H1-2

DV

Contents


```r
library(knitr)
library(kableExtra)
opts_chunk$set(dpi = 600, dev = 'pdf')
options(digits = 5)
```

```r
library(here)
```

```
## here() starts at /home/denis/Documents/Poso/faks/istraživanja/inter-
testing-feedback-2018/analyses
```

```r
# NOTE: this will load {magrittr}, {here}, {conflicted} and {tidyverse}. also,
# `conflict_prefer`s filter from {dplyr}
# furthermore, it loads 3 data.frames: (1) `dat` which contains the pooled data
# through `2-wrangling-main.R`, (2) `datHard` which is `dat` with all the hard
# exclusion criteria applied (as described in `analysis-plan.md`), and (3)
# `datSoft` which is `datHard` with the soft exclusion criteria applied (as
# described in `analysis-plan.md`)
source(here('wrangling', '3-exclusion-criteria.R'))
```

```
## -- Attaching packages ---------------------------------------------------
------ tidyverse 1.2.1 --
```

```
## v ggplot2 3.1.0       v purrr   0.3.1
## v tibble  2.0.1       v dplyr   0.8.0.1
## v tidyr   0.8.3       v stringr 1.4.0
## v readr   1.3.1       v forcats 0.4.0
```

```
## -- Conflicts ------------------------------------------------------------
tidyverse_conflicts() --
## x dplyr::filter()     masks stats::filter()
## x dplyr::group_rows() masks kableExtra::group_rows()
## x dplyr::lag()        masks stats::lag()
```

```
## [conflicted] Will prefer dplyr::filter over any other package
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   when = col_datetime(format = ""),
##   giveFeedback = col_logical(),
##   condition = col_character(),
##   kolikoProcitaoText1 = col_character(),
##   kolikoProcitaoText2 = col_character(),
##   kolikoProcitaoText3 = col_character(),
##   readingDeficits = col_character(),
##   which = col_character(),
##   readingDifficultiesThisExp = col_character(),
##   activityFactor = col_character()
## )

## See spec(...) for full column specifications.
```

```
# for LDA
library(MASS)
# for Henze-Zirkler
library(MVN)
```

```
## sROC 0.1-2 loaded
```

```
# for Box's M
library(heplots)
```

```
## Loading required package: car

## Loading required package: carData

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some
```

```
# colorscale
library(viridis)
```

```
## Loading required package: viridisLite
```

```r
conflict_prefer('select', 'dplyr')
```

```
## [conflicted] Will prefer dplyr::select over any other package
```

```r
theme_set(theme_minimal())

# source helper functions
source(here('helpers', 'h1-2-helpers.R'))
```

Hard exclusion criteria

The following analyses are going to be conducted on a subset of the collected data which contains 203 cases. First, we will take a look at the data going into this analysis. Then, we will check whether the assumptions for conducting a MANOVA are satisfied. Finally, we will conduct the analyses specified in the `analysis-plan.md` file.

Descriptive statistics

This analysis is going to be run on a subset participants who were in no-feedback conditions. This includes the rereading group, and the two no-feedback test groups.

```r
# creating new df with the specified subset, selecting only relevant vars
datHardNofeed <- datHard %>% filter(., giveFeedback == F) %>%
  select(., activityFactor, totalCorrect, totalIntrusors)
```

This leaves us with 122 cases.

```r
datHardNofeed %>% glimpse(.)
```

```
## Observations: 122
## Variables: 3
## $ activityFactor <chr> "content", "general", "rereading", "content", "...
## $ totalCorrect   <dbl> 15, 12, 6, 12, 14, 14, 9, 5, 14, 13, 14, 8, 12,...
## $ totalIntrusors <dbl> 3, 3, 5, 3, 3, 4, 4, 4, 4, 3, 4, 6, 3, 3, 6, 8,...
```

First of all, it's important to mention that the group sizes are imbalanced, but the difference is really small:

```r
datHardNofeed %>% group_by(., activityFactor) %>% tally(.)
```

```
## # A tibble: 3 x 2
##   activityFactor     n
##   <chr>          <int>
## 1 content           42
```

```
## 2 general          40
## 3 rereading        40
```

Here are the descriptives for the whole subset.

```r
datHardNofeed %>% select(., -activityFactor) %>% psych::describe(.)
```

```
##                  vars   n  mean   sd median trimmed  mad min max range skew
## totalCorrect        1 122 11.40 3.04     11   11.39 2.97   4  19    15 0.04
## totalIntrusors      2 122  4.18 1.98      4    4.10 1.48   0  10    10 0.38
##                  kurtosis   se
## totalCorrect        -0.41 0.28
## totalIntrusors      -0.17 0.18
```

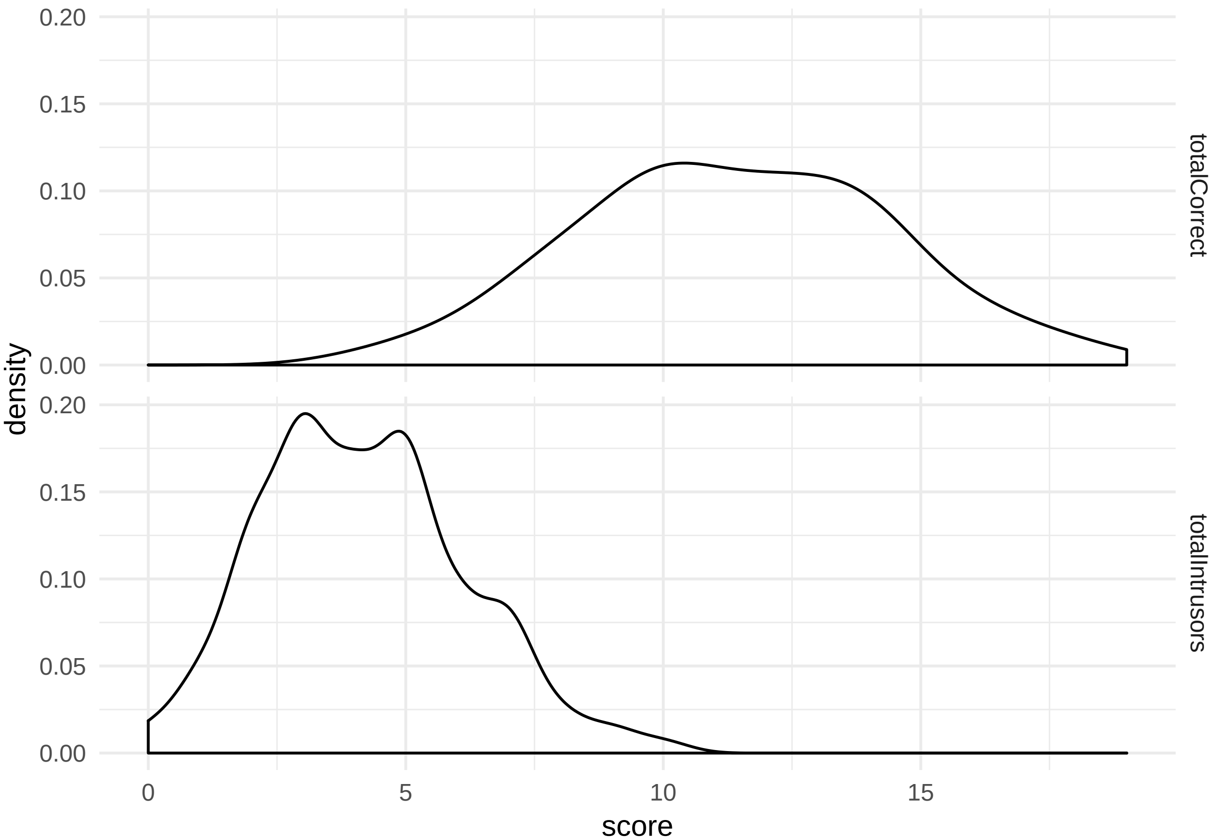
And the descriptives by group:

```r
by(datHardNofeed$totalCorrect, INDICES = datHardNofeed$activityFactor,
   psych::describe) %>% reduce(., rbind) %>%
  mutate(., condition = c("content", "general", "rereading")) %>%
  select(., condition, everything(), -vars)
```

```
##   condition  n   mean     sd median trimmed    mad min max range      skew
## 1   content 42 12.786 3.0165     12  12.765 2.9652   7  19    12  0.039247
## 2   general 40 10.475 2.8374     10  10.531 2.9652   5  16    11 -
0.053301
## 3 rereading 40 10.875 2.8028     11  10.938 2.9652   4  17    13 -
0.140828
##   kurtosis      se
## 1 -0.77457 0.46546
## 2 -0.98633 0.44863
## 3 -0.25332 0.44316
```

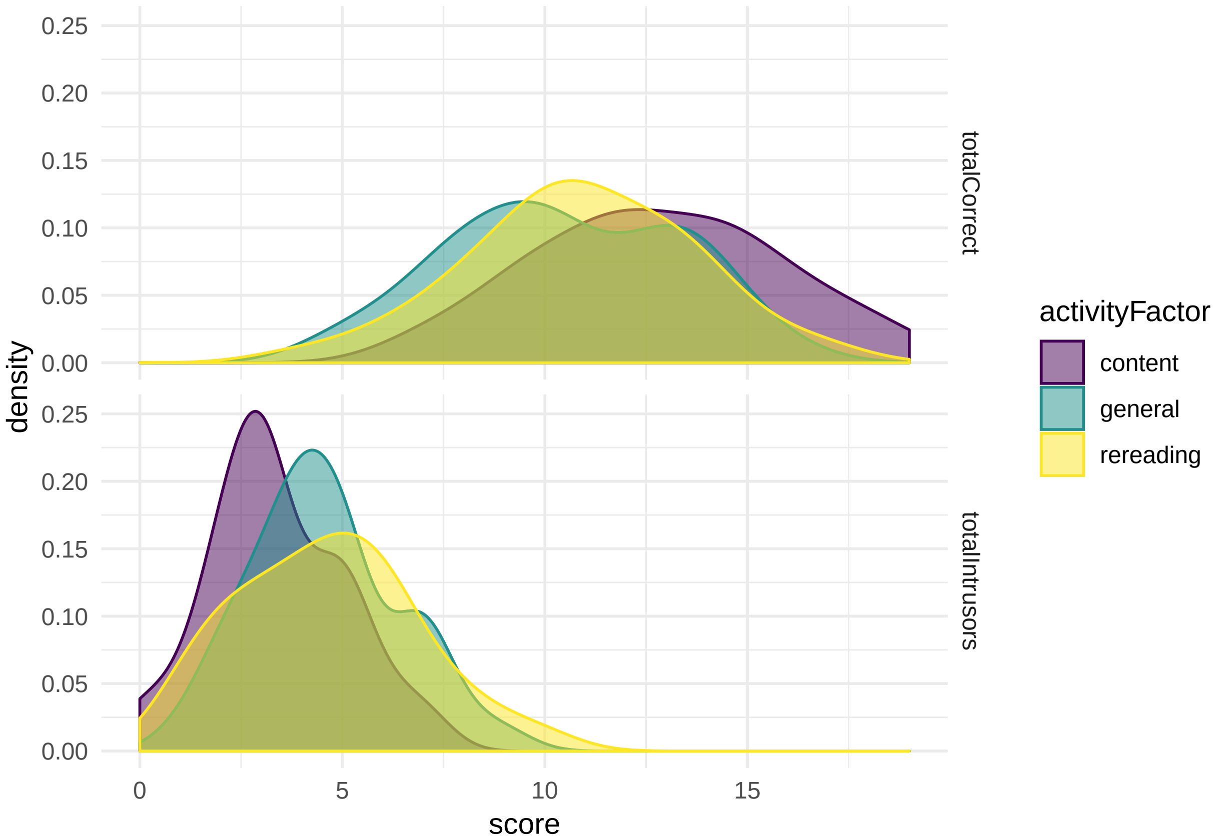
Now, we'll plot the DV distributions, both on the whole subset, and per group.

```r
datHardNofeed %>% gather(., totalCorrect, totalIntrusors, key = 'dependentVar',
                         value = 'score') %>%
  ggplot(., aes(x = score)) +
  geom_density() + facet_grid(dependentVar ~ .)
```



The graph shows that there could be significant deviations from normality. Let's look at the distributions in each group.

```
datHardNofeed %>% gather(., totalCorrect, totalIntrusors, key = 'dependentVar',
                         value = 'score') %>%
  ggplot(., aes(x = score, color = activityFactor, fill = activityFactor)) +
  geom_density(alpha = .5) + facet_grid(dependentVar ~ .) +
  scale_fill_viridis_d() + scale_color_viridis_d()
```

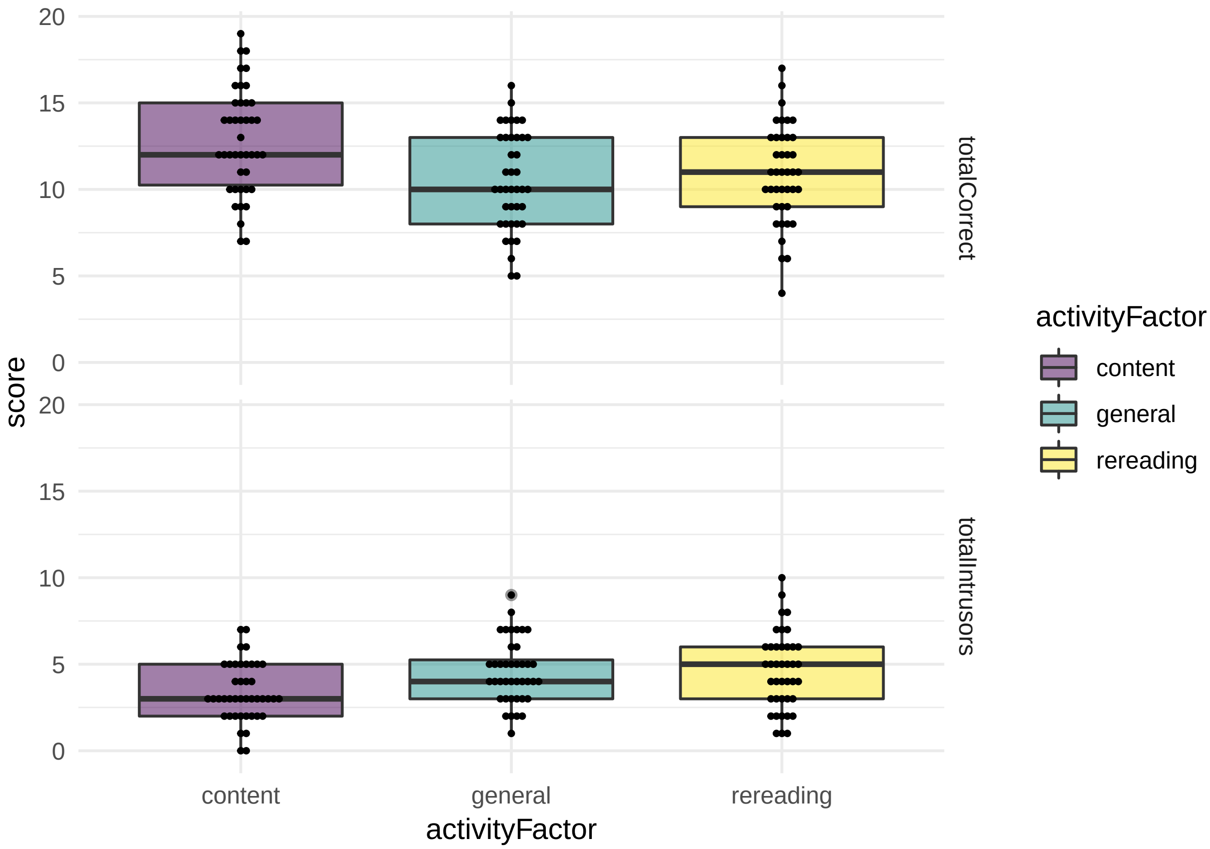


The distributions seem to be fairly similar on both dependent variables, and look a bit more normal than on the whole sample.

Next, here are the boxplots for the three groups, and for both DVs.

```
datHardNofeed %>% add_column(subject = 1:nrow(.), .before = 1) %>%
  gather(., totalCorrect, totalIntrusors, key = 'dependentVar',
         value = 'score') %>%
  ggplot(., aes(x = activityFactor, y = score, fill = activityFactor)) +
  geom_boxplot(alpha = .5) + geom_dotplot(mapping = aes(y = score), binaxis = 'y
                                 stackdir = 'centerwhole', dotsize = .5,
                                 fill = 'black', color = 'black') +
  facet_grid(dependentVar~.) + scale_fill_viridis(discrete = T)
```

```
## `stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.
```



Looks like there could be an outlier on the number of total intrusions in the general knowledge test condition.

Next, let's look at the correlation between the DVs. First, let's look at the correlation in the whole sub-sample.

```
. <- datHardNofeed %>% select(., -activityFactor) %>% psych::corr.test(.)
print(.)
```

```
## Call:psych::corr.test(x = .)
## Correlation matrix
##                 totalCorrect totalIntrusors
## totalCorrect            1.00          -0.67
## totalIntrusors         -0.67           1.00
## Sample Size
## [1] 122
## Probability values (Entries above the diagonal are adjusted for multiple test
##                 totalCorrect totalIntrusors
## totalCorrect               0              0
## totalIntrusors             0              0
##
##  To see confidence intervals of the correlations, print with the short=FALSE
```

We found a statistically significant correlation of .$r[2]. Next, let's look at the correlation in each group.

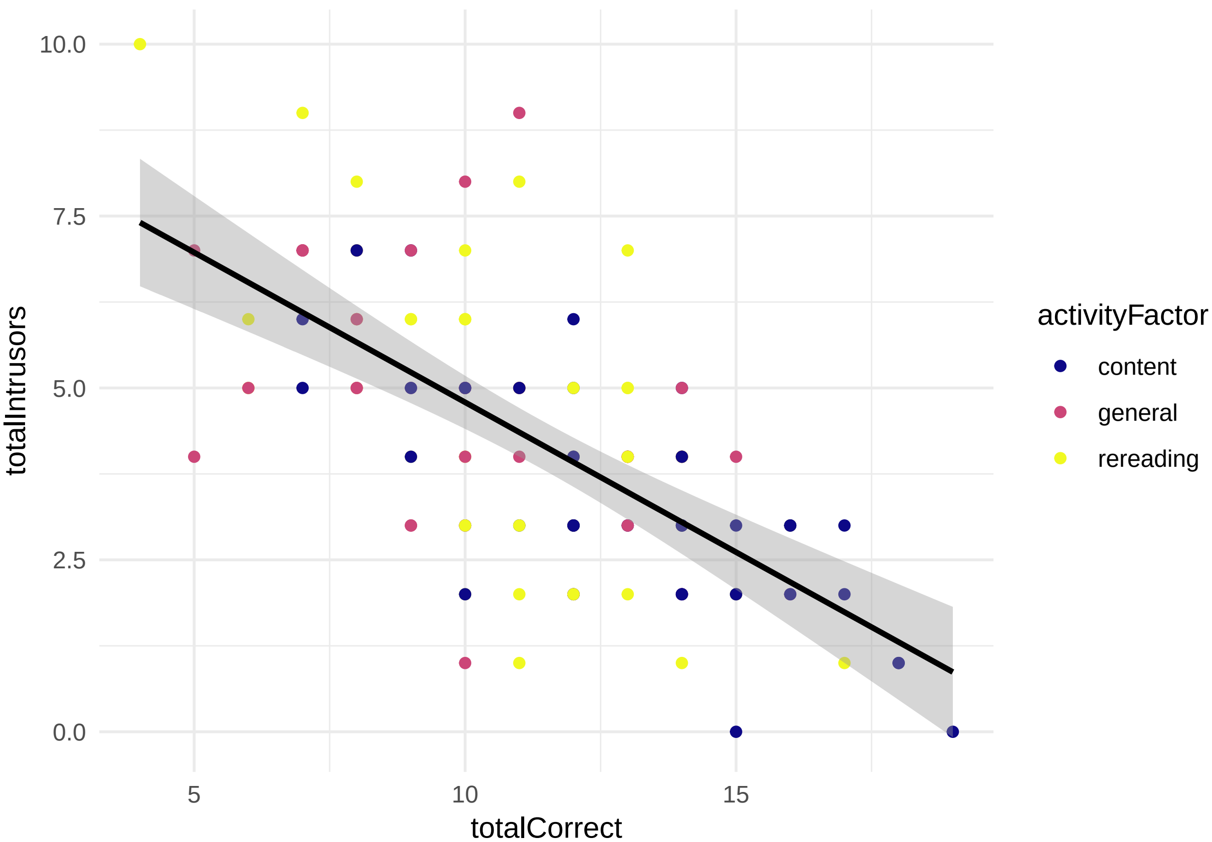
```r
by(datHardNofeed[, c('totalCorrect', 'totalIntrusors')],
   INDICES = datHardNofeed$activityFactor, FUN = psych::corr.test)
```

```
## datHardNofeed$activityFactor: content
## Call:FUN(x = data[x, , drop = FALSE])
## Correlation matrix
##                totalCorrect totalIntrusors
## totalCorrect           1.00          -0.74
## totalIntrusors        -0.74           1.00
## Sample Size
## [1] 42
## Probability values (Entries above the diagonal are adjusted for multiple test
##                totalCorrect totalIntrusors
## totalCorrect              0              0
## totalIntrusors            0              0
##
##  To see confidence intervals of the correlations, print with the short=FALSE
## --------------------------------------------------------
## datHardNofeed$activityFactor: general
## Call:FUN(x = data[x, , drop = FALSE])
## Correlation matrix
##                totalCorrect totalIntrusors
## totalCorrect           1.00          -0.53
## totalIntrusors        -0.53           1.00
## Sample Size
## [1] 40
## Probability values (Entries above the diagonal are adjusted for multiple test
##                totalCorrect totalIntrusors
## totalCorrect              0              0
## totalIntrusors            0              0
##
##  To see confidence intervals of the correlations, print with the short=FALSE
## --------------------------------------------------------
## datHardNofeed$activityFactor: rereading
## Call:FUN(x = data[x, , drop = FALSE])
## Correlation matrix
##                totalCorrect totalIntrusors
## totalCorrect           1.00          -0.65
## totalIntrusors        -0.65           1.00
```

```
## Sample Size
## [1] 40
## Probability values (Entries above the diagonal are adjusted for multiple test
##                 totalCorrect totalIntrusors
## totalCorrect               0              0
## totalIntrusors             0              0
##
##  To see confidence intervals of the correlations, print with the short=FALSE
```

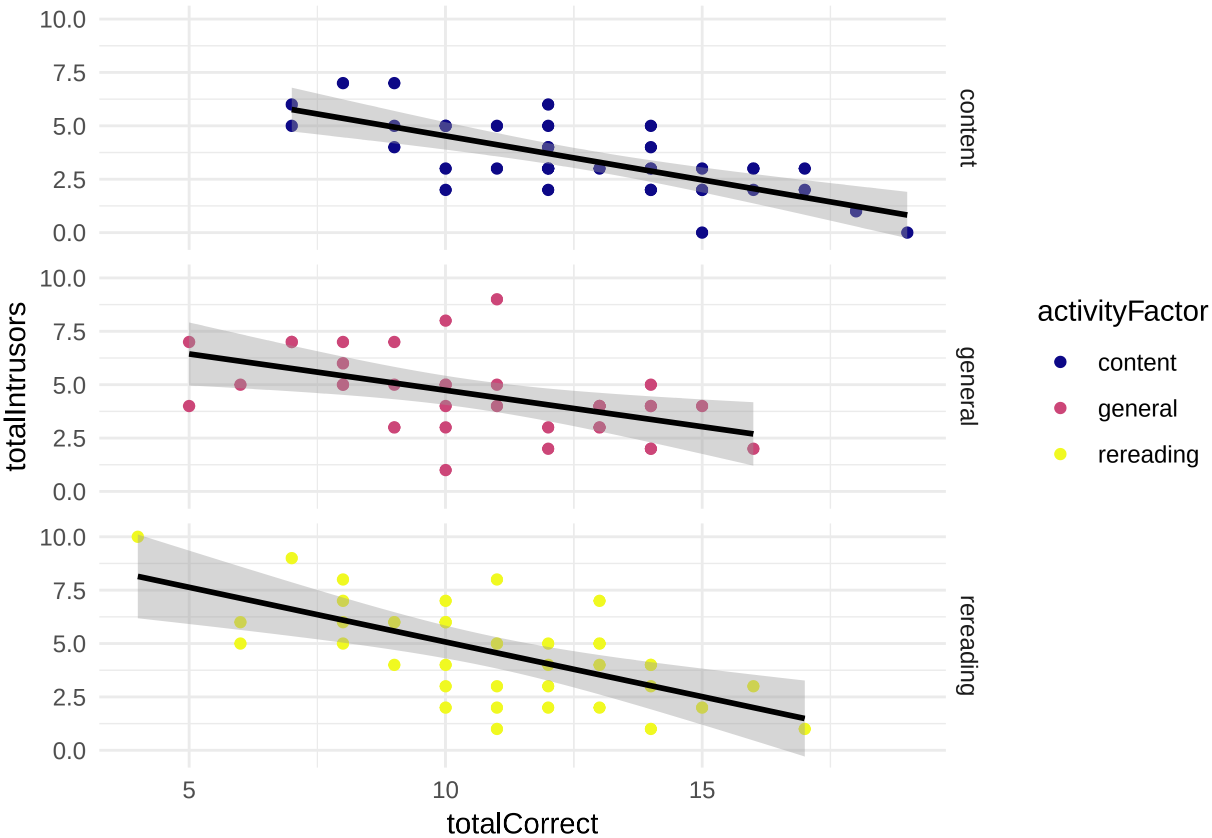
The correlations in all three groups are fairly similar and statistically significant. To check whether the relationship between the DVs could be described as linear, we'll plot the scatterplots for the whole sample and for each group.

```
datHardNofeed %>%
  ggplot(., aes(x = totalCorrect, y = totalIntrusors)) +
  geom_point(aes(fill = activityFactor, color = activityFactor)) +
  geom_smooth(method = 'lm', color = 'black', level = .99) +
  scale_fill_viridis_d(option = 'C') + scale_color_viridis_d(option = 'C')
```



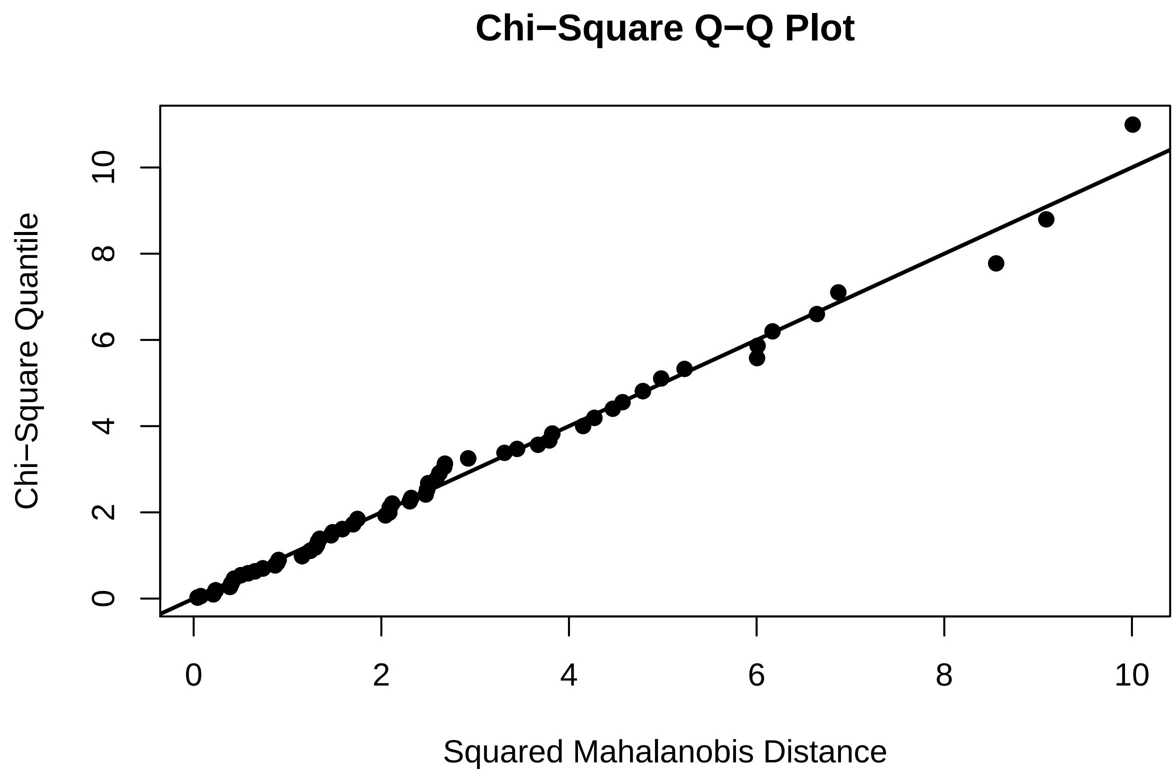
As can be seen from the plot, the relationship seems to be pretty linear, and the 99% confidence interval of the regression slopes is pretty small. Now, let's take a look at the scatterplots for each group separately.

```
datHardNofeed %>%
  ggplot(., aes(x = totalCorrect, y = totalIntrusors)) +
  geom_point(aes(fill = activityFactor, color = activityFactor)) +
  geom_smooth(method = 'lm', level = .99, color = 'black') +
  facet_grid(activityFactor ~ .) +
  scale_fill_viridis_d(option = 'C') + scale_color_viridis_d(option = 'C')
```



Again, we can see that the relationships are linear, as well as similar. Next, we will check the multivariate normality assumption using the Henze-Zirkler test.

```
datHardNofeed %>% select(., -activityFactor) %>%
  mvn(., multivariatePlot = 'qq', mvnTest = 'hz', desc = F)
```




```
## $multivariateNormality
##            Test      HZ p value MVN
## 1 Henze-Zirkler 0.52318 0.58715 YES
##
## $univariateNormality
##           Test        Variable Statistic   p value Normality
## 1 Shapiro-Wilk  totalCorrect      0.9870    0.2972    YES
## 2 Shapiro-Wilk totalIntrusors     0.9663    0.0038    NO
```

The result of Henze-Zirkler's multivariate normality test shows that a statistically significant departure from multivariate normality was not detected. Hence, we will assume that there really is no departure. The points on the Chi-Square Q-Q plot follow the straight line fairly well, which is also indicative of a normal distribution.

Now, we'll take a look at the homogeneity of covariance matrices assumption. First, let's take a look at the matrices themselves.

```r
by(datHardNofeed[, c('totalCorrect', 'totalIntrusors')],
   INDICES = datHardNofeed$activityFactor, FUN = cov) -> .
print(.)
```

```
## datHardNofeed$activityFactor: content
##                totalCorrect totalIntrusors
## totalCorrect         9.0993        -3.7456
## totalIntrusors      -3.7456         2.7782
## --------------------------------------------------------
```

```
## datHardNofeed$activityFactor: general
##                  totalCorrect totalIntrusors
## totalCorrect           8.0506        -2.7417
## totalIntrusors        -2.7417         3.3276
## ------------------------------------------------------------
## datHardNofeed$activityFactor: rereading
##                  totalCorrect totalIntrusors
## totalCorrect           7.8558        -4.0224
## totalIntrusors        -4.0224         4.9071
```

The covariance matrices look quite similar. The ratio of largest to smallest variance of the number of correct answers is 1.1583. The same ratio for the number of chosen intrusors is 1.76629. Finally, the ratio of the largest to the smallest covariance between the two DVs is 0.68159. As we can see, the variance ratios are pretty close to one. Still, let's test them with Box's M test.

```r
boxM(datHardNofeed %>% select(., -activityFactor),
     group = datHardNofeed$activityFactor)
```

```
##
##  Box's M-test for Homogeneity of Covariance Matrices
##
## data:  datHardNofeed %>% select(., -activityFactor)
## Chi-Sq (approx.) = 9.34, df = 6, p-value = 0.16
```

Box's M returns a non-significant p-value, indicating that we cannot reject the null hypothesis. Field, Miles, and Zoe (2012) and Raykov and Marcoulides (2008) warn that Box's M is extremely sensitive, so we'd expect to find a difference if there really was one. On the other hand, Field et al. (2012) warn that the test can return a non-significant p-value when the assumption of multivariate normality is not tenable. However, given the results of the Henze-Zirkler multivariate normality test, we suspect that this is not the case.

References

Field, A., Miles, J., & Zoe, F. (2012). *Discovering Statistics Using R.* Thousand Oaks, CA: SAGE Publications Ltd.

Raykov, T., & Marcoulides, G. A. (2008). *An introduction to applied multivariate analysis.* Routledge.