Statistical inference and linear models

February 20, 2018

If you get bored

- Go to the last slide for bonus exercises
- Work on code for your research and ask question during exercise time
- But try and keep an eye out, just in case

Disclaimer

- Assume you got lectures about statistics and
  - know why we need statistics
  - have heard of the general philosophy
- We may simplify to focus on practical aspects
- Correct us if we say something completely awful

General approach

1. Scientific question

General approach

1. Scientific question

$\downarrow$

2. Model and Statistical question

General approach

$$
\begin{array}{ccc}
\text{1. Scientific question} & & \\
\downarrow & & \\
\text{2. Model and Statistical question} & \longleftrightarrow & \text{3. Data collection}
\end{array}
$$

General approach

1. Scientific question

$\downarrow$

2. Model and Statistical question $\longleftrightarrow$ 3. Data collection

$\downarrow$

4. Estimation

4.b Uncertainty and statistical significance

General approach

1. Scientific question

2. Model and Statistical question ⟷ 3. Data collection

4. Estimation

4.b Uncertainty and statistical significance

5. Diagnostic, check assumptions, prediction

General approach

1. Scientific question

2. Model and Statistical question ⟷ 3. Data collection

4. Estimation

4.b Uncertainty and statistical significance

5. Diagnostic, check assumptions, prediction

6. Interpret and think about the biology

Reminder t.test

Reminder t.test

```
data("iris")
```

```
str(iris)
plot(iris)
```

1. Scientific question: Are the taxa "setosa" and "versicolor" different species?

Reminder t.test

```r
data("iris")
```

```r
str(iris)
plot(iris)
```

1. Scientific question: Are the taxa "setosa" and "versicolor" different species?
2. Model and stat question:
   - 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

Reminder t.test

```r
data("iris")
```

```r
str(iris)
plot(iris)
```

1. Scientific question: Are the taxa "setosa" and "versicolor" different species?
2. Model and stat question:
    - 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
    - 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

Reminder 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 $=$ $\text{Mean}_1 - \text{Mean}_2$
     - 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)
     - Can derive confidence interval and standard error

When do we know it is different?

4. Statistical estimation
   - a Estimation
     - Cannot know true difference $\mu_{species_1} - \mu_{species_2}$
     - Estimated difference $=$ $\text{Mean}_1 - \text{Mean}_2$
     - 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)
     - Can derive confidence interval and standard error

Less uncertainty with

- Larger absolute difference
- Smaller variability
- Larger sample size

When do we know it is different? Simulations

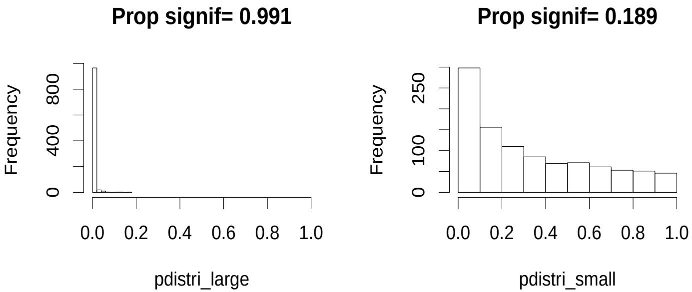
When do we know it is different? Simulations

1. Larger absolute difference

```
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.**

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.**

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

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.**

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

NB: Focus on p-value criticized, but common and they not more evil than other misused statistics!

T-test exercise: p-values and simulations

```
t.test(x = ..., y=...., var.equal = TRUE)
t.test(x = ..., y=...., var.equal = FALSE)
```

What if variance are different by chance only?

```
set.seed(1234)
var(rnorm(20, mean = 0, sd = 1))

[1] 1.027806

var(rnorm(20, mean = 0, sd = 1))

[1] 0.6265501
```

Exercise

What option is more correct for var.equal?

A small example

Animal behavior in response to weather
Load data:

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

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

A small example

Animal behavior in response to weather
Load data:

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

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

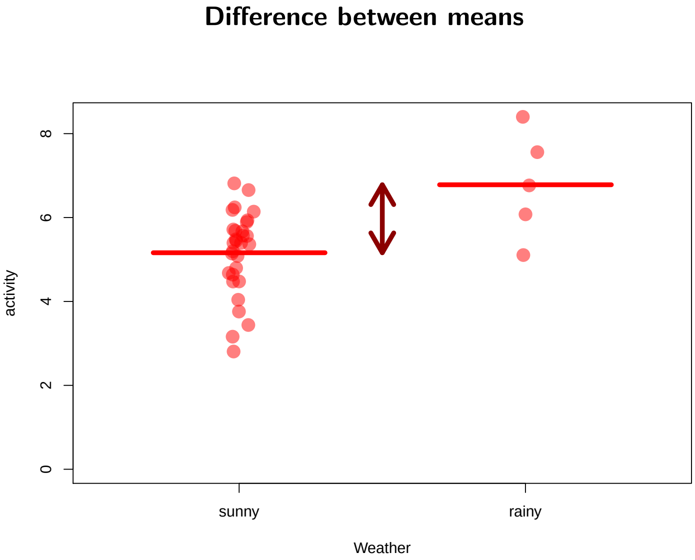
STEP 1: have a look at your data

```
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
```

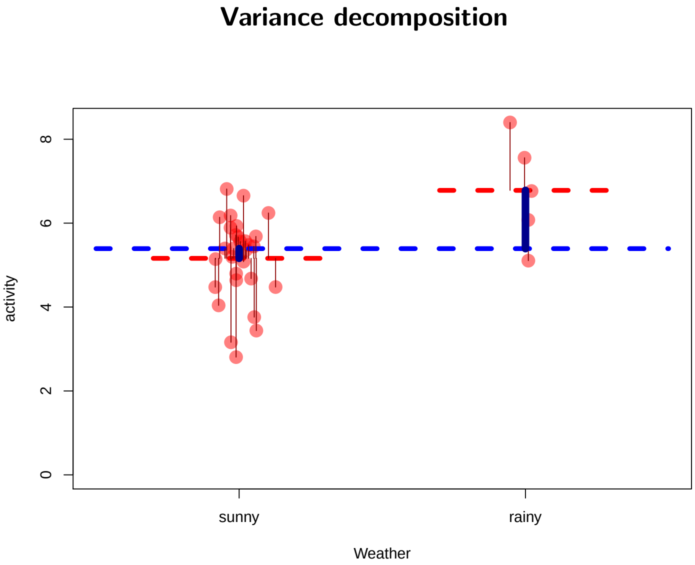
t-test, graphically



ANOVA

```
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
```

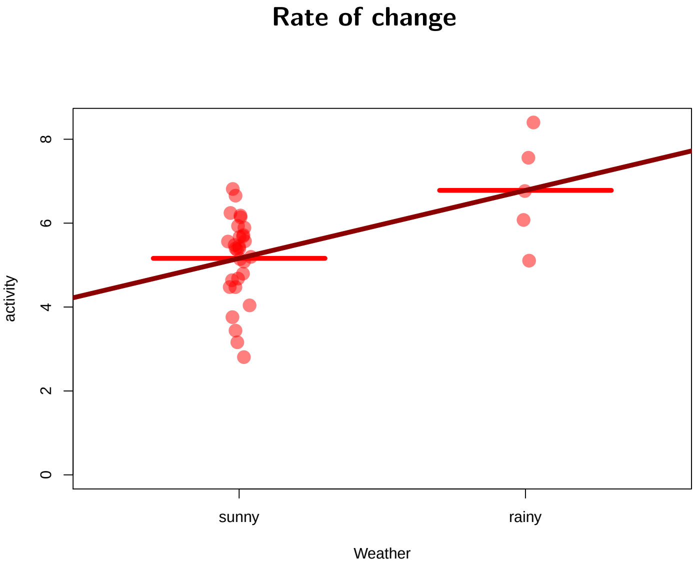
ANOVA, graphically



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()

```
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!

Interpretation

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

Warning in file(file, "rt"):  cannot open file 'Anscombe.csv':
No such file or directory
Error in file(file, "rt"):  cannot open the connection
```

Linear model basic assumptions

- Linear combination of parameters (including transformation, polynoms, interactions...)
  Risk: biologically meaningless

Linear model basic assumptions

- Linear combination of parameters (including transformation, polynoms, interactions. . .)
  Risk: biologically meaningless
- Predictor not perfectly correlated
  Risk: Model won't run, unstable convergence, or huge SE

Linear model basic assumptions

- Linear combination of parameters (including transformation, polynoms, interactions. . .)
  Risk: biologically meaningless
- Predictor not perfectly correlated
  Risk: Model won't run, unstable convergence, or huge SE
- Little error in predictors
  Risk: bias estimates (underestimate with Gaussian error)

Linear model basic assumptions

- Linear combination of parameters (including transformation, polynoms, interactions. . .)
  Risk: biologically meaningless
- Predictor not perfectly correlated
  Risk: Model won't run, unstable convergence, or huge SE
- Little error in predictors
  Risk: bias estimates (underestimate with Gaussian error)
- Gaussian error distribution
  Risk: Poor predictions

Linear model basic assumptions

- Linear combination of parameters (including transformation, polynoms, interactions. . .)
  Risk: biologically meaningless
- Predictor not perfectly correlated
  Risk: Model won't run, unstable convergence, or huge SE
- Little error in predictors
  Risk: bias estimates (underestimate with Gaussian error)
- Gaussian error distribution
  Risk: Poor predictions
- Homoscedasticity (constant error variance)
  Risk: Over-optimistic uncertainty, unreliable predictions

Linear model basic assumptions

- Linear combination of parameters (including transformation, polynoms, interactions...)
  Risk: biologically meaningless
- Predictor not perfectly correlated
  Risk: Model won't run, unstable convergence, or huge SE
- Little error in predictors
  Risk: bias estimates (underestimate with Gaussian error)
- Gaussian error distribution
  Risk: Poor predictions
- Homoscedasticity (constant error variance)
  Risk: Over-optimistic uncertainty, unreliable predictions
- Independence of error
  Risk: Bias and over-optimistic uncertainty

Extra exercises

Linear models

1.