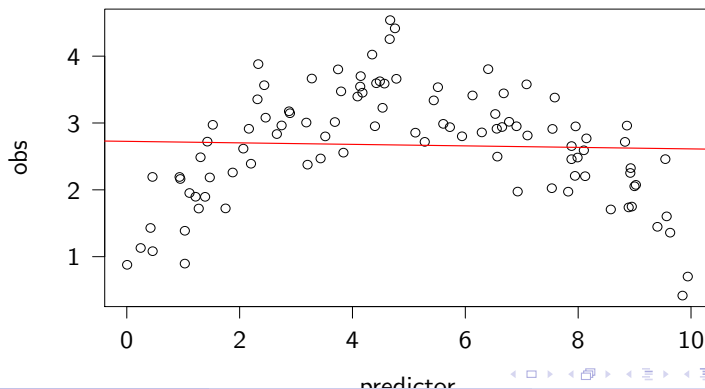
```
par(mfrow=c(2,2))  
plot(m0)
```



# How to check?

```
m0 <- lm(obs ~ 1 + predictor, data=forprediction)
```

```
setPar()  
plot(x=forprediction$predictor, y=forprediction$obs, xlab="predictor", ylab="obs")  
abline(m0, col="red", lwd=3) #simple prediction, without SE
```



# Check checklist

- **Visualize your data**
- Residual in summary(): are they symmetrical?
- plot(lm):
  - ① trend residual/fitted?
  - ② Normal residuals?
  - ③ trend in residual variance?
  - ④ outliers?
- Predictions: range and biological meaning

# Fix?

```
lm(obs ~ 1 + predictor , data=forprediction)
```



# Fix?

```
lm(obs ~ 1 + predictor , data=forprediction)
```

```
m1 <- lm(obs ~ 1 + predictor + I(predictor^2), data=forprediction)  
plot(m1)
```

How about prediction? (abline(m1) won't work here)

# Introduction to prediction

```
m1 <- lm(obs ~ 1 + predictor + I(predictor^2), data=forprediction)
coef(m1)
```

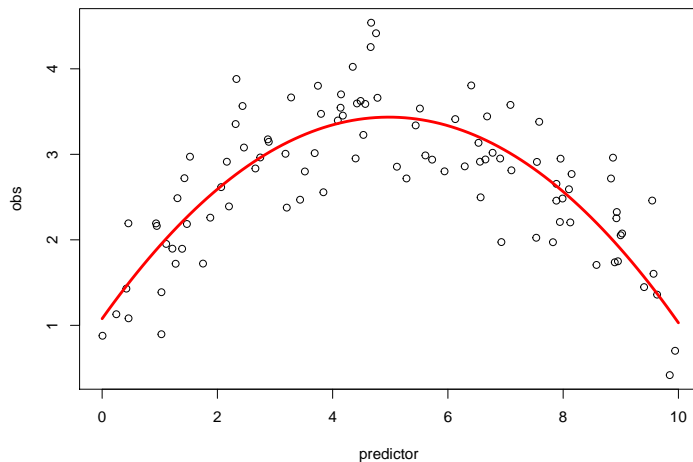
(Intercept)	predictor	I(predictor^2)
1.07782598	0.94760312	-0.09524182

## Small exercise

Use regression coefficients to predict "obs" from "predictor", and add a prediction line on the plot obs/predictor.

Is the fit satisfactory?

# Introduction to prediction



# Over-fit and collinearity

## Small exercise

Load Cdata.csv, fit models of y predicted by x1 and x2, or x2 and x3. Something is weird, what is going on? What to do?

Call:

```
lm(formula = y ~ x1 + x2, data = cdata)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.9679	-0.4763	-0.1581	0.4476	1.5434

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-22.45	127.66	-0.176	0.862
x1	23.43	127.74	0.183	0.856
x2	22.36	127.62	0.175	0.862

Residual standard error: 0.6513 on 32 degrees of freedom

# 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?**

# 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?**

- 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?

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# Multiple regression



# Transformations

# Linear model basic assumptions

Not necessarily wrong, but typical interpretation assumes:

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*Risk: Over-optimistic uncertainty, unreliable predictions*
- Independence of error  
*Risk: Bias and over-optimistic uncertainty*

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# Extra exercises

## General R coding

- 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)

## Linear models

- 1 Load `Cdata.csv`, fit models of  $y$  predicted by  $x_1$  and  $x_2$ , or  $x_2$  and  $x_3$ . Something is weird, what is going on? What to do?
- 2 For model that can be fitted with `t.test`, `aov`, and `lm`, is one of the function faster?
- 3 Write your own code to obtain a prediction from a `lm` (that is, a simpler version of the `predict` function), with confidence interval. (extra toughness: do it using the matrix formulation of the analytical solution to a linear model)

# What do you want to learn about?

## Topics

