"Simple and multiple regression are two of the most-used statistical procedures in biology. Statistical results from both procedures are commonly interpreted as metrics of the degree of relationship between (sometimes multiple) explanatory and response variables. This rough interpretation may generally be satisfactory for simple regressions, i.e., models involving only one explanatory variable. However, this interpretation can lead to confusion for multiple regression, where the coefficients of a multiple regression model measure something subtly but crucially different. . . "

Morrissey & Ruxton (2018) **Multiple Regression Is Not Multiple Regressions: The Meaning of Multiple Regression and the Non-Problem of Collinearity**. PTPBIO 10(3)

Multiple regressions

Timothée Bonnet

May 17, 2019

BDSI / RSB

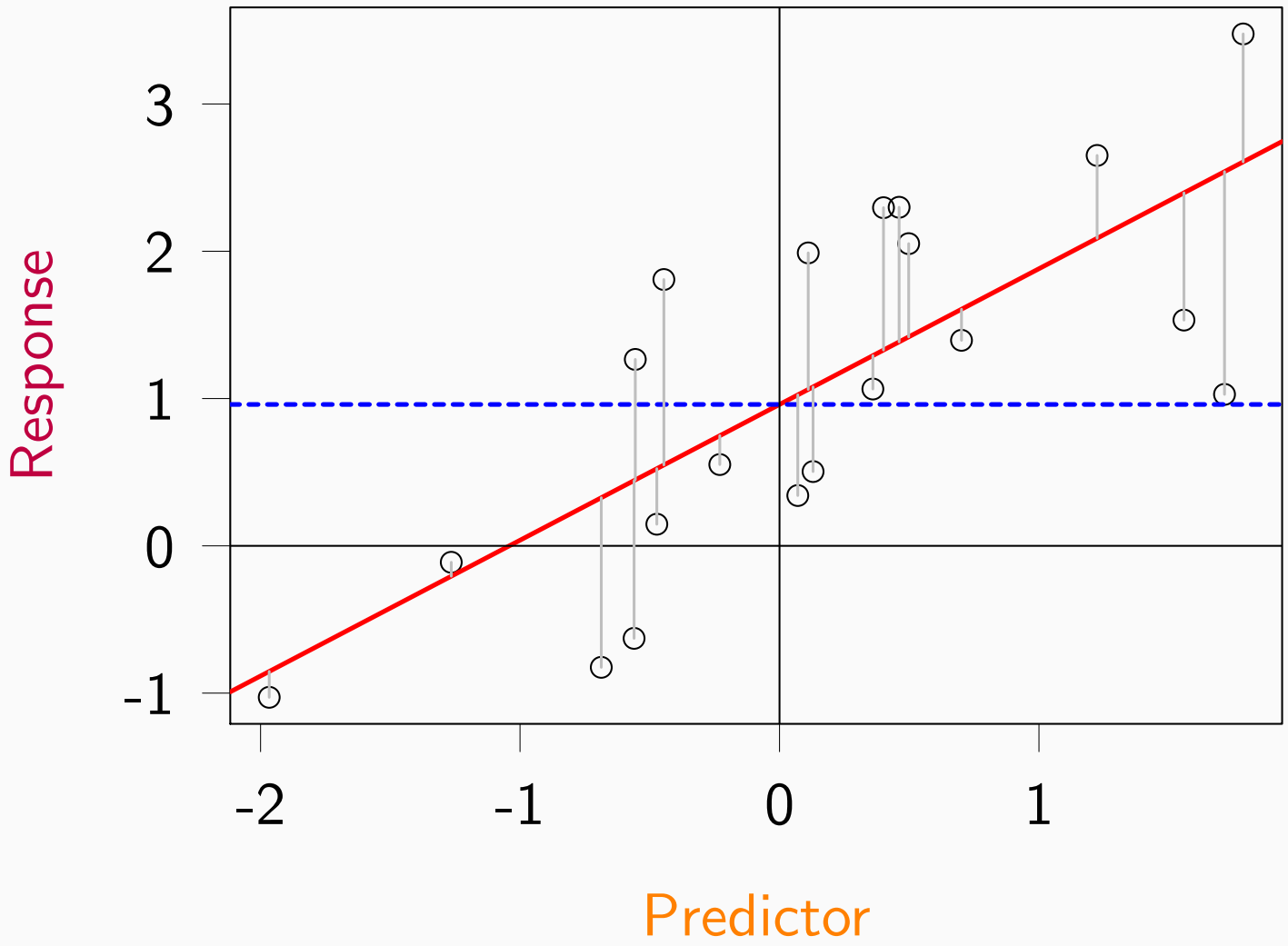
Linear model, reminder

Multiple regression

Interaction

A simple linear model

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



A multiple linear model

$$\text{Response} = \text{Intercept} + \text{Slope1} \times \text{Predictor1} + \text{Slope2} \times \text{Predictor2} + \text{Error}$$

In R:

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

Linear model, reminder

Multiple regression

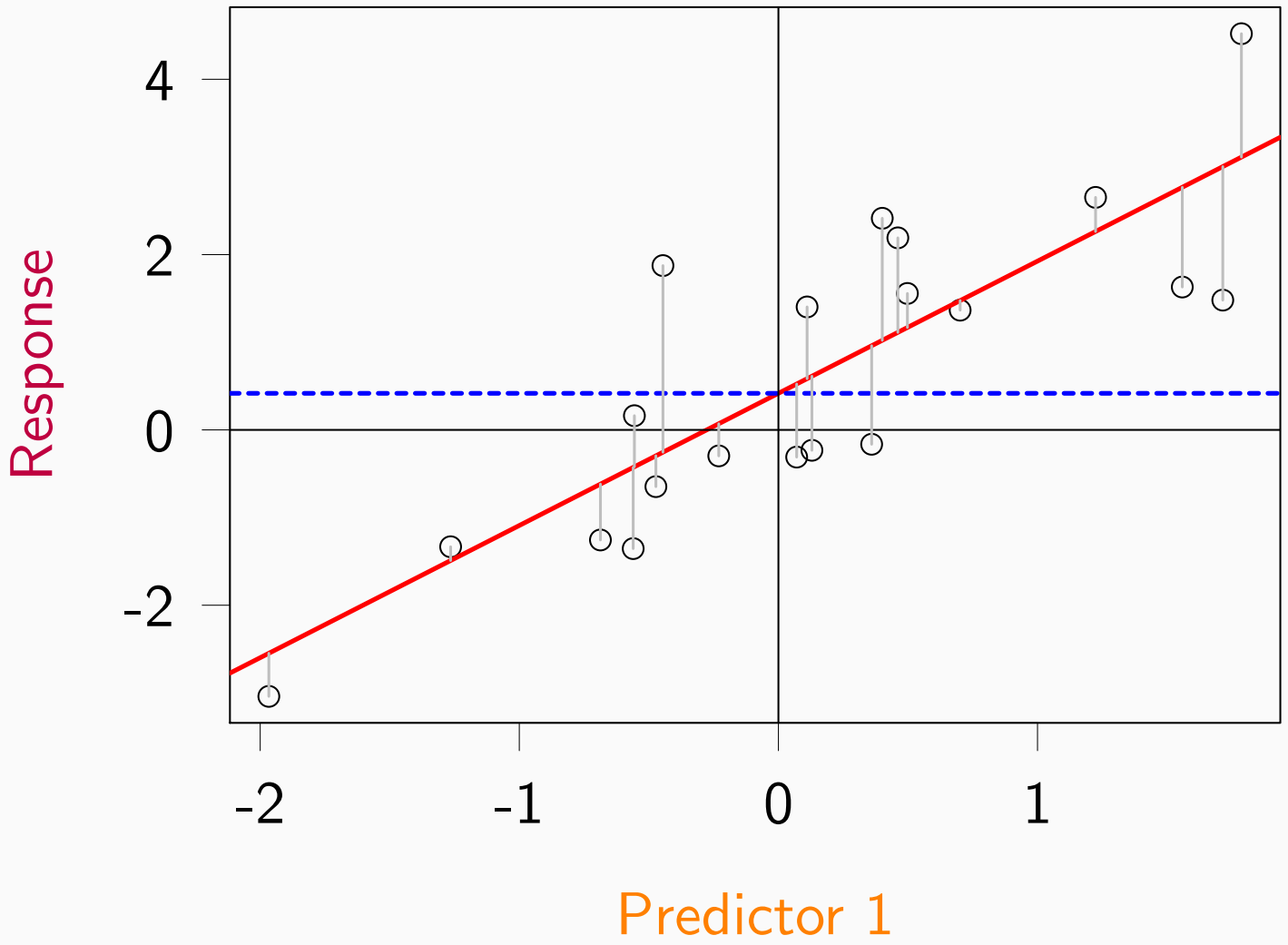
Interaction

Sequential regression

We want to explain a response by three predictors

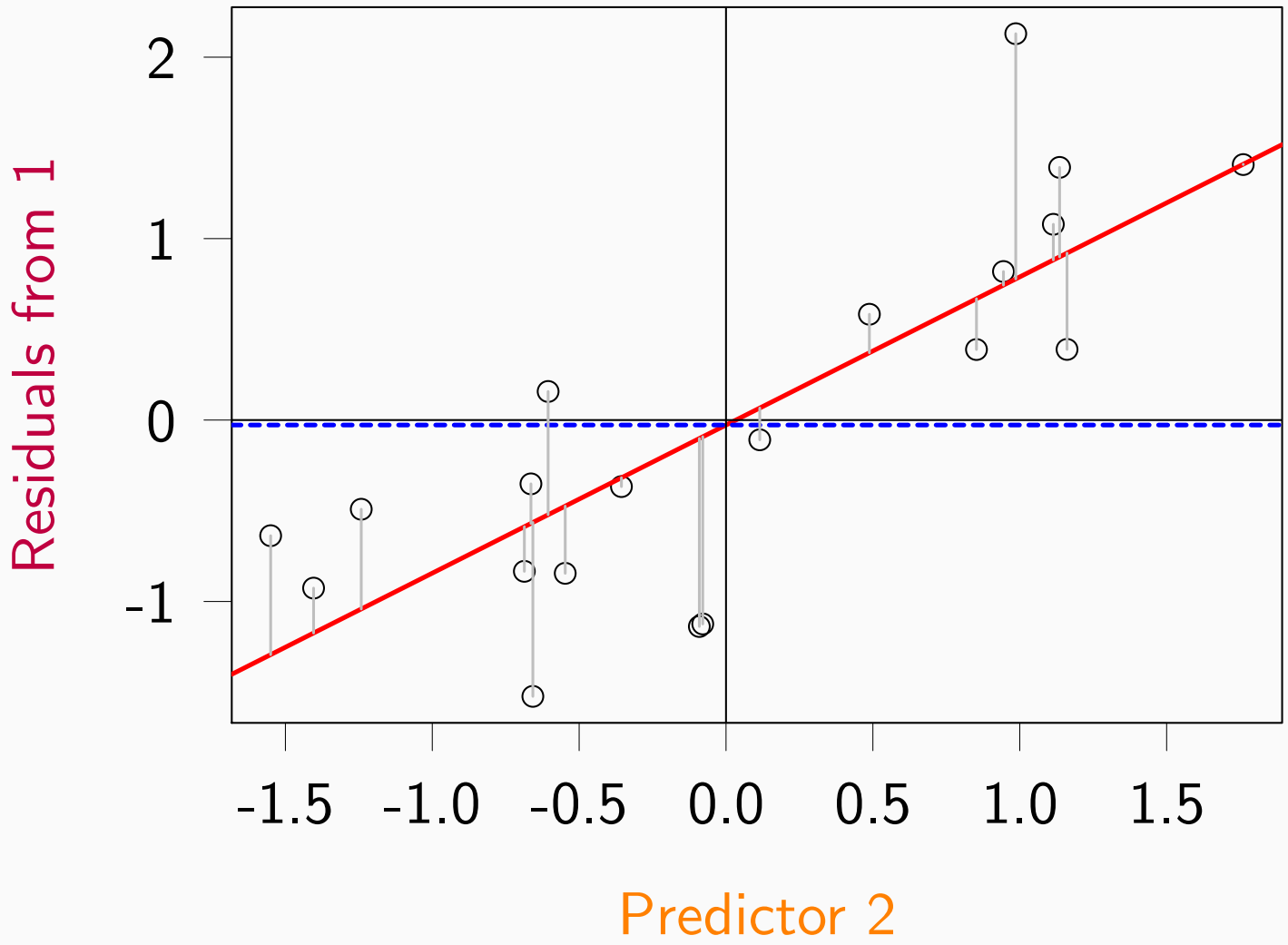
Sequential regression

We want to explain a response by three predictors



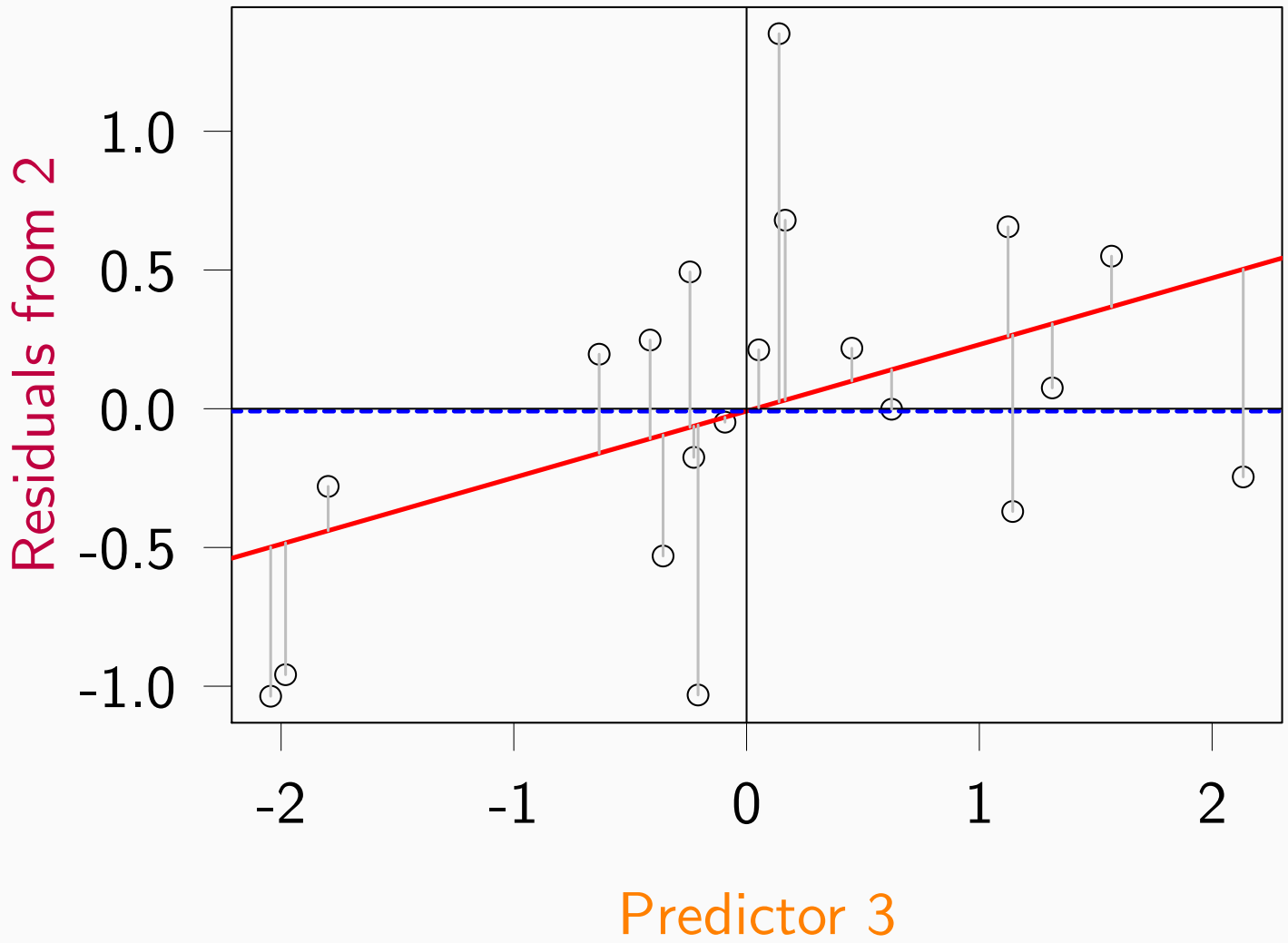
Sequential regression

We want to explain a response by three predictors



Sequential regression

We want to explain a response by three predictors



Sequential regression

```
m1 <- lm(y ~ x1)
m2 <- lm(m1$residuals ~ x2)
m3 <- lm(m2$residuals ~ x3)
```

Sequential regression

But estimates in

```
m1 <- lm(y ~ x1)
m2 <- lm(m1$residuals ~ x2)
m3 <- lm(m2$residuals ~ x3)
c(coefficients(m1)[2], coefficients(m2)[2], coefficients(m3)[2])
```

```
      x1        x2        x3
1.5080427 0.8163980 0.2397068
```

are different from

```
m1 <- lm(y ~ x3)
m2 <- lm(m1$residuals ~ x2)
m3 <- lm(m2$residuals ~ x1)
c(coefficients(m1)[2], coefficients(m2)[2], coefficients(m3)[2])
```

```
       x3         x2         x1
-0.6143369  1.4517052  0.3677874
```

Sequential regression

Also what happens with classical ANOVA (aov in R)

```
  summary(aov(y ~ x1 + x2 + x3))

            Df Sum Sq Mean Sq F value   Pr(>F)
x1           1  40.88   40.88 251.862 3.27e-11 ***
x2           1  16.40   16.40 101.051 2.55e-08 ***
x3           1   0.02    0.02   0.135    0.719
Residuals   16   2.60    0.16
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  summary(aov(y ~ x2 + x3 + x1))

            Df Sum Sq Mean Sq F value   Pr(>F)
x2           1  46.20   46.20  284.62 1.30e-11 ***
x3           1   2.46    2.46   15.16  0.00129 **
x1           1   8.65    8.65   53.27 1.79e-06 ***
Residuals   16   2.60    0.16
```

Multiple regression

In contrast lm() optimizes relationships simultaneously
Order does **not** matter:

```
  coefficients(lm(y ~ x1 + x2 + x3))

(Intercept)          x1          x2          x3
 0.45794446  0.94570383  1.12062799  0.03583753

  coefficients(lm(y ~ x2 + x3 + x1))

(Intercept)          x2          x3          x1
 0.45794446  1.12062799  0.03583753  0.94570383
```

Multiple regression

BUT estimates may change with extra covariates

```
    coefficients(lm(y ~ x1 + x2 ))

(Intercept)          x1          x2
  0.4625304   0.9214930   1.1242262

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(Intercept)          x1          x2          x3
 0.45794446  0.94570383  1.12062799  0.03583753
```

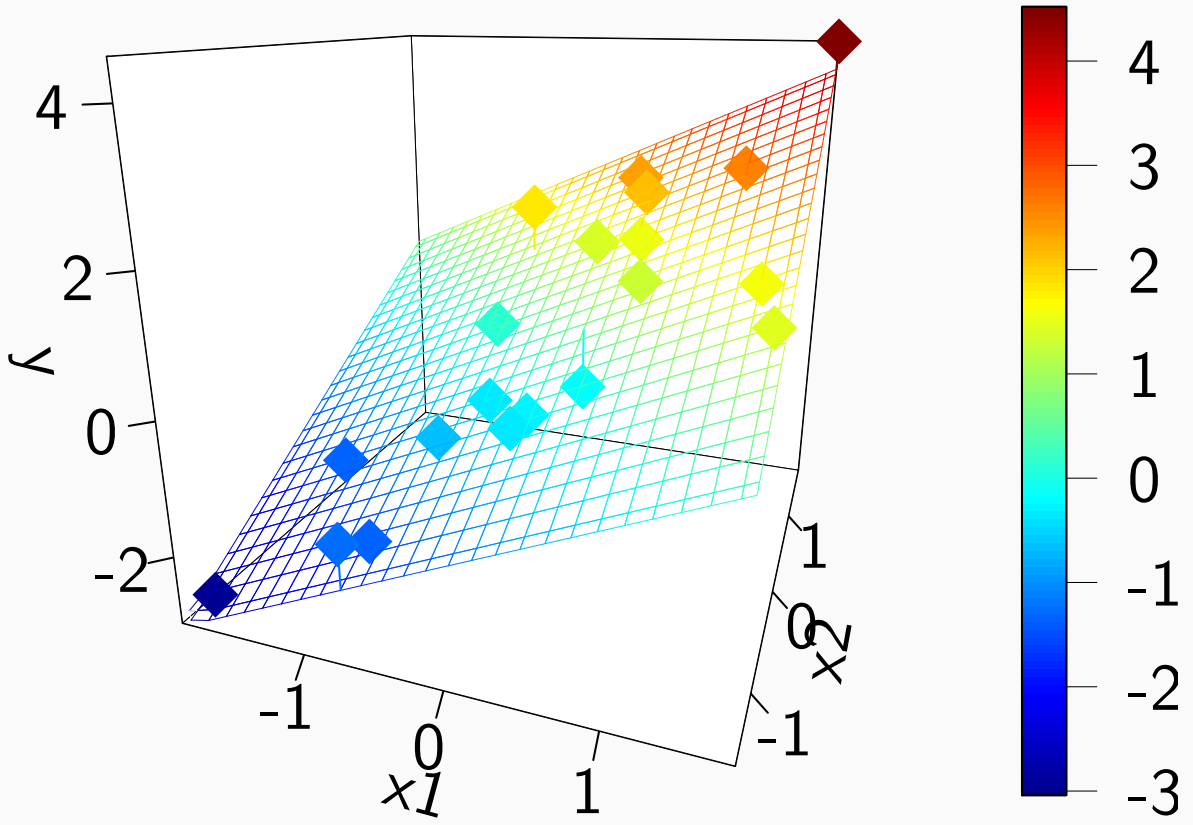
??

- That is a good thing
- Estimates are independent effects, conditional on the other parameters

Multiple regression

```
        library("plot3D")
fit <- lm(y ~ x1 + x2)
# predict values on regular xy grid
grid.lines = 26
x1.pred <- seq(min(x1), max(x1), length.out = grid.lines)
x2.pred <- seq(min(x2), max(x2), length.out = grid.lines)
x1x2 <- expand.grid( x1 = x1.pred, x2 = x2.pred)
y.pred <- matrix(predict(fit, newdata = x1x2),
                 nrow = grid.lines, ncol = grid.lines)
fitpoints <- predict(fit)
scatter3D(x1, x3, y, pch = 18, cex = 2,
    theta =18, phi = -18, ticktype = "detailed",
    xlab = "x1", ylab = "x2", zlab = "y",
    surf = list(x = x1.pred, y = x2.pred, z = y.pred,
    facets = NA, fit = fitpoints), main = "")
```

Multiple regression



Multiple regression

```
    library("plot3Drgl")
plotrgl(lighting = FALSE, new=TRUE)
```

Conditional estimation

Exercise 1

1. load `jumpingdistance.csv`
2. Use plots and lm() to test whether mass increases jumping distance

```
jumping <- read.csv(file = "jumpingdistance.csv")
```

A first approach suggests mass increases jumping distance:

```
summary(lm(jump ~ mass, data=jumping))
plot(mass, jump)
```

But that is incorrect and due to the correlation between mass and height:

```
summary(lm(jump ~ mass + height, data=jumping))
```

The direct (causal) effect of mass is negative, as revealed by a multiple regression

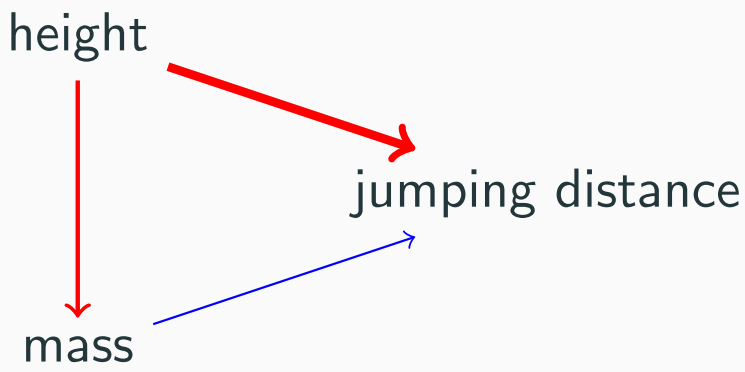
Conditional estimation

Total / marginal effects

Conditional estimation

Total / marginal effects

Direct / conditional effects



- Marginal effects $\approx$ raw correlations, sum of direct and indirect effects
- Multiple regression estimates direct effects (conditional on other predictors)
  $\rightarrow$ may reveal causal relationships

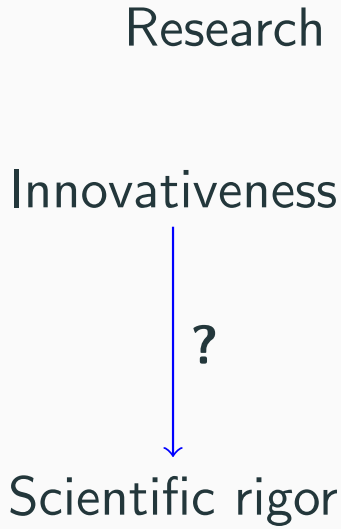
Conditional estimation

Exercise 2

1. Load `babies.csv`
2. What drives change in number of babies born?

Conditional estimation warning: more covariates is not always better

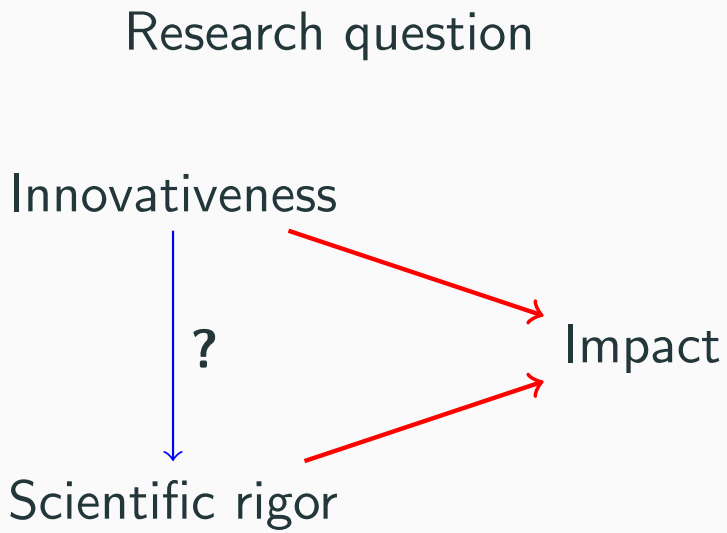
Are more innovative papers less rigorous?



Should you correct for publication impact?

Conditional estimation warning: more covariates is not always better

Are more innovative papers less rigorous?



Should you correct for publication impact?

Conditional estimation final warning: more is not always better

Should you include publication impact?

```
    summary(lm(rigor ~ innovativeness + impact))$coefficients

                 Estimate Std. Error    t value      Pr(>|t|)
(Intercept)     0.0301366 0.02188752   1.376885  1.688569e-01
innovativeness -0.3150363 0.03051417 -10.324262  8.238502e-24
impact          0.5135830 0.01538756  33.376503 1.361378e-164
```

Apparent negative effect of innovativeness ?

```
    summary(lm(rigor ~ innovativeness))$coefficients

                 Estimate Std. Error   t value     Pr(>|t|)
(Intercept)    0.04104524 0.03182923  1.289545 1.975073e-01
innovativeness 0.38804729 0.03210760 12.085841 1.758144e-31
```

Apparent positive effect of innovativeness ?

Conditional estimation final warning: more is not always better

Should you include publication impact?

Conditional estimation final warning: more is not always better

Should you include publication impact?

Data simulated with positive effect of innovativeness on rigor (simulated slope 0.3)

Conditional estimation final warning: more is not always better

Should you include publication impact?

Data simulated with positive effect of innovativeness on rigor (simulated slope 0.3)

You should NOT correct for impact

Conditional estimation final warning: more is not always better

Should you include publication impact?

Data simulated with positive effect of innovativeness on rigor (simulated slope 0.3)

You should NOT correct for impact

Rule of Thumb: Do not correct for variables influenced by your predictor outside the causal path of interest

Want more on multiple regression?

Morrissey & Ruxton (2018) **Multiple Regression Is Not Multiple Regressions: The Meaning of Multiple Regression and the Non-Problem of Collinearity**. PTPBIO 10(3)

dx.doi.org/10.3998/ptpbio.16039257.0010.003

> *Simple regression, and multiple regression, typically correspond to very different biological questions. The former use regression lines to describe univariate associations. The latter describe the partial, or direct, effects of multiple variables, conditioned on one another. We suspect that the superficial similarity of simple and multiple regression leads to confusion in their interpretation. [...] There is no general sense in which collinearity is a problem. [...] Purported solutions to the perceived problems of collinearity are detrimental to most biological analyses.*

Linear model, reminder

Multiple regression

Interaction

Warnings

Vocabulary warning!

- **correlation**: linear association between two variables *"how well does x explain y ?"*

Warnings

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- **interaction**: non-additive effect of two or more variables *"does the effect of x_1 on y change as a function of x_2?"*. Adds a predictor (or several) to a model.

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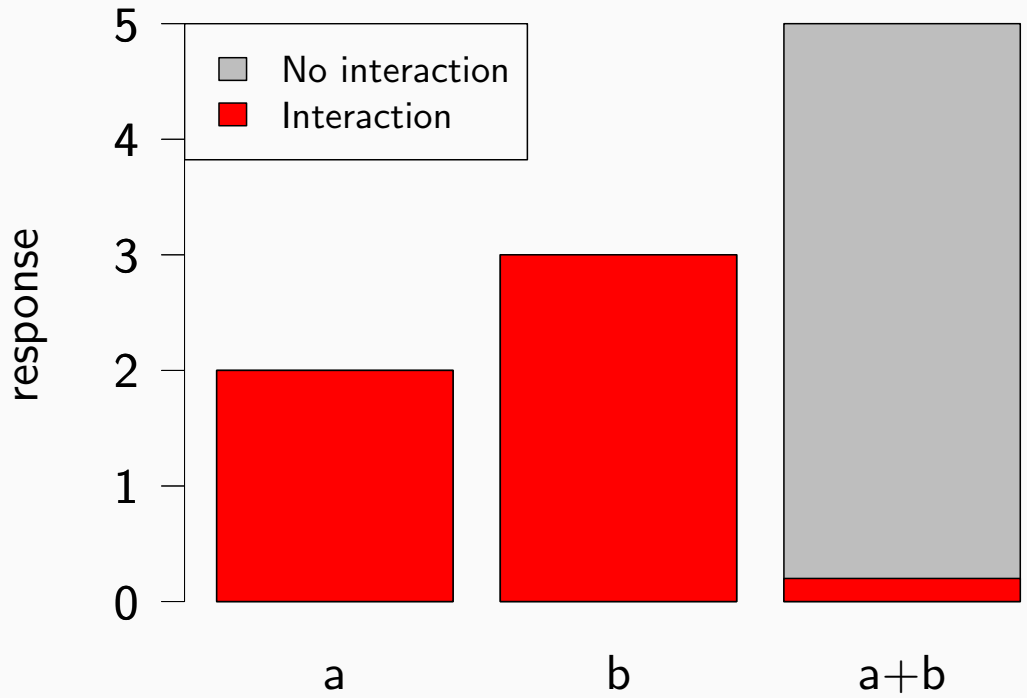

Fitting an interaction

```
lm(y ~ 1 + x1 * x2)
lm(y ~ 1 + x1 + x2 + x1:x2)
```

Fitting an interaction

```
lm(y ~ 1 + x1 * x2)
lm(y ~ 1 + x1 + x2 + x1:x2)
```

```
summary(lm(y~ 1 + x1*x2))
```

```
Call:
lm(formula = y ~ 1 + x1 * x2)

Residuals:
    Min      1Q  Median      3Q     Max
-1.8719 -0.6777 -0.1086  0.5897  2.3166

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.14098    0.09578  11.913  < 2e-16 ***
x1          -0.49281    0.10834  -4.549 1.58e-05 ***
x2           0.53434    0.09881   5.408 4.67e-07 ***
```

Fitting an interaction

Why the multiplication sign?

Fitting an interaction

Why the multiplication sign?

```
x1Xx2 <- x1*x2
```

Fitting an interaction

Why the multiplication sign?

```
x1Xx2 <- x1*x2
```

```
     summary(lm(y~ 1 + x1 + x2 + x1Xx2))



Call:
lm(formula = y ~ 1 + x1 + x2 + x1Xx2)

Residuals:
    Min      1Q  Median      3Q     Max
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x2           0.53434    0.09881   5.408 4.67e-07 ***
```

Warnings

Modeling warning!

- ~~DO NOT COMPARE P-VALUES OF TWO MODELS TO TEST FOR AN INTERACTION~~

Exercise

1. Load the data masssex.csv
2. Fit a simple regression explaining movement by mass for each sex separately. Is the relationship different between sexes?
3. Fit the multiple regression explaining movement by mass, sex, and mass:sex, using the full dataset. Is the relationship different between sexes?
4. Try to understand the discreapancy by plotting the data

Warnings

1.

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

Warnings

1.

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

2.

```
summary(lm(movement ~ mass, data=masssex[masssex$sex==0,]))
summary(lm(movement ~ mass, data=masssex[masssex$sex==1,]))
```

Warnings

1.

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

2.

```
summary(lm(movement ~ mass, data=masssex[masssex$sex==0,]))
summary(lm(movement ~ mass, data=masssex[masssex$sex==1,]))
```

3.

```
summary(lm(movement ~ mass*sex, data=masssex))
```

Warnings

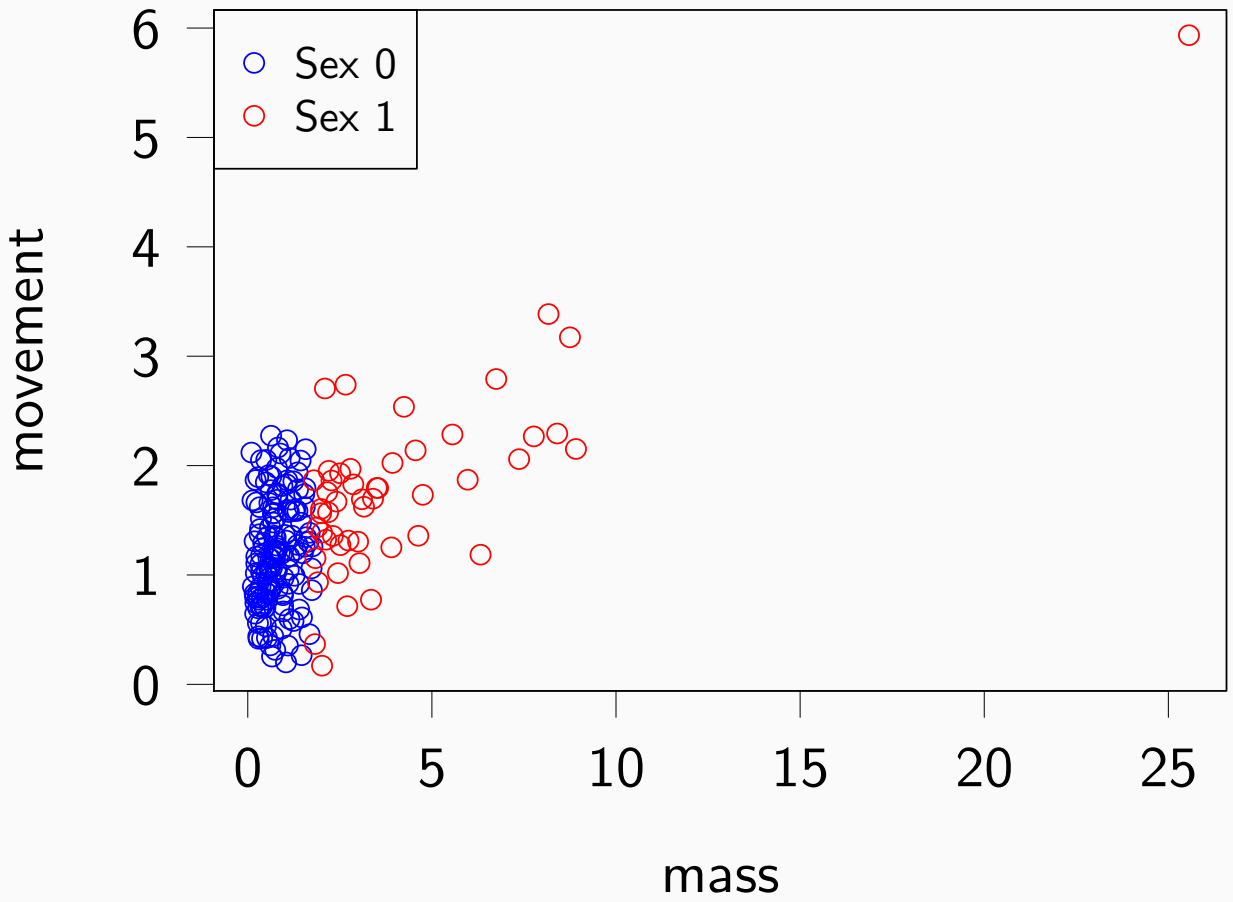
4. Visualize the problem (result on next slide):

```
plot(masssex[masssex$sex==0,"mass"],masssex[masssex$sex==0,"movement"],
 col="blue", xlim=range(masssex$mass), ylim=range(masssex$movement),
   xlab="mass", ylab="movement")
points(masssex[masssex$sex==1,"mass"],
       masssex[masssex$sex==1,"movement"], col="red")
legend(x="topleft", col=c("blue", "red"),
       legend = c("Sex 0", "Sex 1"), pch=1)
```

The slope of movement on mass is the same for both sexes, but the range of values is much smaller for sex 0, so that there is no power to detect a significant effect. Analysing sexes separately is unsound. You must fit an interaction in a model with both sexes to test for an interaction.

Warnings

4.



Prediction

Exercise

1. Load plantsize.csv and plot the data
2. Fit an additive model explaining plant size by x and y coordinates

```
plantsize <- read.csv("plantsize.csv")
m0 <- lm(plantsize ~ x_location + y_location, data=plantsize)
```

Prediction

Exercise

1. Load plantsize.csv and plot the data
2. Fit an additive model explaining plant size by x and y coordinates
3. Create a prediction for plant size as a function of x for two values of y

```
plantsize <- read.csv("plantsize.csv")
m0 <- lm(plantsize ~ x_location + y_location, data=plantsize)
```

Prediction

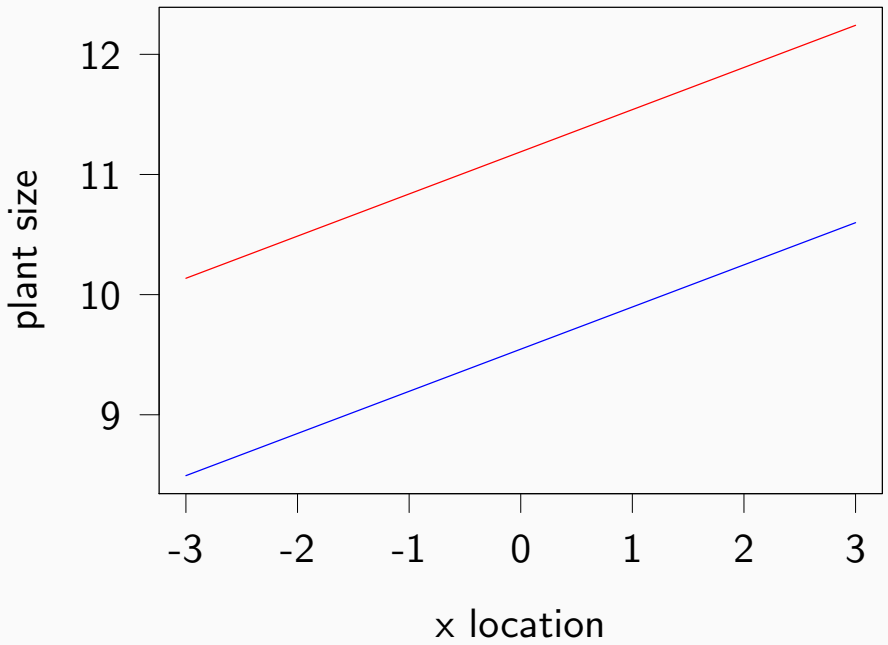
3.1. Predict

```
newdata <- data.frame(x_location = rep(seq(-3,3, length.out = 100),2),
                      y_location = c(rep(-3, 100), rep(4,100)))
newdata$prediction <- predict(m0, newdata = newdata)
```

Prediction

3.2 Visualize

```
plot(newdata$x_location[newdata$y_location==-3],
     newdata$prediction[newdata$y_location==-3],
     xlab="x location", ylab="plant size", type="l",
     ylim = range(newdata$prediction), col="blue")
lines(newdata$x_location[newdata$y_location==4],
      newdata$prediction[newdata$y_location==4], col="red")
```

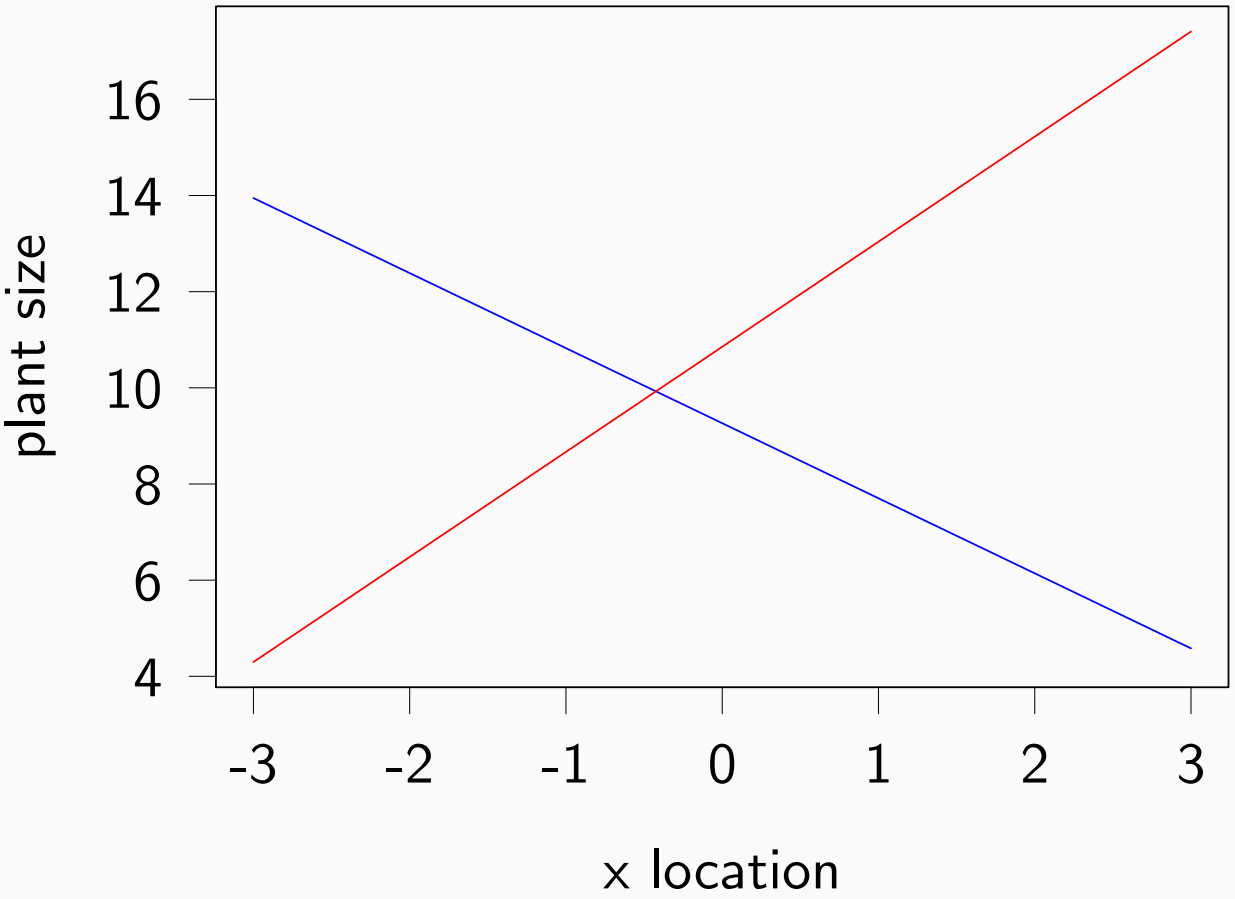


Prediction with interaction

Exercise

1. Load plantsize.csv and plot the data
2. Fit an additive model explaining plant size by x and y coordinates
3. Create a prediction for plant size as a function of x for two values of y and plot it
4. Fit an interaction between x and y coordinates
5. Create a new prediction with interaction, and plot it

Prediction with interaction



Prediction with interaction

Exercise

1. Load plantsize.csv and plot the data
2. Fit an additive model explaining plant size by x and y coordinates
3. Create a prediction for plant size as a function of x for two values of y and plot it
4. Fit an interaction between x and y coordinates
5. Create a new prediction with interaction, and plot it
6. Compare estimates and p-values across models. Do you think x location has an effect or not?

Prediction with interaction

```
m1 <- lm(plantsize ~ x_location * y_location, data=plantsize)
newdata <- data.frame(x_location = rep(seq(-3,3, length.out = 10),10),
                      y_location = rep(seq(-3,4, length.out = 10), each=10))
newdata$prediction <- predict(m1, newdata = newdata)
plot(newdata$x_location[newdata$y_location==-3],
     newdata$prediction[newdata$y_location==-3],
       xlab="x location", ylab="plant size", type="l",
     ylim = range(newdata$prediction), col="blue")
lines(newdata$x_location[newdata$y_location==4],
      newdata$prediction[newdata$y_location==4], col="red")
```

Prediction with interaction

```
 library(reshape2)
matpred <- acast(newdata, x_location~y_location, value.var="prediction")
layout(mat = matrix(data = c(1,2),nrow = 1), widths = c(3,1) )
image(t(matpred), col = topo.colors(10), xlab = "x location",
      ylab = "y location")

par(mar=c(5, 0,4, 6)+0.1)
image(matrix(data = seq(min(newdata$prediction),
            max(newdata$prediction), length.out = 10), nrow= 1 ),
      col=topo.colors(10), xaxt = "n", yaxt="n", main="legend")
axis(side = 4, at = c(0,0.2,0.4,0.6,0.8,1),
labels = round(seq(min(newdata$prediction), max(newdata$prediction),
                   length.out =6),1))
```

Prediction with interaction