

# Solutions to problems from: A Crash Course in Practical Data Analysis\*

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\*For the latest version, visit <https://github.com/sashahafner/CCPDA>

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# Contents

1	Packages and functions	3
2	Problem 1. Inoculum effects on BMP	3
3	Problem 2. Wood hardness and density	13
4	Problem 3. Fruit fly longevity and sexual activity	20
5	Problem 4: Growth and nitrate accumulation by <i>Lemna minor</i>	26
6	Bibliography	33

# 1 Packages and functions

```
source('functions/dfsumm.R')
```

```
library(tidyr)
library(dplyr)
library(ggplot2)
```

## 2 Problem 1. Inoculum effects on BMP

Koch et al. [2017] studied the effect of inoculum origin on biochemical methane potential (BMP) for four substrates. Data are given in the file BMP\_inoc.csv, where the unit of observation is a single BMP bottle. Take a look at the data and answer these questions:

1. Did BMP depend on inoculum type?
2. Did any effect vary by substrate?

The original data are in a intermediate structure, with replicates across columns.

```
bi <- read.csv('data/BMP_inoc.csv')
```

```
bi
#      substrate inoc  BMP1  BMP2  BMP3  BMP4  BMP5  BMP6  BMP7  BMP8
# 1 Sewage Sludge WWTP 293.8 272.8 303.9 260.2 275.7 276.6 309.9 330.1
# 2      Maize WWTP 319.7 320.2 344.5 324.7 328.3 338.6 324.8 351.9
# 3 Food Waste WWTP 453.9 444.5 462.9 451.1 453.9 473.7 423.8 419.5
# 4 Cellulose WWTP 333.3 315.6 341.0 322.8 330.4 338.9 338.9 343.0
# 5 Sewage Sludge ABP 294.8 294.2 293.9 267.0 269.6 272.5 332.4 319.8
# 6      Maize ABP 320.1 325.6 348.6 362.5 343.8 412.5 326.6 330.9
# 7 Food Waste ABP 441.1 432.2 466.2 490.0 398.3 429.3 423.3 432.5
# 8 Cellulose ABP 344.1 347.7 374.8 348.5 351.3 378.0 354.9 367.5
# 9 Sewage Sludge BWTP 296.6 307.6 307.5 309.1 315.0 319.4 342.3 325.0
# 10      Maize BWTP 328.2 341.6 356.8 339.4 357.3 372.6 336.6 339.5
# 11 Food Waste BWTP 459.0 450.8 484.4 453.2 449.3 483.8 442.9 429.7
# 12 Cellulose BWTP 379.0 389.4 376.8 360.1 357.0 389.0 362.5 369.7
#      BMP9
# 1 328.3
# 2 352.1
# 3 432.0
# 4 350.0
# 5 319.4
# 6 335.5
# 7 439.8
# 8 366.9
# 9 347.1
# 10 356.0
# 11 458.2
# 12 376.7
```

This structure could work well in a spreadsheet analysis. For analysis in R, the structure can be changed to long using the `gather()` function.

```
bil <- gather(bi, key = 'rep', value = 'BMP', contains('BMP'))
head(bil)
```

```
#      substrate inoc rep  BMP
# 1 Sewage Sludge WWTP BMP1 293.8
# 2      Maize WWTP BMP1 319.7
# 3   Food Waste WWTP BMP1 453.9
# 4   Cellulose WWTP BMP1 333.3
# 5 Sewage Sludge ABP BMP1 294.8
# 6      Maize ABP BMP1 320.1
```

```
dim(bil)
```

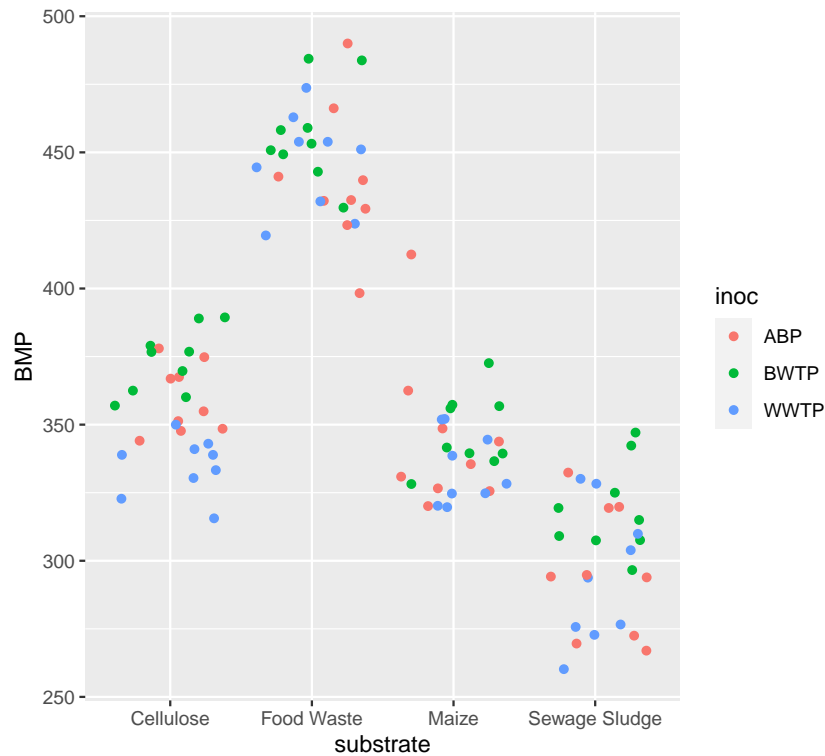
```
# [1] 108  4
```

```
dfsumm(bil)
```

```
#
# 108 rows and 4 columns
# 108 unique rows
#
#      substrate  inoc      rep  BMP
# Class          factor factor character numeric
# Minimum      Cellulose  ABP    BMP1    260
# Maximum      Sewage Sludge WWTP    BMP9    490
# Mean          Food Waste BWTP    BMP5    362
# Unique (excl. NA)      4      3      9    103
# Missing values      0      0      0      0
# Sorted          FALSE  FALSE    TRUE  FALSE
```

Here are the values, with a single point representing a BMP value from a single bottle.

```
ggplot(bil, aes(substrate, BMP, colour = inoc)) +
  geom_jitter(height = 0)
```



Calculate means and standard deviation.

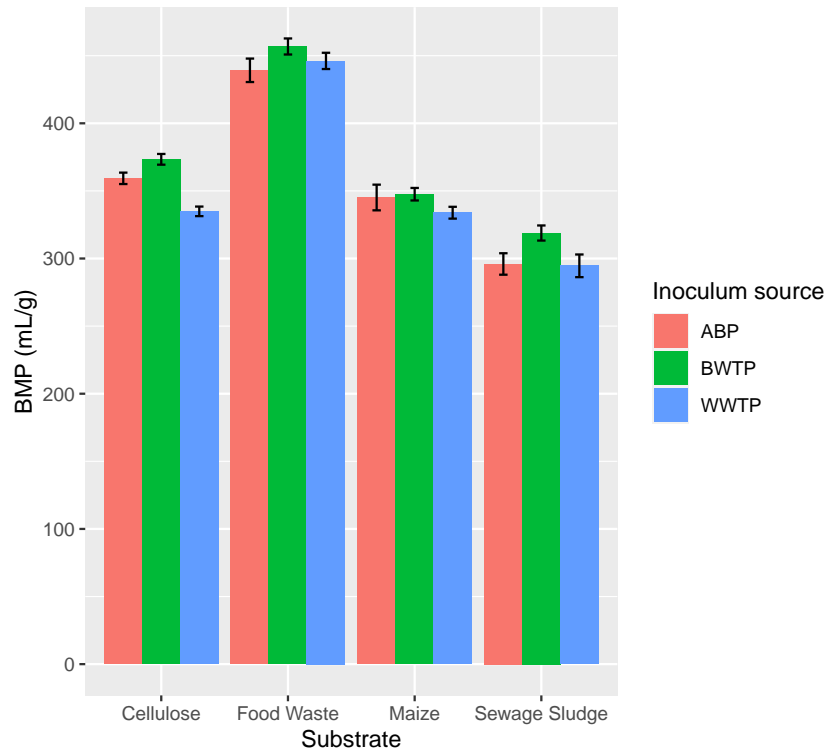
```
bm <- as.data.frame(summarise(group_by(bil, substrate, inoc), BMP.mn = mean(BMP),
                                BMP.sd = sd(BMP), n = length(BMP)))
bm$BMP.se = bm$BMP.sd / sqrt(bm$n)
```

bm

#	substrate	inoc	BMP.mn	BMP.sd	n	BMP.se
# 1	Cellulose	ABP	359.3000	12.65178	9	4.217260
# 2	Cellulose	BWTP	373.3556	11.89276	9	3.964254
# 3	Cellulose	WWTP	334.8778	10.63329	9	3.544431
# 4	Food Waste	ABP	439.1889	26.05554	9	8.685180
# 5	Food Waste	BWTP	456.8111	17.78479	9	5.928262
# 6	Food Waste	WWTP	446.1444	18.01694	9	6.005648
# 7	Maize	ABP	345.1222	28.50604	9	9.502014
# 8	Maize	BWTP	347.5556	13.87661	9	4.625536
# 9	Maize	WWTP	333.8667	13.12355	9	4.374516
# 10	Sewage Sludge	ABP	295.9556	23.81765	9	7.939215
# 11	Sewage Sludge	BWTP	318.8444	16.75717	9	5.585724
# 12	Sewage Sludge	WWTP	294.5889	25.14202	9	8.380673

And plot them.

```
ggplot(bm, aes(substrate, BMP.mn, fill = inoc)) +
  geom_bar(position = position_dodge(), stat = 'identity') +
  geom_errorbar(aes(ymin = BMP.mn - BMP.se, ymax = BMP.mn + BMP.se), position = position_dodge(0.9),
    labs(x = 'Substrate', y = 'BMP (mL/g)', fill = 'Inoculum source'))
```



Here is a case where we really do need a statistical analysis to help understand the data.

```
m1 <- lm(BMP ~ substrate * inoc, data = bil)
summary(m1)
```

```
#
# Call:
# lm(formula = BMP ~ substrate * inoc, data = bil)
#
# Residuals:
#      Min       1Q   Median       3Q      Max
# -40.889 -11.719  -1.700   9.261  67.378
#
# Coefficients:
#              Estimate Std. Error t value Pr(>|t|)
# (Intercept)      359.300      6.377   56.343 < 2e-16
# substrateFood Waste    79.889      9.018    8.858 4.21e-14
# substrateMaize    -14.178      9.018   -1.572 0.11922
# substrateSewage Sludge -63.344      9.018   -7.024 3.10e-10
# inocBWTP          14.056      9.018    1.559 0.12240
# inocWWTP         -24.422      9.018   -2.708 0.00801
# substrateFood Waste:inocBWTP    3.567     12.754    0.280 0.78035
# substrateMaize:inocBWTP   -11.622     12.754   -0.911 0.36444
# substrateSewage Sludge:inocBWTP    8.833     12.754    0.693 0.49024
# substrateFood Waste:inocWWTP    31.378     12.754    2.460 0.01567
# substrateMaize:inocWWTP    13.167     12.754    1.032 0.30450
# substrateSewage Sludge:inocWWTP    23.056     12.754    1.808 0.07378
#
# (Intercept) ***
```

```

# substrateFood Waste      ***
# substrateMaize
# substrateSewage Sludge   ***
# inocBWTP
# inocWWTP                 **
# substrateFood Waste:inocBWTP
# substrateMaize:inocBWTP
# substrateSewage Sludge:inocBWTP
# substrateFood Waste:inocWWTP *
# substrateMaize:inocWWTP
# substrateSewage Sludge:inocWWTP .
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# Residual standard error: 19.13 on 96 degrees of freedom
# Multiple R-squared:  0.8995, Adjusted R-squared:  0.888
# F-statistic: 78.14 on 11 and 96 DF,  p-value: < 2.2e-16

anova(m1)

# Analysis of Variance Table
#
# Response: BMP
#
#      Df Sum Sq Mean Sq F value    Pr(>F)
# substrate    3 302030   100677 275.0758 < 2.2e-16 ***
# inoc         2   8804     4402  12.0276 2.181e-05 ***
# substrate:inoc 6   3740      623   1.7031  0.1285
# Residuals   96 35136      366
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

There is clear evidence of an inoculum effect, and a slight suggestion of a possible interaction.

```

m2 <- aov(BMP ~ substrate * inoc, data = bil)
summary(m2)

#      Df Sum Sq Mean Sq F value    Pr(>F)
# substrate    3 302030   100677 275.076 < 2e-16 ***
# inoc         2   8804     4402  12.028 2.18e-05 ***
# substrate:inoc 6   3740      623   1.703  0.129
# Residuals   96 35136      366
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

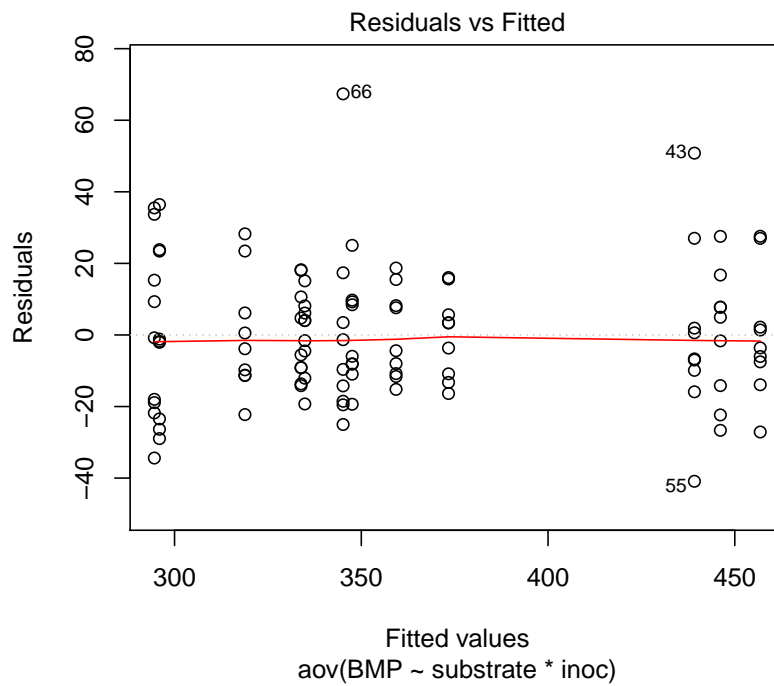
TukeyHSD(m2, 'inoc')

# Tukey multiple comparisons of means
# 95% family-wise confidence level
#
# Fit: aov(formula = BMP ~ substrate * inoc, data = bil)

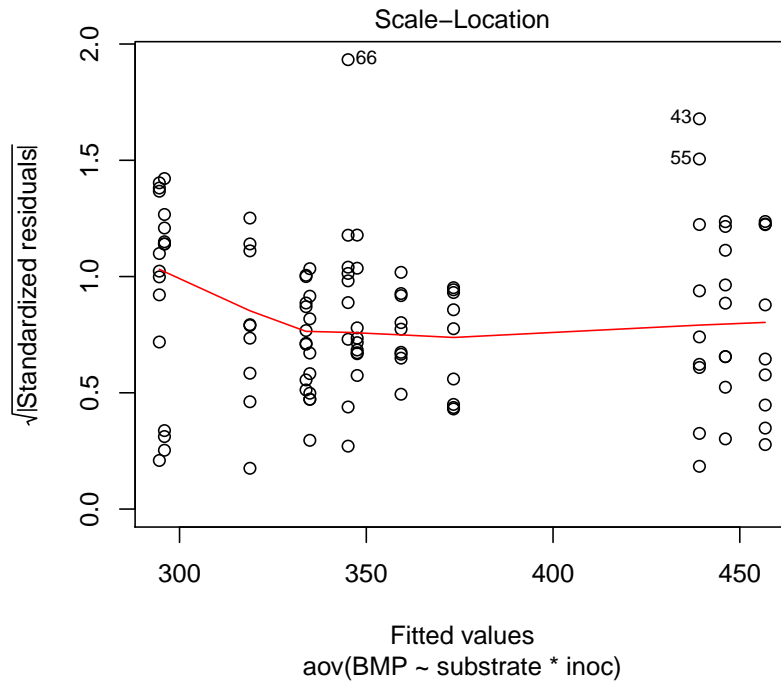
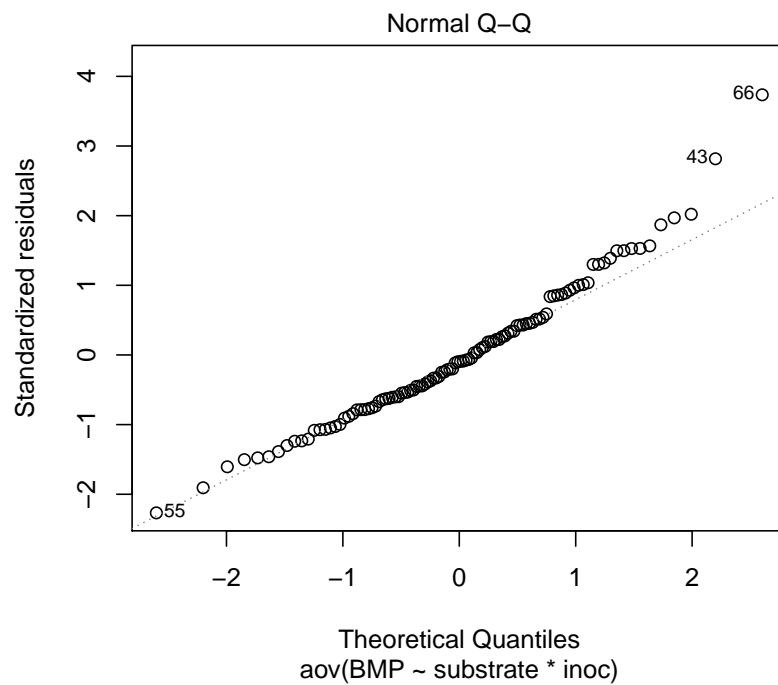
```

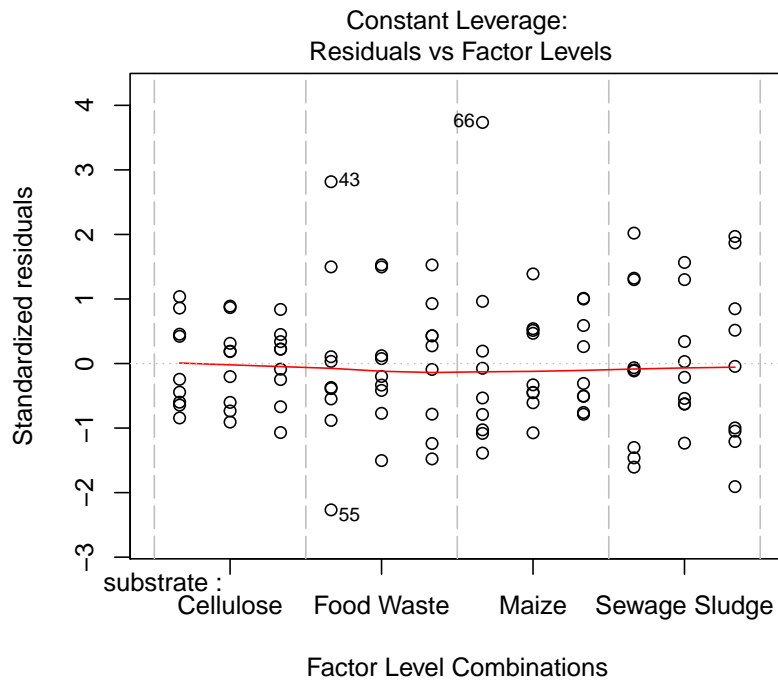
```
#
# $inoc
#           diff           lwr           upr       p adj
# BWTP-ABP   14.250000    3.515301   24.984699 0.0059271
# WWTP-ABP   -7.522222  -18.256921    3.212477 0.2227058
# WWTP-BWTP -21.772222  -32.506921  -11.037523 0.0000154
```

```
plot(m2, ask = FALSE)
```









```
m3 <- aov(log10(BMP) ~ substrate * inoc, data = bil)
summary(m3)
```

```
#           Df Sum Sq Mean Sq F value    Pr(>F)
# substrate    3  0.4081  0.13604  244.417 < 2e-16 ***
# inoc          2  0.0141  0.00703   12.623 1.36e-05 ***
# substrate:inoc 6  0.0062  0.00103    1.853  0.097 .
# Residuals    96  0.0534  0.00056
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

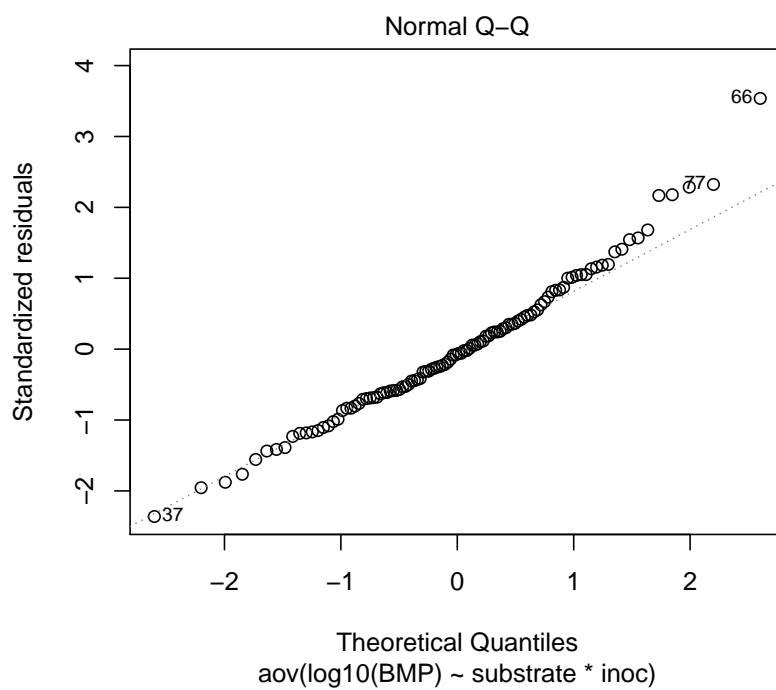
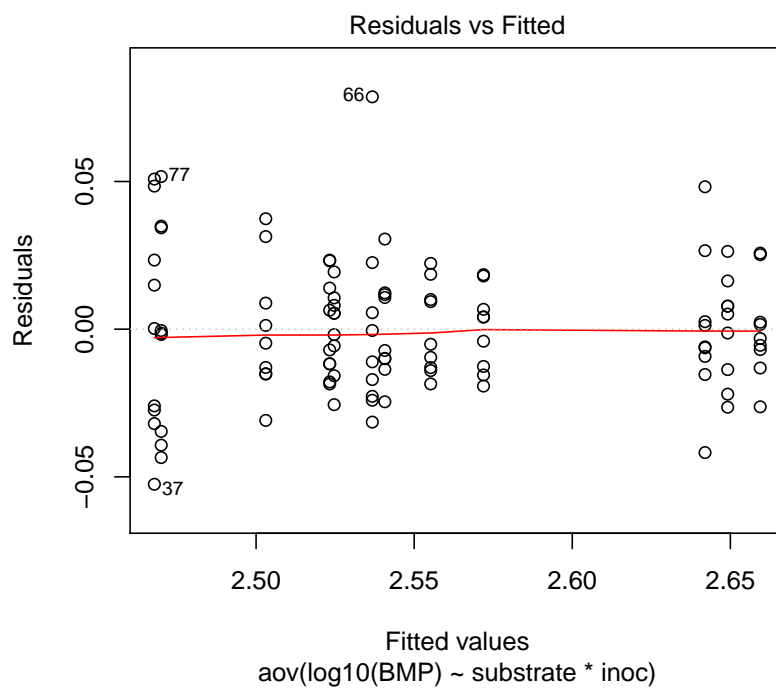
```
(tr <- TukeyHSD(m3, 'inoc'))
```

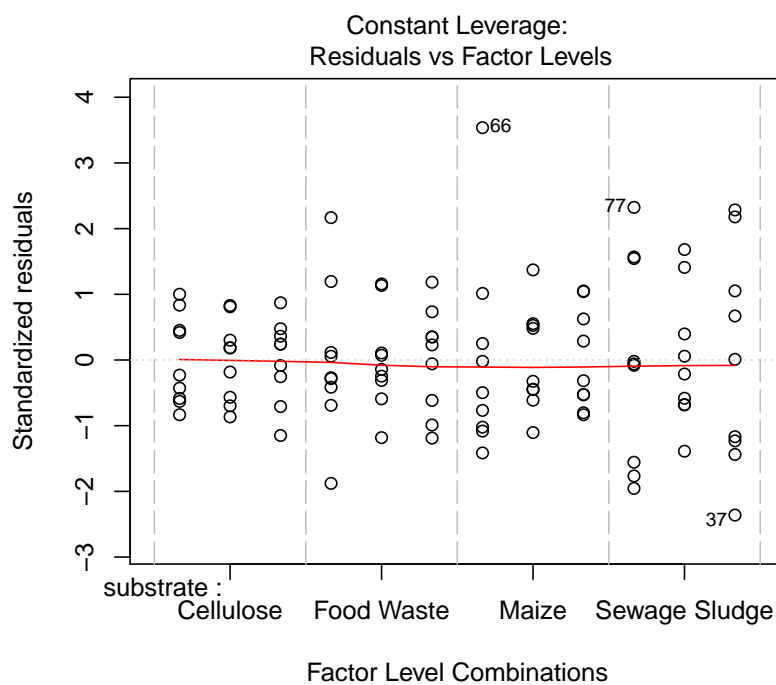
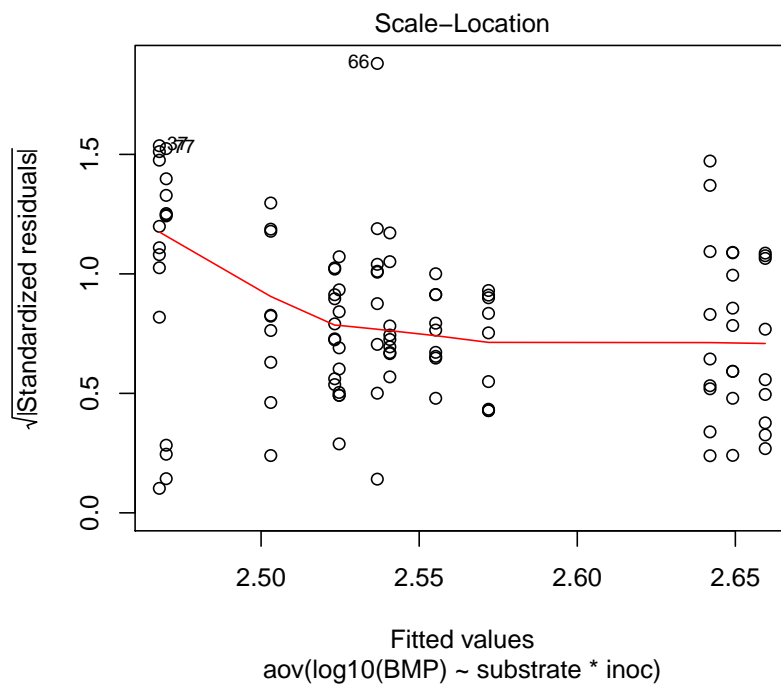
```
#      Tukey multiple comparisons of means
#      95% family-wise confidence level
#
# Fit: aov(formula = log10(BMP) ~ substrate * inoc, data = bil)
#
# $inoc
#           diff          lwr          upr      p adj
# BWTP-ABP  0.017803269  0.004565351  0.03104119 0.0052233
# WWTP-ABP -0.009747578 -0.022985495  0.00349034 0.1911260
# WWTP-BWTP -0.027550847 -0.040788764 -0.01431293 0.0000092
```

```
100 * (10^tr$inoc[, 'diff'] - 1)
```

```
# BWTP-ABP WWTP-ABP WWTP-BWTP
#  4.184538 -2.219462 -6.146785
```

```
plot(m3, ask = FALSE)
```





We can conclude that the BWTP inoculum resulted in BMP values about 4-6% higher than the other two.

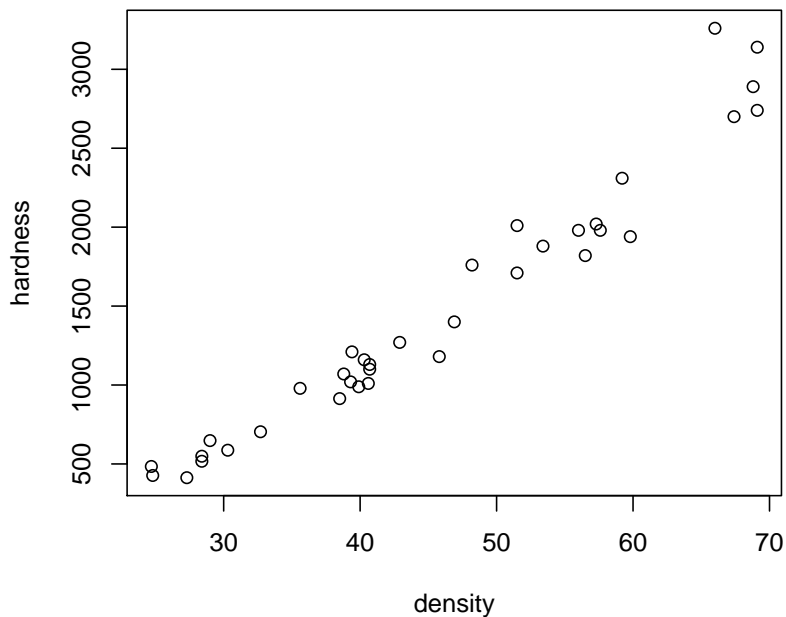
### 3 Problem 2. Wood hardness and density

```
hard <- read.csv("data/janka.csv")
dfsumm(hard)

#
# 36 rows and 2 columns
# 36 unique rows
#
#           density hardness
# Class           numeric   integer
# Minimum          24.7      413
# Maximum          69.1     3260
# Mean             45.7     1180
# Unique (excl. NA)    32      35
# Missing values       0       0
# Sorted             TRUE     FALSE
```

Let's start out by seeing what the data look like.

```
plot(hardness ~ density, data = hard)
```



We might be interested in doing two things with these data: determining if wood hardness (difficult to measure) is related to wood density (easy to measure), and, if so, predicting hardness from the density. Are these data experimental or observational? Try to fit an appropriate regression model to these data, and take a look at the residuals to check the structure. Can you improve it?

```

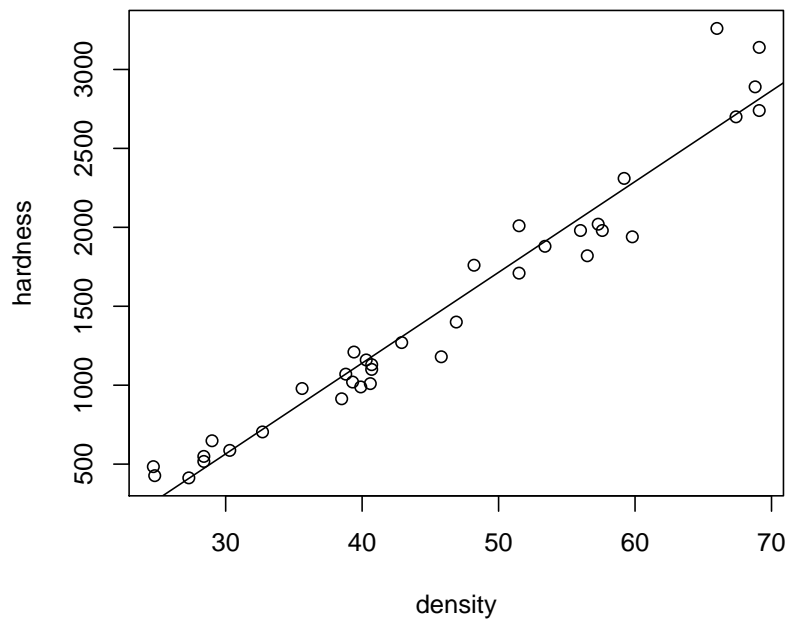
m1 <- lm(hardness ~ density, data = hard)
summary(m1)

#
# Call:
# lm(formula = hardness ~ density, data = hard)
#
# Residuals:
#      Min       1Q   Median       3Q      Max
# -338.40  -96.98  -15.71   92.71  625.06
#
# Coefficients:
#              Estimate Std. Error t value Pr(>|t|)
# (Intercept) -1160.500    108.580  -10.69 2.07e-12 ***
# density       57.507      2.279   25.24 < 2e-16 ***
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# Residual standard error: 183.1 on 34 degrees of freedom
# Multiple R-squared:  0.9493, Adjusted R-squared:  0.9478
# F-statistic: 637 on 1 and 34 DF, p-value: < 2.2e-16

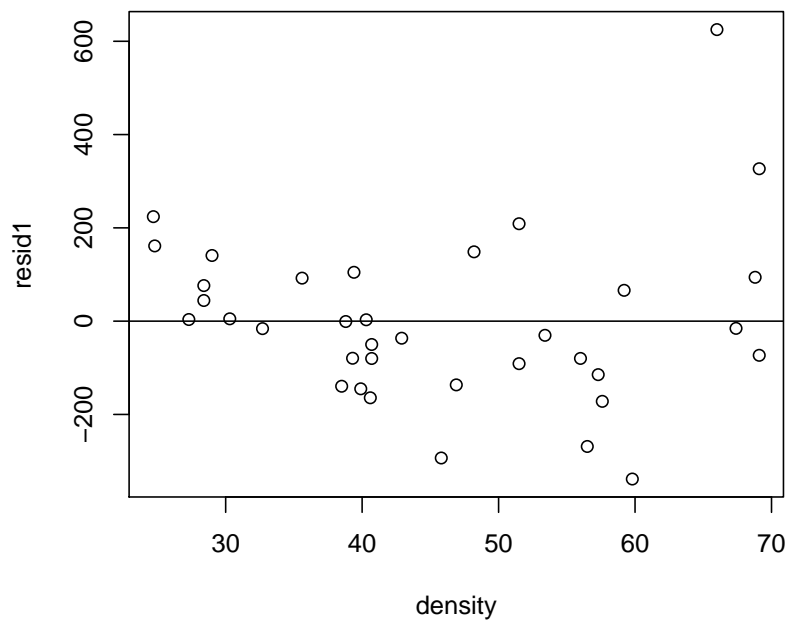
hard$pred1 <- predict(m1)
hard$resid1 <- resid(m1)

plot(hardness ~ density, data = hard)
abline(m1)

```



```
plot(resid1 ~ density, data = hard)  
abline(h = 0)
```



```

m2 <- lm(hardness ~ poly(density, 3), data = hard)
summary(m2)

#
# Call:
# lm(formula = hardness ~ poly(density, 3), data = hard)
#
# Residuals:
#      Min       1Q   Median       3Q      Max
# -310.98  -92.52  -14.94   61.41  537.92
#
# Coefficients:
#              Estimate Std. Error t value Pr(>|t|)
# (Intercept)      1469.47      27.29  53.841 < 2e-16 ***
# poly(density, 3)1  4620.14     163.76  28.213 < 2e-16 ***
# poly(density, 3)2   525.40     163.76   3.208  0.00303 **
# poly(density, 3)3    72.14     163.76   0.441  0.66252
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# Residual standard error: 163.8 on 32 degrees of freedom
# Multiple R-squared:  0.9618, Adjusted R-squared:  0.9583
# F-statistic: 268.8 on 3 and 32 DF,  p-value: < 2.2e-16

m2 <- lm(hardness ~ poly(density, 2), data = hard)
hard$pred2 <- predict(m2)
hard$resid2 <- resid(m2)

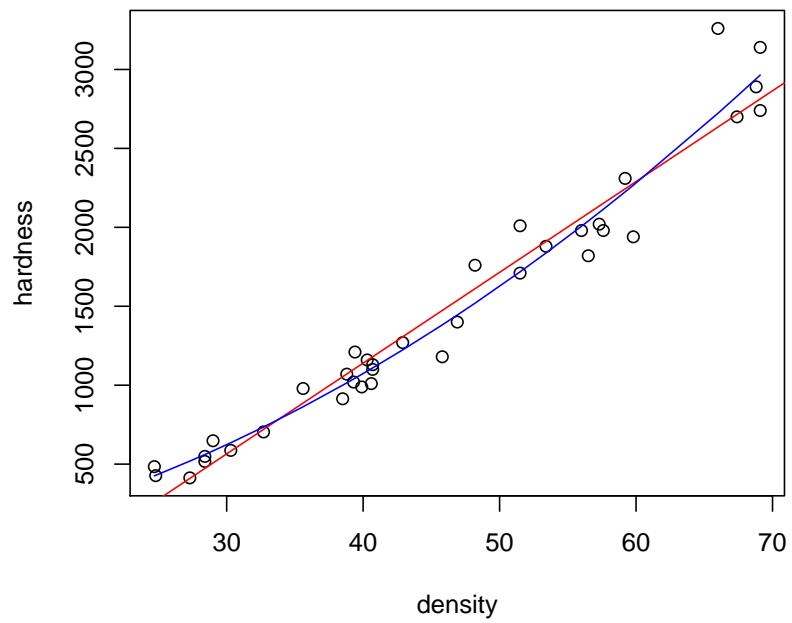
```

```

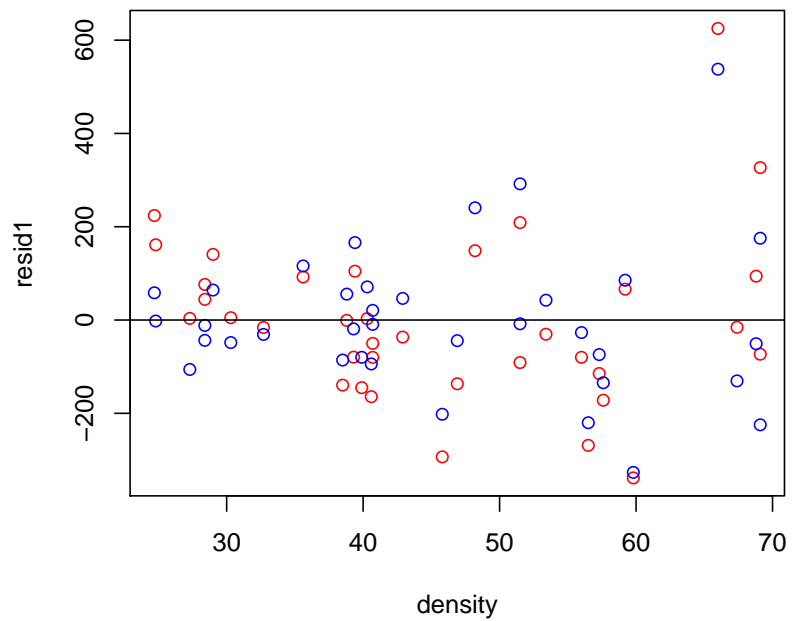
plot(hardness ~ density, data = hard)
abline(m1, col = 'red')
lines(pred2 ~ density, data = hard, col = 'blue')

```





```
plot(resid1 ~ density, data = hard, col = 'red')
points(resid2 ~ density, data = hard, col = 'blue')
abline(h = 0)
```



```

m3 <- lm(log10(hardness) ~ poly(density, 2), data = hard)
summary(m3)

#
# Call:
# lm(formula = log10(hardness) ~ poly(density, 2), data = hard)
#
# Residuals:
#      Min       1Q   Median       3Q      Max
# -0.096983 -0.024792 -0.004795  0.032573  0.081955
#
# Coefficients:
#              Estimate Std. Error t value Pr(>|t|)
# (Intercept)    3.099195   0.007294  424.896 < 2e-16 ***
# poly(density, 2)1  1.470617   0.043764   33.603 < 2e-16 ***
# poly(density, 2)2 -0.234322   0.043764   -5.354 6.49e-06 ***
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# Residual standard error: 0.04376 on 33 degrees of freedom
# Multiple R-squared:  0.9723, Adjusted R-squared:  0.9706
# F-statistic: 578.9 on 2 and 33 DF,  p-value: < 2.2e-16

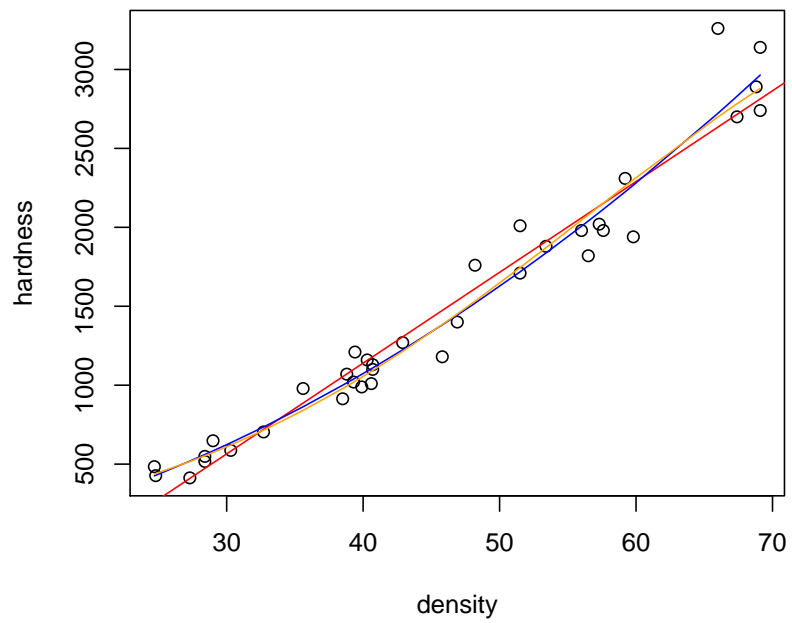
hard$pred3 <- 10^predict(m3)
hard$resid3 <- hard$pred3 - hard$hardness

```

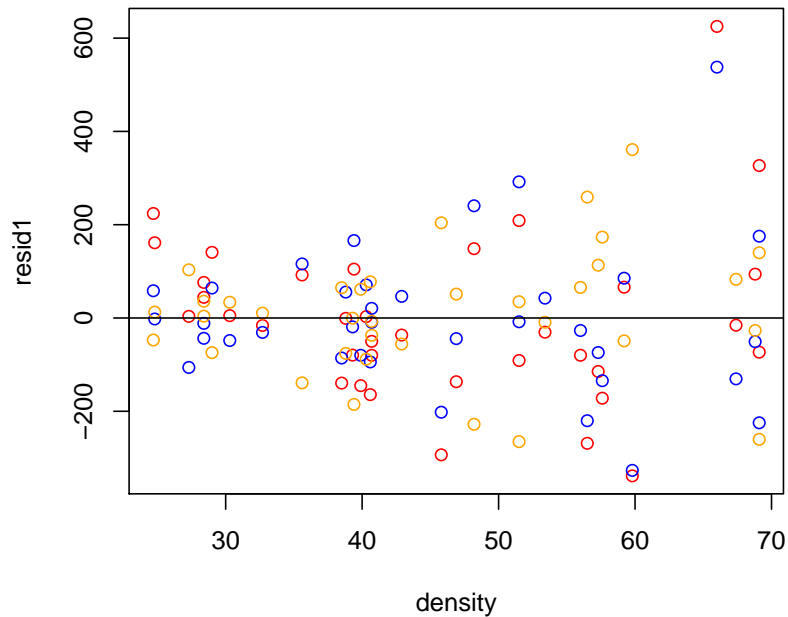
```

plot(hardness ~ density, data = hard)
abline(m1, col = 'red')
lines(pred2 ~ density, data = hard, col = 'blue')
lines(pred3 ~ density, data = hard, col = 'orange')

```



```
plot(resid1 ~ density, data = hard, col = 'red')
points(resid2 ~ density, data = hard, col = 'blue')
points(resid3 ~ density, data = hard, col = 'orange')
abline(h = 0)
```



## 4 Problem 3. Fruit fly longevity and sexual activity

The data in the file `fruitfly.csv` are from an experiment on fruitfly longevity and are also from [Faraway \[2005\]](#). The original objective of this famous experiment was to assess the effect of sexual activity (manipulated by controlling the number of females placed with a single male, `activity` column) on fruitfly longevity (how long the flies live, `longevity` column). But longevity is known to be correlated with thorax length (`thorax` column).

```
ff <- read.csv('data/fruitfly.csv')
head(ff)
```

```
#   thorax longevity activity
# 1  0.68         37    many
# 2  0.68         49    many
# 3  0.72         46    many
# 4  0.72         63    many
# 5  0.76         39    many
# 6  0.76         46    many
```

1. How might you plot these data to assess the effect of activity?
2. How can you fit a statistical model that utilizes the correlation with thorax length to increase power?
3. What approach should you use to compare the levels of `activity` to each other?

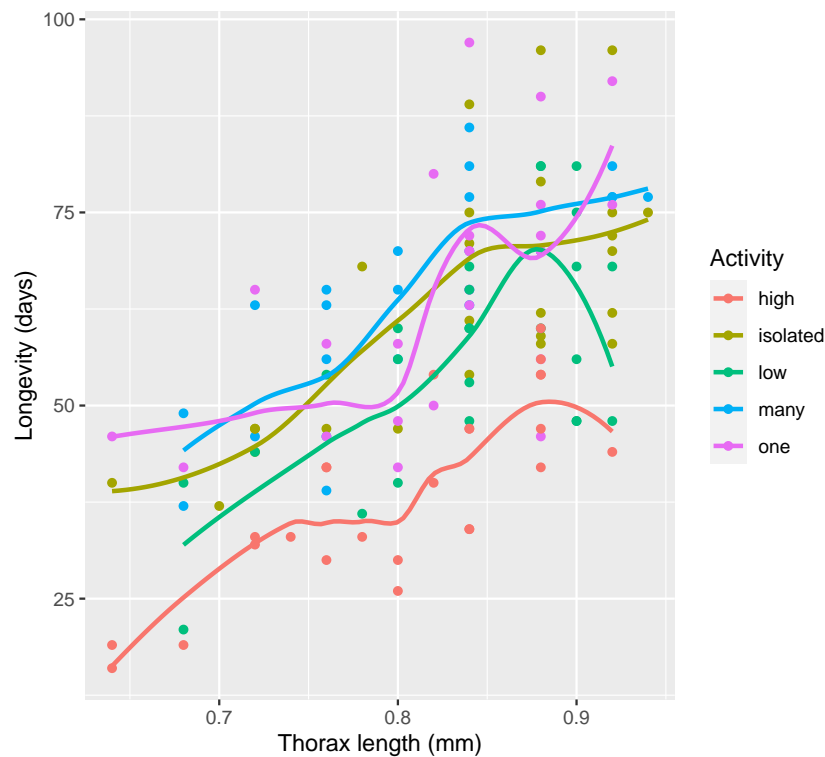
```
ggplot(ff, aes(thorax, longevity, colour = activity)) +
  geom_point() +
  geom_smooth(se = FALSE) +
  labs(x = 'Thorax length (mm)', y = 'Longevity (days)', colour = 'Activity')

# 'geom_smooth()' using method = 'loess' and formula 'y ~ x'

# Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, :
# pseudoinverse used at 0.84

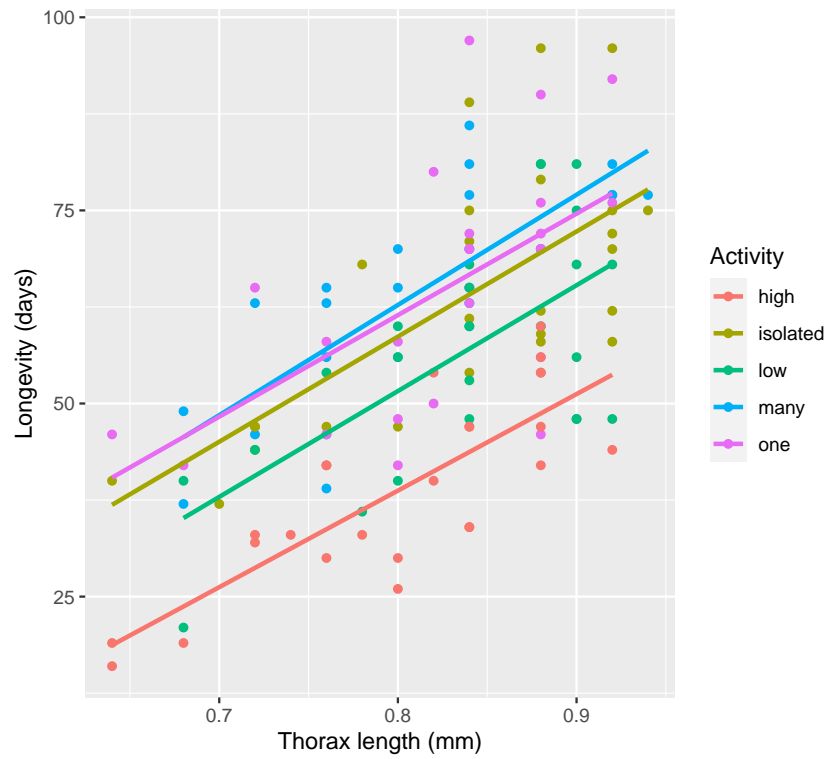
# Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, :
# neighborhood radius 0.04

# Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric, :
# reciprocal condition number 8.6863e-22
```



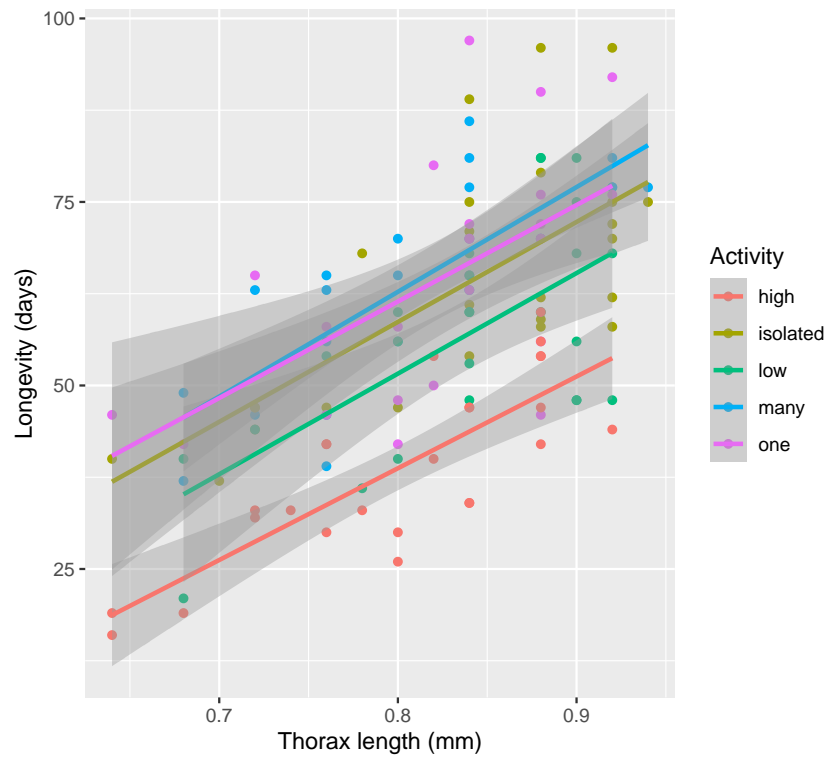
```
ggplot(ff, aes(thorax, longevity, colour = activity)) +
  geom_point() +
  geom_smooth(method = lm, se = FALSE) +
  labs(x = 'Thorax length (mm)', y = 'Longevity (days)', colour = 'Activity')

# 'geom_smooth()' using formula 'y ~ x'
```



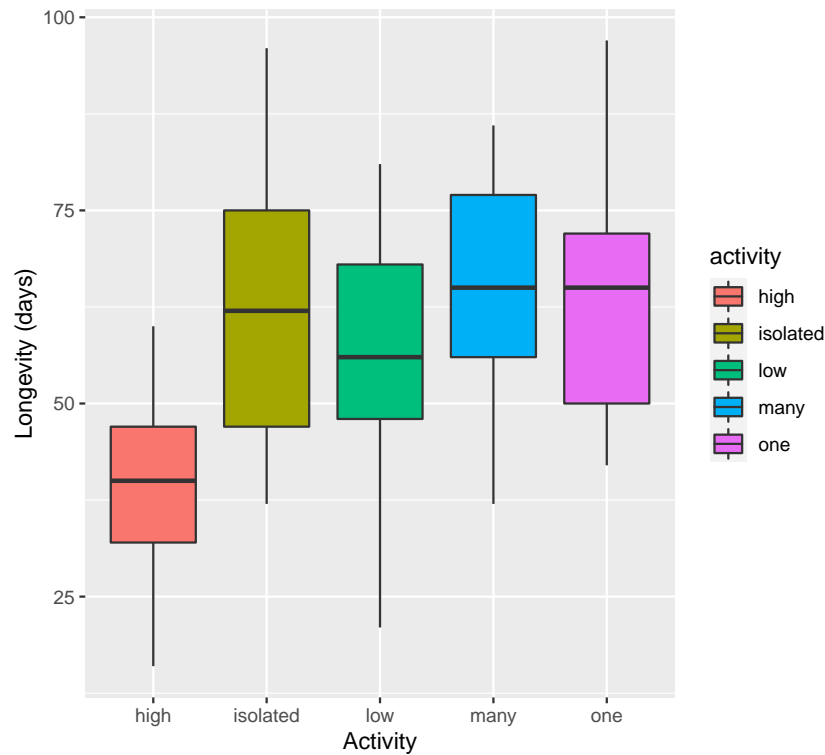
```
ggplot(ff, aes(thorax, longevity, colour = activity)) +
  geom_point() +
  geom_smooth(method = lm) +
  labs(x = 'Thorax length (mm)', y = 'Longevity (days)', colour = 'Activity')

# 'geom_smooth()' using formula 'y ~ x'
```



Compare to a boxplot—more difficult to see separation of groups.

```
ggplot(ff, aes(activity, longevity, fill = activity)) +
  geom_boxplot() +
  labs(x = 'Activity', y = 'Longevity (days)', colour = 'Activity')
```



```
levels(ff$activity)
```

```
# [1] "high"      "isolated" "low"       "many"      "one"
```

First level will be reference. Let's change it to isolated.

```
ff$activity <- relevel(ff$activity, ref= 'isolated')
```

```
m1 <- lm(longevity ~ activity * thorax, data = ff)
anova(m1)
```

```
# Analysis of Variance Table
#
# Response: longevity
#
#      Df Sum Sq Mean Sq F value Pr(>F)
# activity      4 12269.5   3067.4   26.728 1.2e-15 ***
# thorax        1 12368.4 12368.4 107.774 < 2e-16 ***
# activity:thorax  4    24.3     6.1   0.053 0.9947
# Residuals    114 13083.0   114.8
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m2 <- lm(longevity ~ activity + thorax, data = ff)
anova(m2)
```



```
# Analysis of Variance Table
#
# Response: longevity
#           Df Sum Sq Mean Sq F value    Pr(>F)
# activity    4  12270   3067.4   27.614 3.481e-16 ***
# thorax      1  12368  12368.4  111.348 < 2.2e-16 ***
# Residuals 118  13107    111.1
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m2)
```

```
#
# Call:
# lm(formula = longevity ~ activity + thorax, data = ff)
#
# Residuals:
#      Min       1Q   Median       3Q      Max
# -26.108  -7.014  -1.101   6.234  30.265
#
# Coefficients:
#              Estimate Std. Error t value Pr(>|t|)
# (Intercept)   -48.749     10.850   -4.493 1.65e-05 ***
# activityhigh  -20.004      3.016   -6.632 1.05e-09 ***
# activitylow   -7.015      2.981   -2.353  0.0203 *
# activitymany    4.139      3.027    1.367  0.1741
# activityone     2.637      2.984    0.884  0.3786
# thorax        134.341     12.731   10.552 < 2e-16 ***
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# Residual standard error: 10.54 on 118 degrees of freedom
# Multiple R-squared:  0.6527, Adjusted R-squared:  0.638
# F-statistic: 44.36 on 5 and 118 DF, p-value: < 2.2e-16
```

We can use Bonferroni adjustment,  $0.05 / 5 = 0.01$ . So only **high** level is clearly different—20 days shorter longevity, which is a lot!

```
confint(m2)
```

```
#              2.5 %      97.5 %
# (Intercept) -70.235303 -27.263477
# activityhigh -25.976247 -14.031174
# activitylow  -12.918256  -1.111636
# activitymany  -1.855011  10.132389
# activityone   -3.271842   8.546143
# thorax       109.130197 159.552553
```

Strange that “many” level is so different from others.

```
confint(m2)

#               2.5 %      97.5 %
# (Intercept) -70.235303 -27.263477
# activityhigh -25.976247 -14.031174
# activitylow  -12.918256  -1.111636
# activitymany  -1.855011  10.132389
# activityyone  -3.271842   8.546143
# thorax       109.130197 159.552553
```

## 5 Problem 4: Growth and nitrate accumulation by *Lemna minor*

Duckweeds are very tiny floating plants that can be used for wastewater treatment and recovery of nitrogen. Harvested material can be used as an animal feed. [Devlamynck et al. \[2020\]](#) measured biomass production and nitrate accumulation in a duckweed species *Lemna minor*. The data are in `lemna.csv`. Use them to explore the following questions.

1. Did medium affect growth (`grow`)?
2. Did medium affect  $\text{NO}_3^-$  accumulation (`N03.accum`)?
3. Is  $\text{NO}_3^-$  accumulation related to  $\text{NO}_3^-$  concentration in the medium (`N03.med`)?

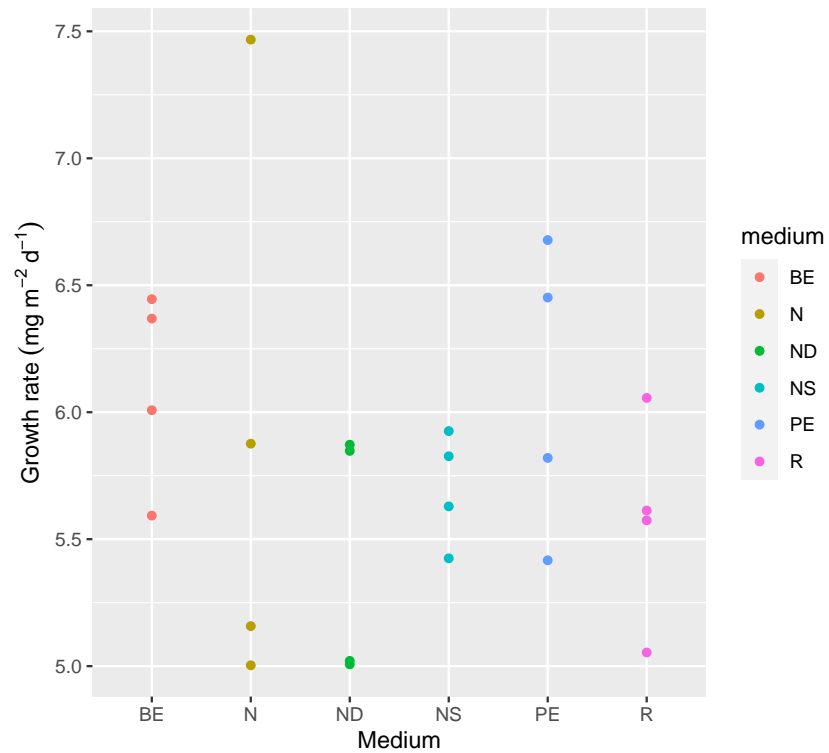
```
lem <- read.csv('data/lemna.csv')
```

```
summary(lem)
```

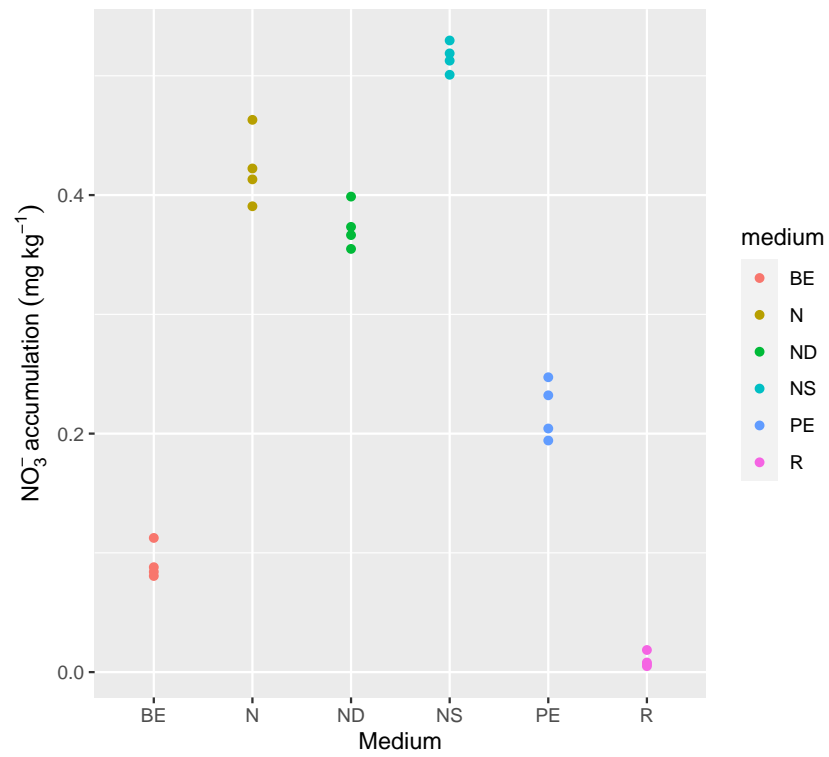
#	med.descrip	medium	grow
# Concentrated C medium	:4	BE:4	Min. :5.003
# Diluted N medium	:4	N :4	1st Qu.:5.423
# Fish wastewater effluent	:4	ND:4	Median :5.823
# Pig wastewater effluent	:4	NS:4	Mean :5.797
# Rainwater	:4	PE:4	3rd Qu.:6.020
# Synthetic N medium	:4	R :4	Max. :7.467
#	N03.accum	pH.med	N03.med
# Min.	:0.005025	Min. :5.760	Min. : 0.009594
# 1st Qu.	:0.087042	1st Qu.:6.388	1st Qu.: 2.215323
# Median	:0.301076	Median :7.390	Median : 4.138554
# Mean	:0.271930	Mean :7.461	Mean : 7.795348
# 3rd Qu.	:0.415473	3rd Qu.:8.525	3rd Qu.: 9.410879
# Max.	:0.529639	Max. :9.632	Max. :27.129694

```
library(ggplot2)
```

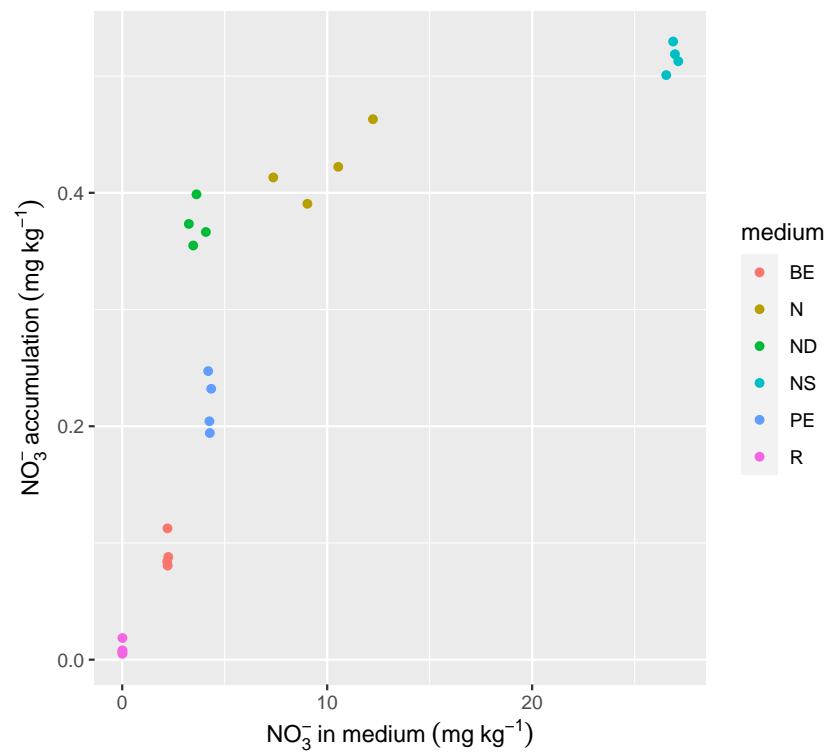
```
ggplot(lem, aes(medium, grow, colour = medium)) +
  geom_point() +
  labs(x = 'Medium', y = expression('Growth rate'~(mg~m^-2~d^-1)))
```



```
ggplot(lem, aes(medium, NO3.accum, colour = medium)) +
  geom_point() +
  labs(x = 'Medium', y = expression(NO[3]^'-~'accumulation'~(mg~kg^-1)))
```



```
ggplot(lem, aes(NO3.med, NO3.accum, colour = medium)) +
  geom_point() +
  labs(x = expression(NO[3]^{"-"}~"in medium"~(mg~kg^{"-1"})), y = expression(NO[3]^{"-"}~"accumulation"~(mg~kg^{"-1"})))
```



First growth. Check plot—no clear effect, no stats needed. We can calculate average and sd at least.

```
lemsum <- as.data.frame(summarise(group_by(lem, medium),
  grow.mean = mean(grow), grow.sd = sd(grow),
  NO3.med.mean = mean(NO3.med), NO3.med.sd = sd(NO3.med),
  NO3.accum.mean = mean(NO3.accum),
  NO3.accum.sd = sd(NO3.accum)))

lemsum
```

#	medium	grow.mean	grow.sd	NO3.med.mean	NO3.med.sd	NO3.accum.mean
# 1	BE	6.103780	0.3904054	2.217319070	0.0227861966	0.091324595
# 2	N	5.876119	1.1268901	9.794380141	2.0779095490	0.422308931
# 3	ND	5.437048	0.4885779	3.604850206	0.3524655526	0.373366822
# 4	NS	5.701615	0.2220019	26.879508387	0.2478468075	0.515520870
# 5	PE	6.091729	0.5780991	4.266298899	0.0601486883	0.219471297
# 6	R	5.574388	0.4101557	0.009733427	0.0001607362	0.009586386

```
# NO3.accum.sd
# 1 0.014458101
# 2 0.030275823
# 3 0.018557293
# 4 0.011995311
# 5 0.024499245
# 6 0.006123297
```

For nitrate accumulation, there seem to be effects.

```
levels(lem$medium)

# [1] "BE" "N" "ND" "NS" "PE" "R"

lem$medium <- relevel(lem$medium, ref= 'R')

m1 <- lm(NO3.accum ~ medium, data = lem)
anova(m1)

# Analysis of Variance Table
#
# Response: NO3.accum
#          Df Sum Sq Mean Sq F value    Pr(>F)
# medium      5 0.78574  0.157147   418.76 < 2.2e-16 ***
# Residuals 18 0.00675  0.000375
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(m1)

#
# Call:
```

```
# lm(formula = NO3.accum ~ medium, data = lem)
#
# Residuals:
#      Min       1Q   Median       3Q      Max
# -0.031673 -0.009509 -0.002861  0.009905  0.040788
#
# Coefficients:
#              Estimate Std. Error t value Pr(>|t|)
# (Intercept)  0.009586   0.009686   0.990   0.335
# mediumBE     0.081738   0.013698   5.967 1.21e-05 ***
# mediumN      0.412723   0.013698  30.130 < 2e-16 ***
# mediumND     0.363780   0.013698  26.557 6.87e-16 ***
# mediumNS     0.505934   0.013698  36.935 < 2e-16 ***
# mediumPE     0.209885   0.013698  15.322 9.03e-12 ***
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# Residual standard error: 0.01937 on 18 degrees of freedom
# Multiple R-squared:  0.9915, Adjusted R-squared:  0.9891
# F-statistic: 418.8 on 5 and 18 DF,  p-value: < 2.2e-16
```

As expected, very clear differences. Does it matter exactly which ones differed? Seems everything was higher than R.

```
m2 <- aov(NO3.accum ~ medium, data = lem)
anova(m2)

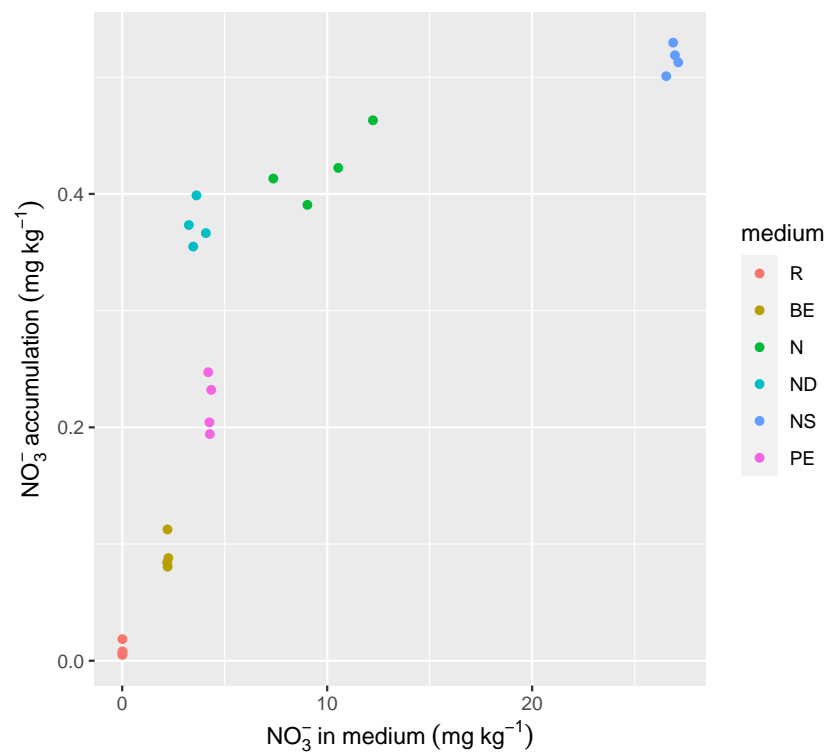
# Analysis of Variance Table
#
# Response: NO3.accum
#      Df Sum Sq Mean Sq F value    Pr(>F)
# medium     5  0.78574  0.157147  418.76 < 2.2e-16 ***
# Residuals  18  0.00675  0.000375
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(m2)
```

```
# Tukey multiple comparisons of means
# 95% family-wise confidence level
#
# Fit: aov(formula = NO3.accum ~ medium, data = lem)
#
# $medium
#      diff      lwr      upr    p adj
# BE-R    0.08173821 0.03820541 0.125271009 0.0001514
# N-R     0.41272254 0.36918974 0.456255345 0.0000000
# ND-R    0.36378044 0.32024763 0.407313236 0.0000000
# NS-R    0.50593448 0.46240168 0.549467284 0.0000000
# PE-R    0.20988491 0.16635211 0.253417711 0.0000000
# N-BE    0.33098434 0.28745154 0.374517136 0.0000000
```

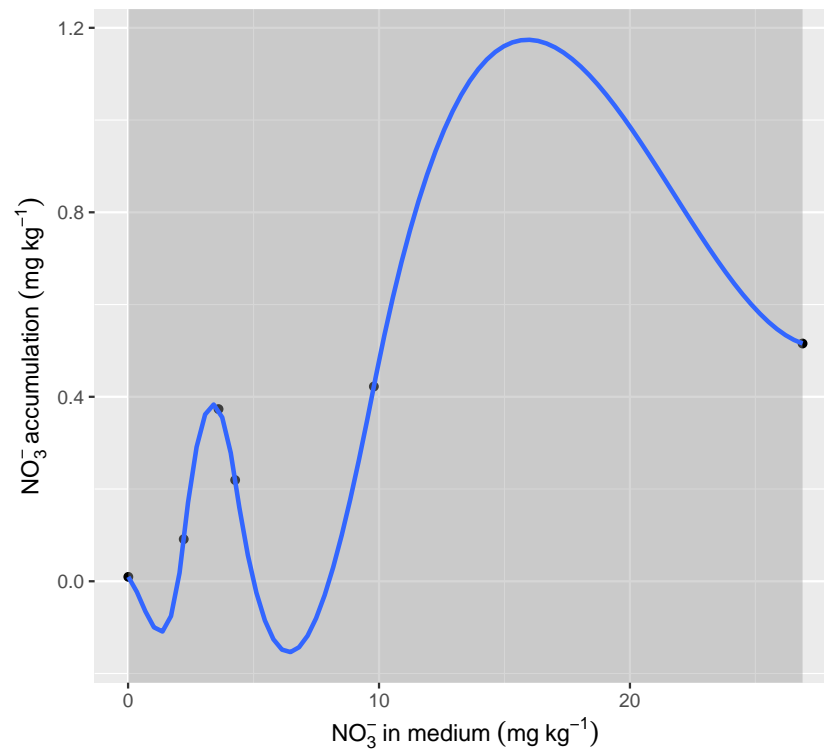
```
# ND-BE 0.28204223 0.23850943 0.325575027 0.0000000
# NS-BE 0.42419628 0.38066347 0.467729076 0.0000000
# PE-BE 0.12814670 0.08461390 0.171679503 0.0000003
# ND-N -0.04894211 -0.09247491 -0.005409309 0.0224993
# NS-N 0.09321194 0.04967914 0.136744740 0.0000291
# PE-N -0.20283763 -0.24637043 -0.159304833 0.0000000
# NS-ND 0.14215405 0.09862125 0.185686849 0.0000001
# PE-ND -0.15389552 -0.19742832 -0.110362724 0.0000000
# PE-NS -0.29604957 -0.33958237 -0.252516773 0.0000000
```

```
ggplot(lem, aes(NO3.med, NO3.accum, colour = medium)) +
  geom_point() +
  labs(x = expression(NO[3]^-1~'in medium'~(mg~kg^-1)), y = expression(NO[3]^-1~'accumulation'~(mg~kg^-1)))
```



```
ggplot(lemsum, aes(NO3.med.mean, NO3.accum.mean)) +
  geom_point() +
  geom_smooth() +
  labs(x = expression(NO[3]^-1~'in medium'~(mg~kg^-1)), y = expression(NO[3]^-1~'accumulation'~(mg~kg^-1)))

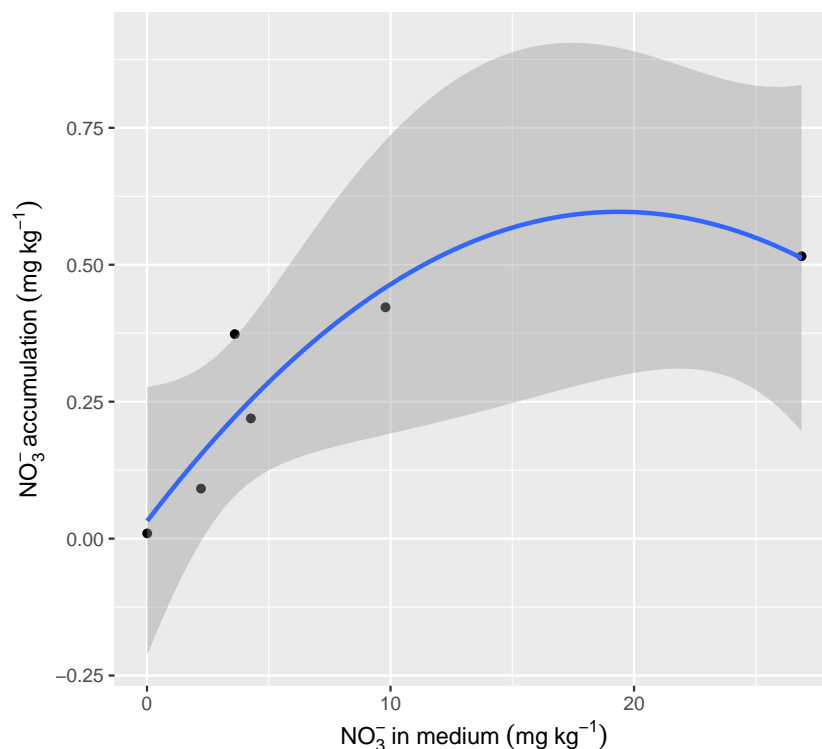
# 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



Whoa! Overfitting by default!

```
ggplot(lemsum, aes(NO3.med.mean, NO3.accum.mean)) +
  geom_point() +
  geom_smooth(method = lm, formula = y ~ poly(x, 2)) +
  labs(x = expression(NO[3]^'- '~'in medium'~(mg~kg^-1)'), y = expression(NO[3]^'- '~'accumulation'~(mg
```





## 6 Bibliography

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- J. J. Faraway. *Linear Models with R*. Number v. 63 in Texts in Statistical Science. Chapman & Hall/CRC, Boca Raton, 2005. ISBN 1-58488-425-8.
- K. Koch, T. Lippert, and J. E. Drewes. The role of inoculum's origin on the methane yield of different substrates in biochemical methane potential (BMP) tests. *Bioresour. Technology*, 243 (Supplement C):457–463, Nov. 2017. ISSN 0960-8524. doi: 10.1016/j.biortech.2017.06.142.