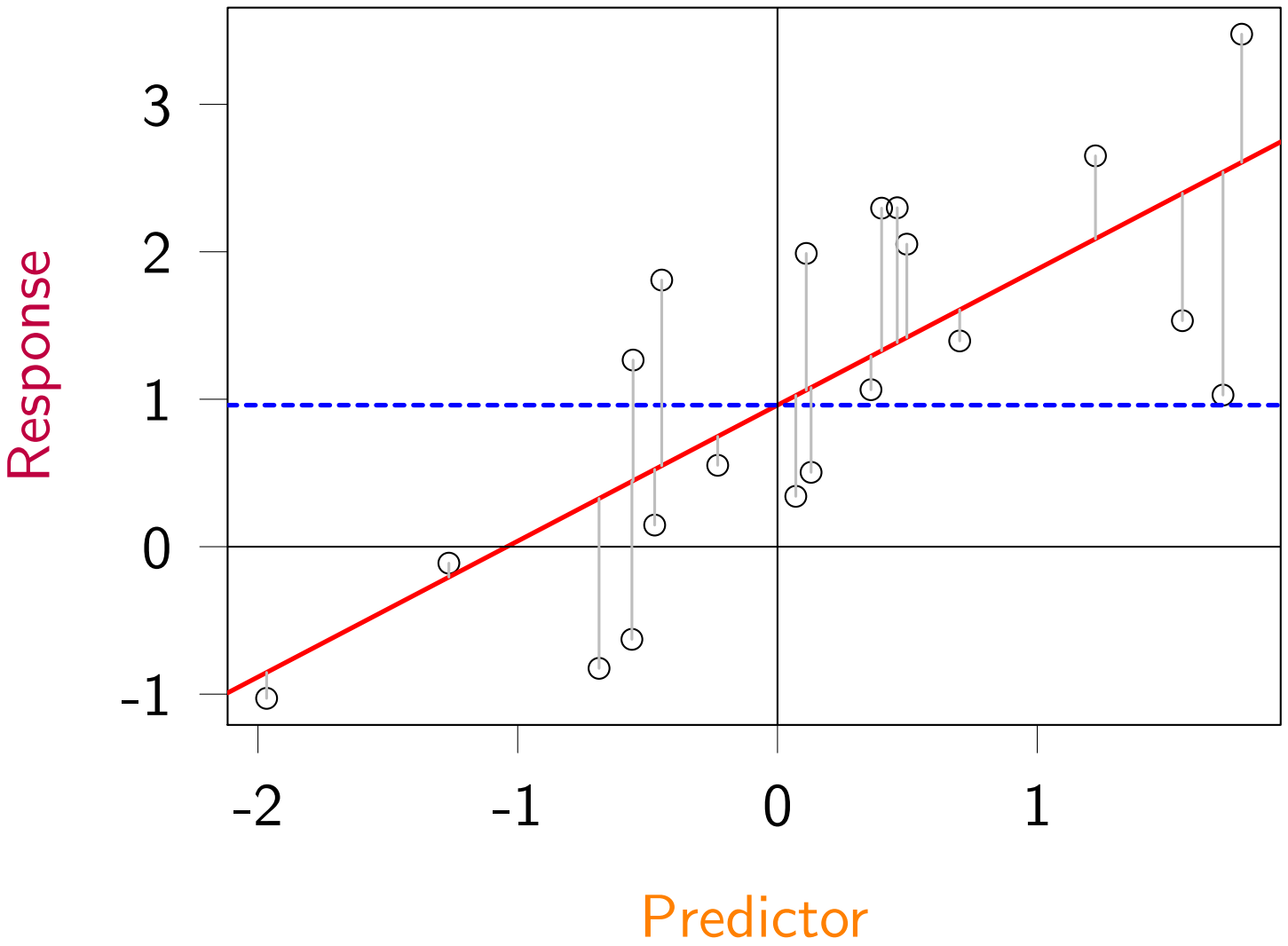
What on earth is going on with my linear models??!

March 9, 2018

A simple linear model

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



A simple linear model

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

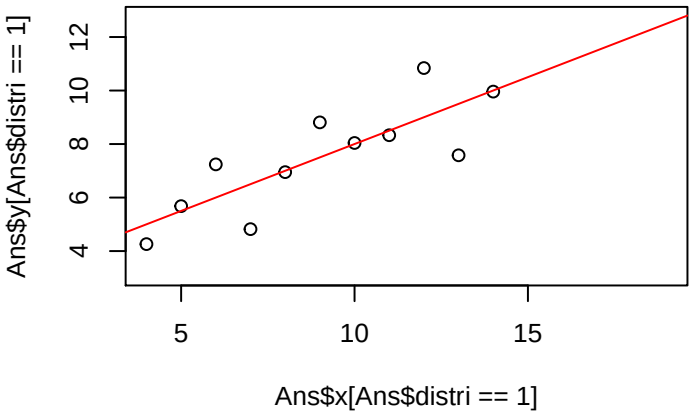
In R:

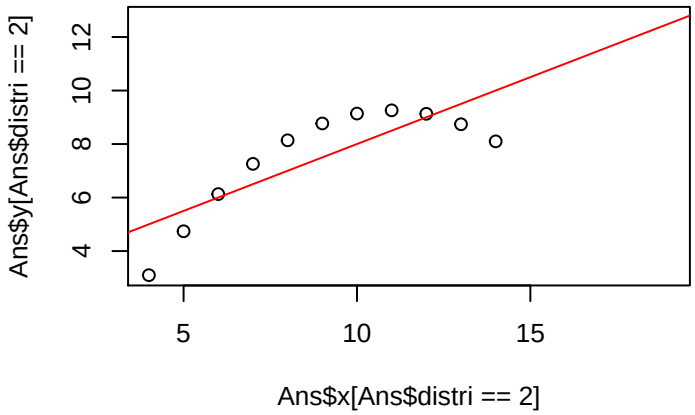
```
lm(response ~ 1 + predictor1 + predictor2, data=data)
```

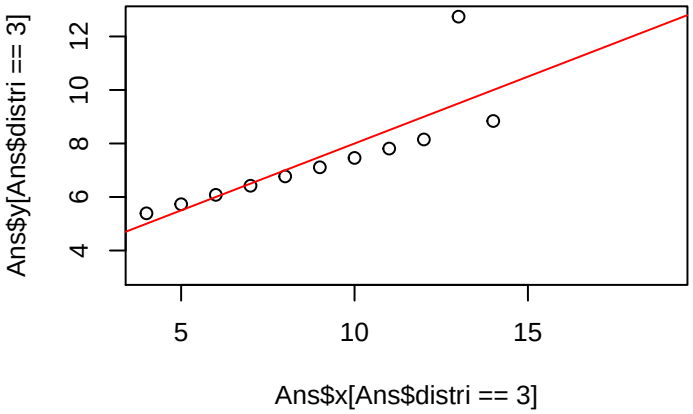
- Intercept can be explicit or implicit
- Can remove intercept with `...~ 0 + ...`
- Error is implicit
- Feed the option `data=` to keep code short, reliable and flexible
- Order of predictors do not matter

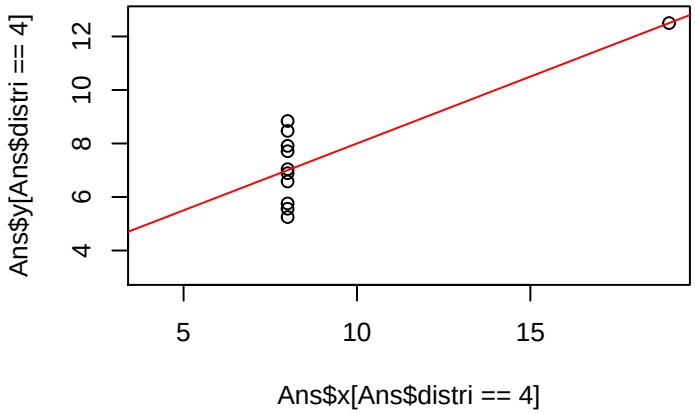
Why we need checks: summary(lm) isn't enough

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

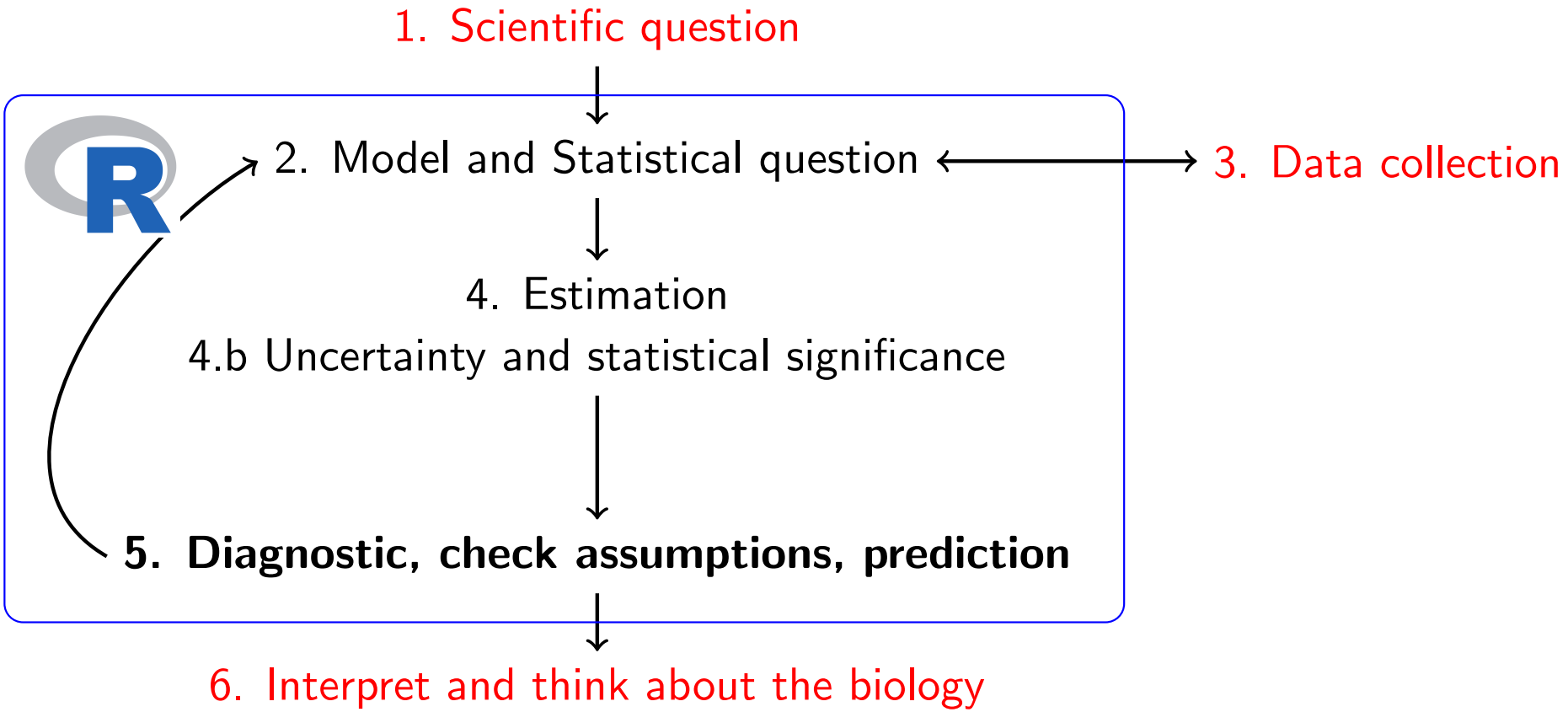








General approach



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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

Why we need checks: missing a relationship

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

Does "predictor" predict "obs"?

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```
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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
Multiple R-squared:  0.001487,Adjusted R-squared:  -0.008702
F-statistic: 0.1459 on 1 and 98 DF,  p-value: 0.7033
```

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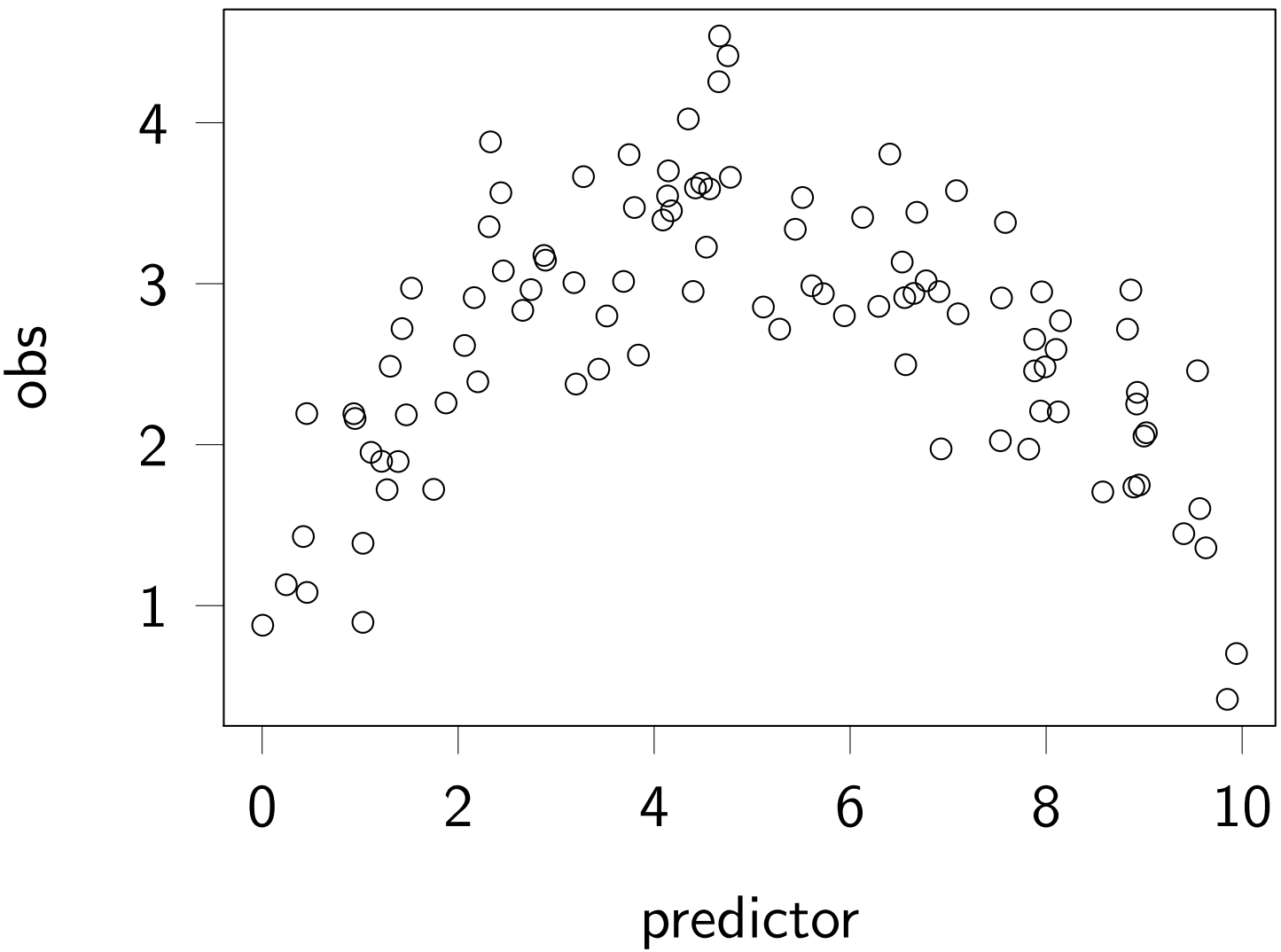

How to check?

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


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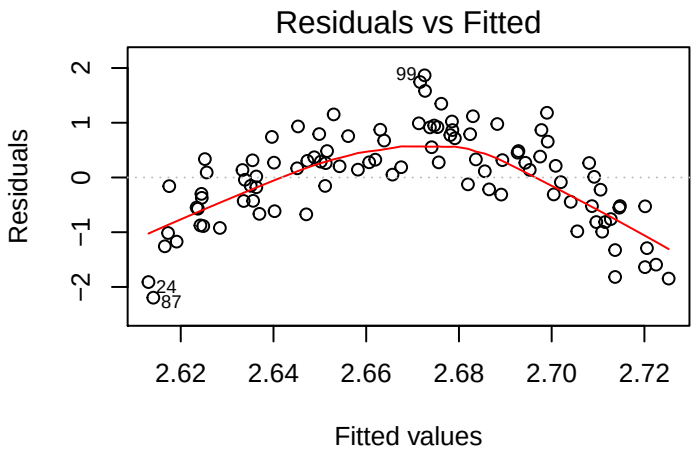
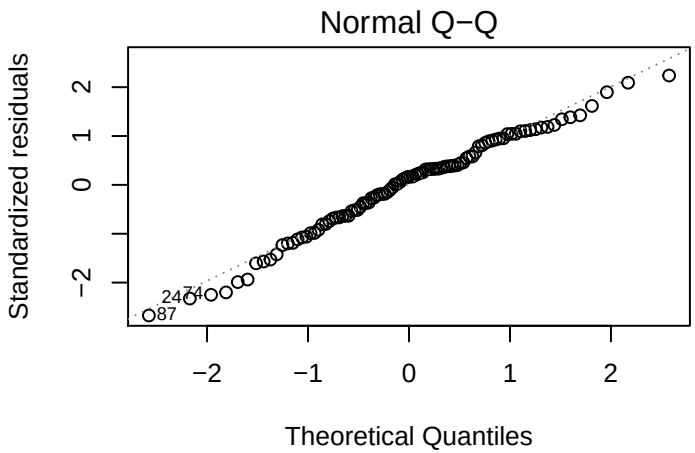
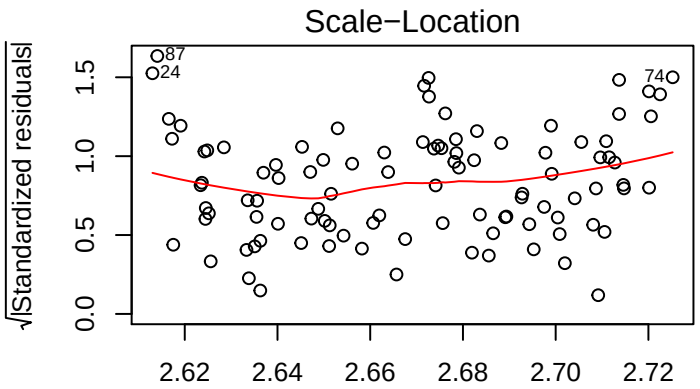
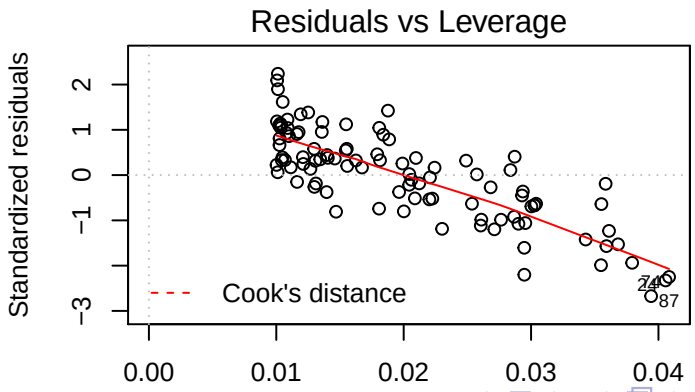
```
par(mfrow=c(2,2))
  plot(m0)
```





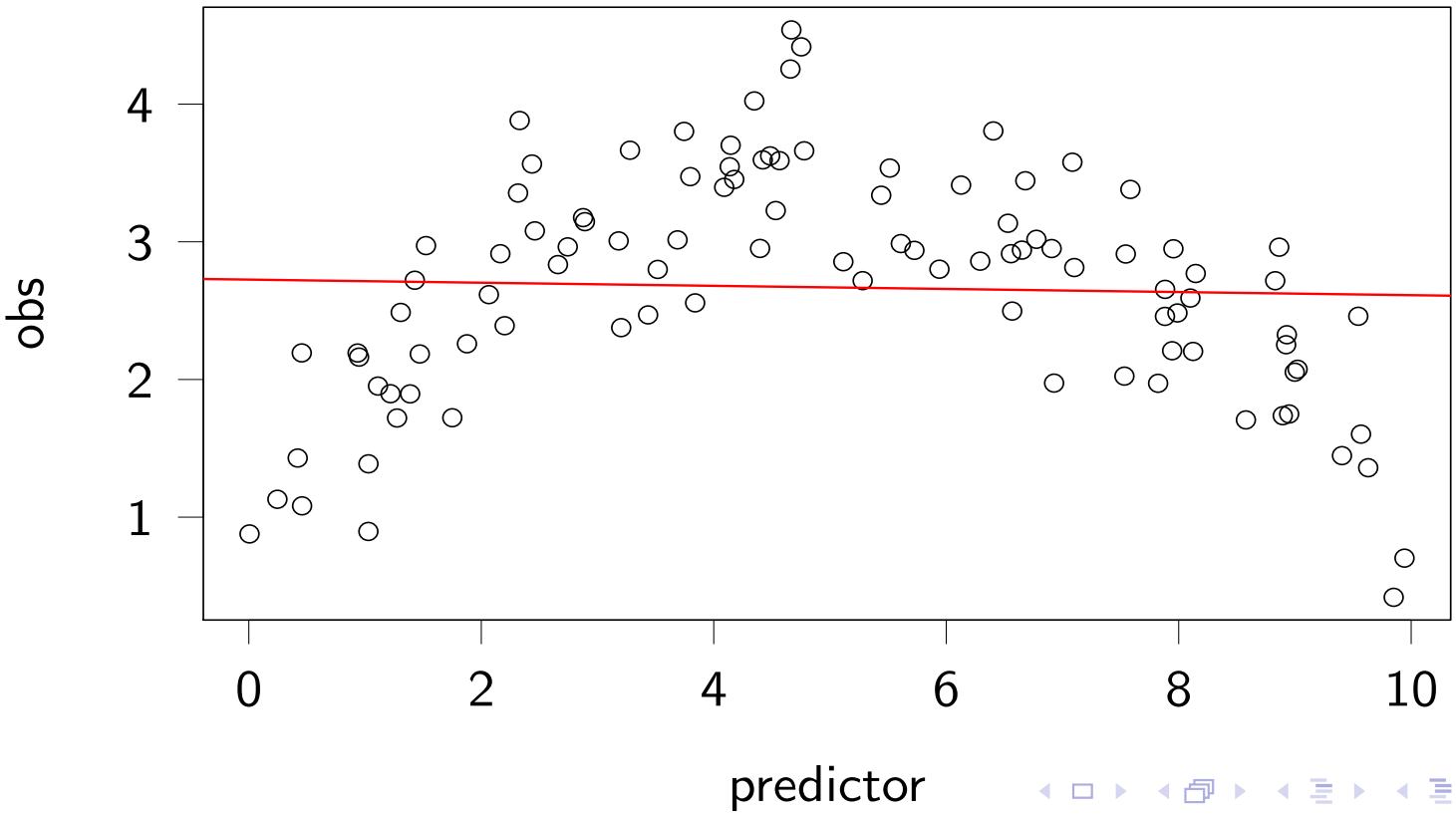




How to check?

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

```
    setPar()
plot(x=forprediction$predictor, y=forprediction$obs, xlab="predictor", ylab
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?

Plot suggests a quadratic relationship

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

Fix?

Plot suggests a quadratic relationship

```
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 because not straight line)

Introduction to prediction

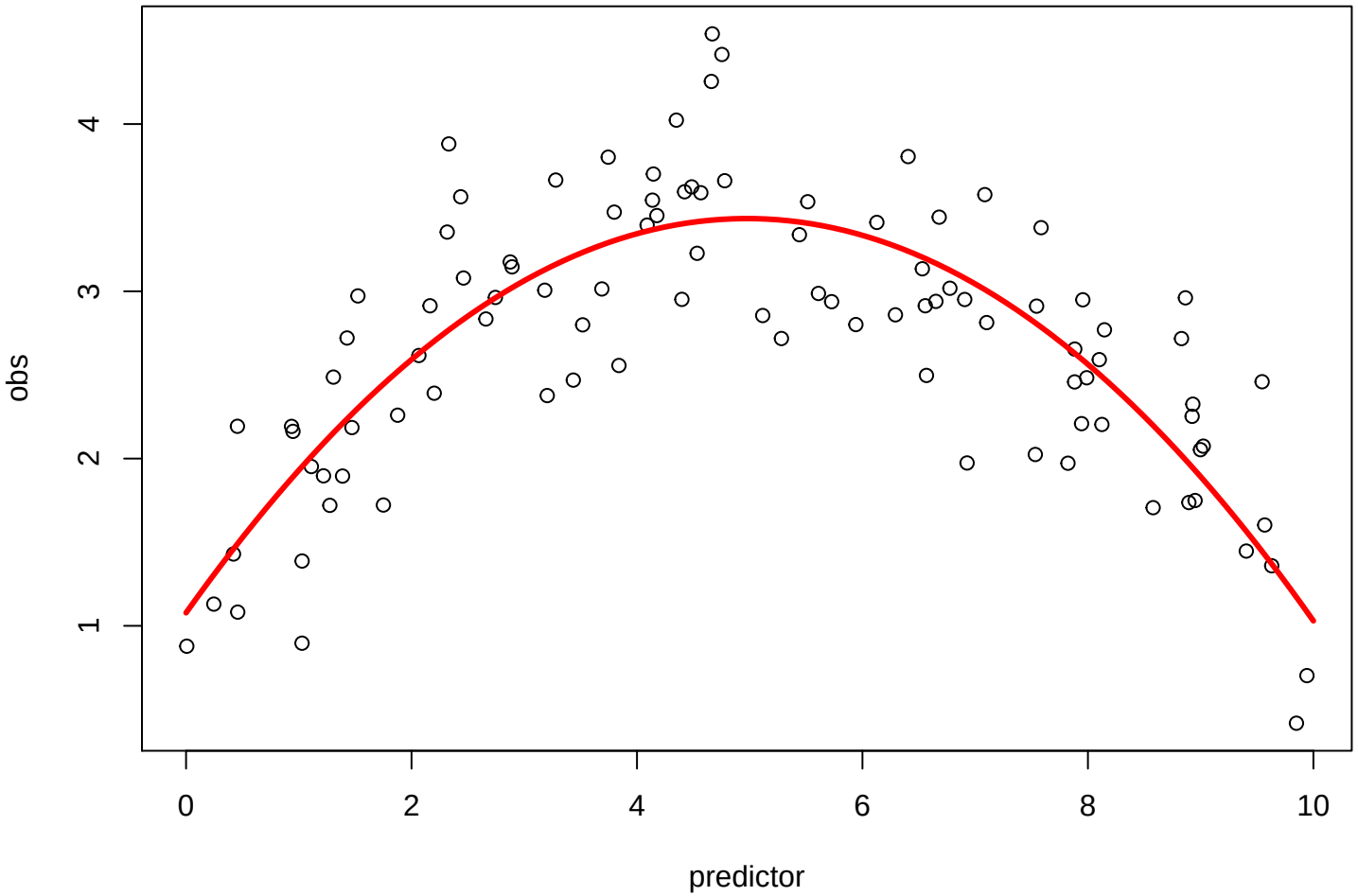
```
m1 <- lm(obs ~ 1 + predictor + I(predictor^2), data=forprediction)
coef(m1)

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

Exercise

1. Write mathematically the relationship between obs and predictor
2. Input regression coefficients in there to predict "obs" from "predictor"
3. 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 predited by x1 and x2, or x2 and x3.
Something is weird, what is going on? What to do?

Exponential data

Load the dataset `htrsdt.csv`.

```
plot(htrsdt$x, htrsdt$obs, ylim = c(-20, max(obs)))
abline(lm(obs ~ x, data=htrsdt))
summary(lm(obs ~ x, data=htrsdt))
plot(lm(obs ~ x, data=htrsdt))
```

Exponential data: prediction

Make a prediction over the range of x, with prediction interval

Exponential data: prediction

Make a prediction over the range of x, with prediction interval "By-hand"

```
lmhtrsdt <- lm(obs ~ x, data=htrsdt)
x <- seq(from=min(x), to=max(x), length.out = 100)
predhtrsdt <- coef(lmhtrsdt)[1] + x * coef(lmhtrsdt)[2]
```

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```

Function predict

```
Xnewdata <- data.frame(x=seq(from=min(x), to=max(x),
                             length.out = 100))
Xpred <- predict(object =  lm(obs ~ x, data=htrsdt), newdata = Xnewdata,
                 se.fit = TRUE, interval = "prediction")
```

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                 se.fit = TRUE, interval = "prediction")
```
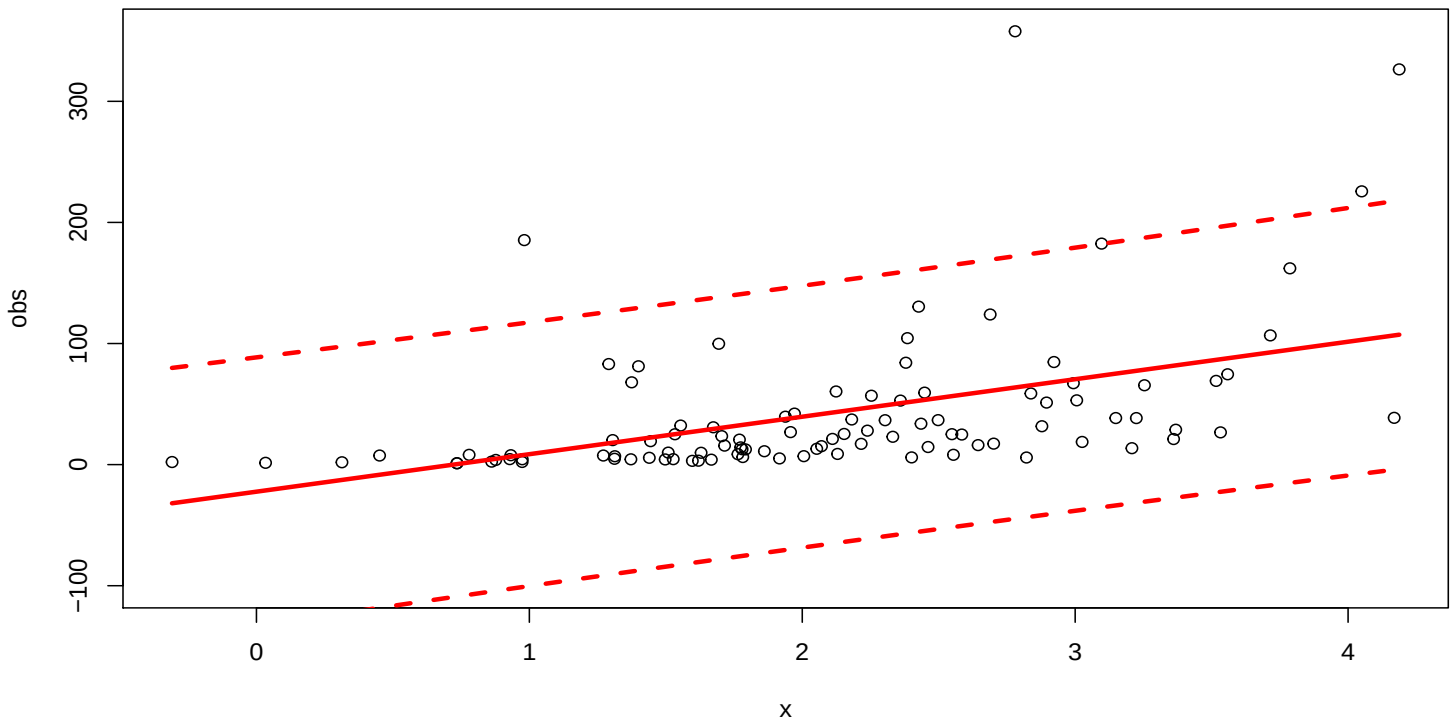

```
Xnewdata <- cbind(Xnewdata, Xpred)
```

```
head(Xnewdata)
```

Exponential data: prediction

```
plot(x, obs, ylim = c(-100, max(obs)))
lines(Xnewdata$x, Xnewdata$fit.fit, col="red", lwd=3)
lines(Xnewdata$x, Xnewdata$fit.lwr, col="red", lty=2, lwd=3)
lines(Xnewdata$x, Xnewdata$fit.upr, col="red", lty=2, lwd=3)
```



Exponential data: confidence

Prediction interval: Where the model predicts new data would be sampled, including variation unrelated to predictor

Exponential data: confidence

Prediction interval: Where the model predicts new data would be sampled, including variation unrelated to predictor
Confidence interval: Where your model predicts the MEAN new data would be sampled; or where is the true relationship with predictor

```
Xconf <- predict(object = lm(obs ~ x), newdata = Xnewdata,
                 se.fit = TRUE, interval = "confidence")
Xnewdata[,c("conf.lwr", "conf.upr")] <-  Xconf$fit[,2:3]
```

Exponential data: confidence

```
plot(x, obs, ylim = c(-100, max(obs)))
lines(Xnewdata$x, Xnewdata$fit.fit, col="red", lwd=3)
lines(Xnewdata$x, Xnewdata$fit.lwr, col="red", lty=2, lwd=3)
lines(Xnewdata$x, Xnewdata$fit.upr, col="red", lty=2, lwd=3)
lines(Xnewdata$x, Xnewdata$conf.lwr, col="blue", lty=2, lwd=3)
lines(Xnewdata$x, Xnewdata$conf.upr, col="blue", lty=2, lwd=3)
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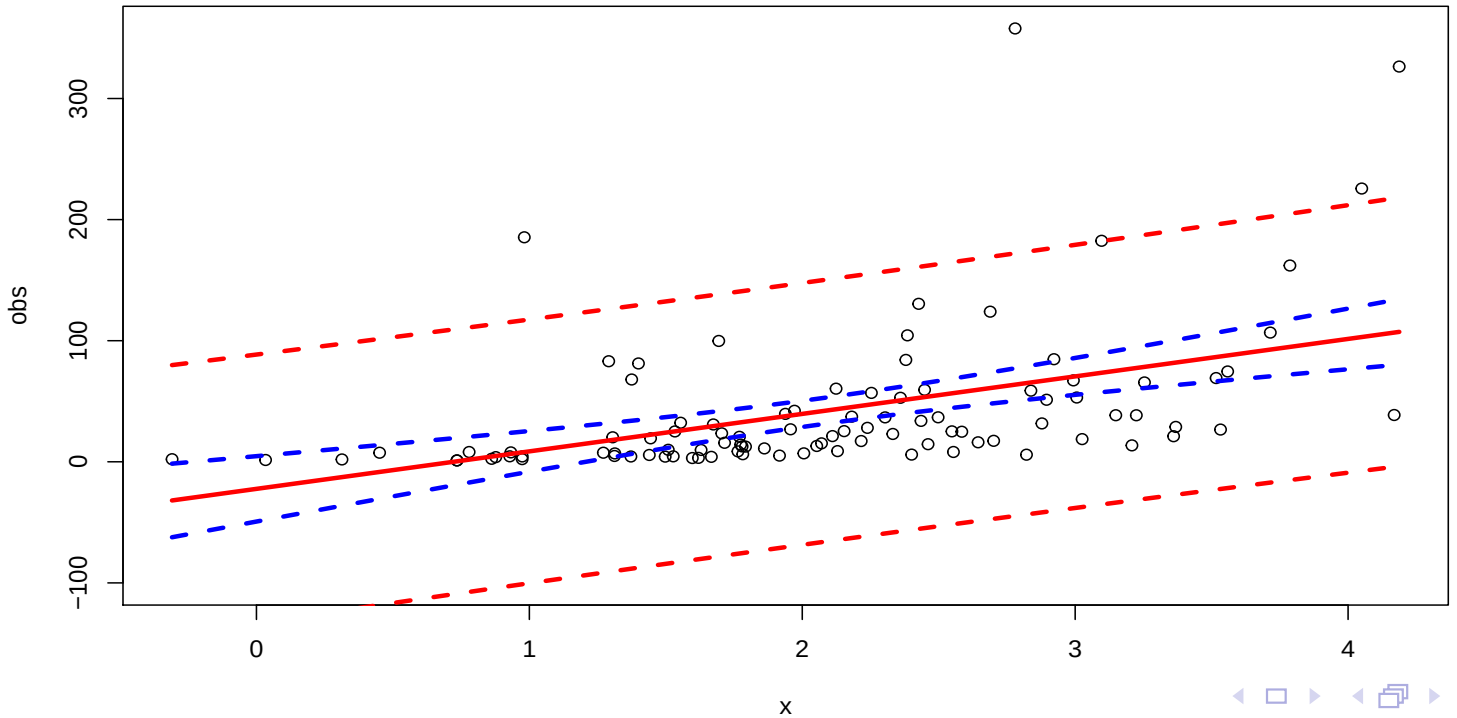

Exponential data: fix

Model sufficient to show positive relationship. . . BUT

- no negative values should exist
- too many outliers
- too much uncertainty on the left. . .

Consequences:

- impossible to understand the biological mechanism
- impossible to predict future observations

What to do?

Exponential data: fix

Log-transform

```
plot(x, log(obs)); abline(lm(log(obs) ~ x))
summary(lm(log(obs) ~ x))
plot(lm(log(obs) ~ x))
```

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summary(lm(log(obs) ~ x))
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```

By the way, the simulation process:

```
set.seed(123)
x <- 2+rnorm(100)
y <- 1 + x + rnorm(100)
obs <- exp(y)
```

Exponential data: other fix

Non-parametric statistics:
Rank observations, do greater ranks go together?

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Rank observations, do greater ranks go together?
Case of two continuous variable: Spearman's rank correlation

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Non-parametric statistics:
Rank observations, do greater ranks go together?
Case of two continuous variable: Spearman's rank correlation

```
cor.test(x = x, y = obs, method = "spearman")
```

```
Spearman's rank correlation rho

data:  x and obs
S = 60622, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.6362316
```

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Significant positive correlation confirmed, BUT, no biological mechanism, little predictive power.

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?

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- Generalized Linear Models
- (Generalized) Linear Mixed Models
- Non-linear models

Improvisation