

Shiny apps overview

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Chapter 1

```
#interactive content: a button to draw a sample from a population of points uniformly distributed over .  
knitr::include_app("http://82.196.4.233:3838/apps/random-variable/", height="360px")
```

```
#interactive content: three histograms: a uniformly distributed discrete population of five colors on t  
knitr::include_app("http://82.196.4.233:3838/apps/sampling-distribution/", height="620px")
```

```
#Generate a binomial probability distribution for the number of yellow candies in a random sample of te  
knitr::include_app("http://82.196.4.233:3838/apps/probability-distribution/", height="590px")
```

```
#Generate a binomial probability distribution for the number of yellow candies in a random sample of te  
knitr::include_app("http://82.196.4.233:3838/apps/expected-value/", height="420px")
```

```
# Generate a normal sampling distribution representing average candy weight in a sample bag (M = 2.8, S  
knitr::include_app("http://82.196.4.233:3838/apps/p-values/", height="260px")
```

```
#Generate a population and sample distribution of candy weight, and (in the middle) sampling distribut  
knitr::include_app("http://82.196.4.233:3838/apps/three-means/", height="560px")
```

Chapter 2

```
# Variant of app random-variable (Ch. 1).  
# Generate and display a not too small (N = 50?) representative sample from a uniformly distributed pop  
knitr::include_app("http://82.196.4.233:3838/apps/bootstrapping/", height="530px")
```

```
# variant of app sampling-distribution.  
# Draw a sample of the user-specified size (slider) from a uniformly distributed population (five candy  
knitr::include_app("http://82.196.4.233:3838/apps/bootstrap-lim/", height="560px")
```

```
# Variant of app: p-values.  
# Let a button generate a normal sampling distribution (with mean 2.8 and a random SD between 0.2 and 0
```



Take a random sample of 10

Figure 1: How many yellow candies will our sample bag contain?

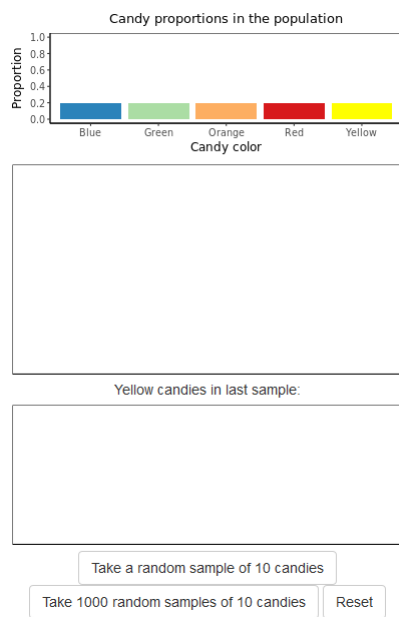


Figure 2: What is a sampling distribution?

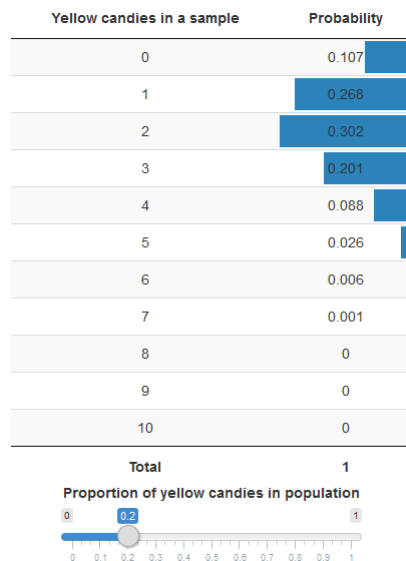


Figure 3: How does the probability of drawing a sample bag with two out of ten candies yellow depend on the proportion of yellow candies in the population?

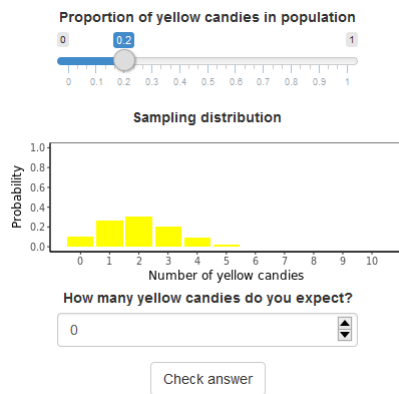


Figure 4: What is the expected value of a probability distribution?

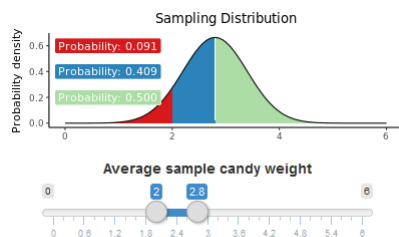


Figure 5: How do we display p values in a continuous sampling distribution?

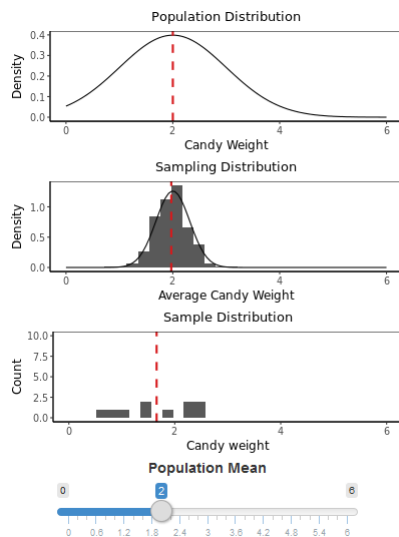


Figure 6: What is the relation between the three distributions?

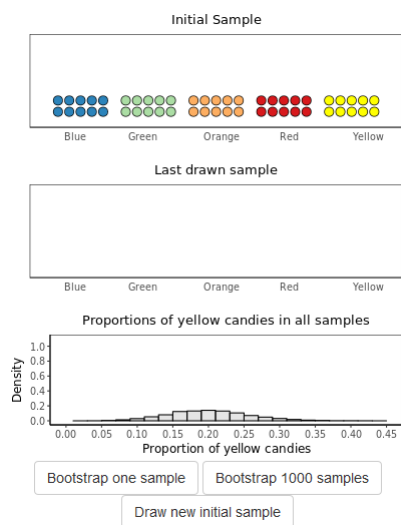


Figure 7: How do we create a sampling distribution with bootstrapping?



Figure 8: How is bootstrapping influenced by sample size?

Please draw a sample

Generate sampling distribution

Figure 9: Normal function as theoretical approximation of a sampling distribution.

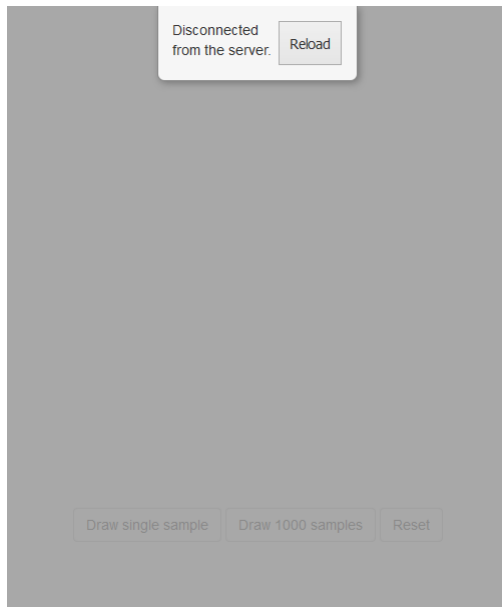


Figure 10: How do we obtain a sampling distribution for the mean difference of to independent samples?

```
knitr::include_app("http://82.196.4.233:3838/apps/normal-approximation/", height="300px")
```

```
# Demonstrate the construction of a sampling distribution of mean differences for independent samples;  
knitr::include_app("http://82.196.4.233:3838/apps/mean-independent/", height="580px")
```

Chapter 3

```
# Combination of apps interval-level, interval-size, and crit-values: A normal curve (M = 2.8, SE = 0.1)  
knitr::include_app("http://82.196.4.233:3838/apps/estimation/", height="460px")
```

```
# (as in ci-borders) Graph a normal distribution with mean 2.8 and standard deviation equal to a random  
knitr::include_app("http://82.196.4.233:3838/apps/interval-level/", height="310px")
```

```
# same as interval-level but the slider adjusts sample size (N between 5 and 100, steps of 5) ; update  
knitr::include_app("http://82.196.4.233:3838/apps/interval-size/", height="310px")
```

```
# same as interval-size but the slider adjusts the standard error (start value = 0.1, so one standard error)  
knitr::include_app("http://82.196.4.233:3838/apps/crit-values/", height="360px")
```

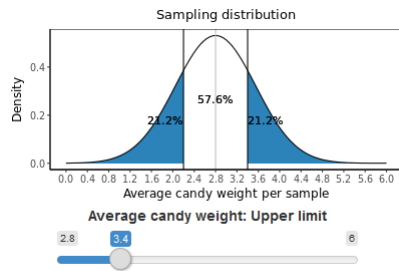


Figure 11: Within which interval do we find the sample results that are closest to the population value?

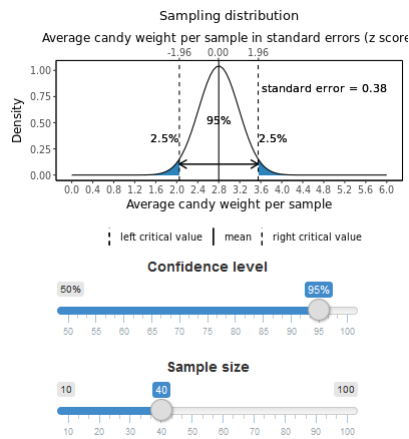


Figure 12: Point and interval estimates, confidence intervals.

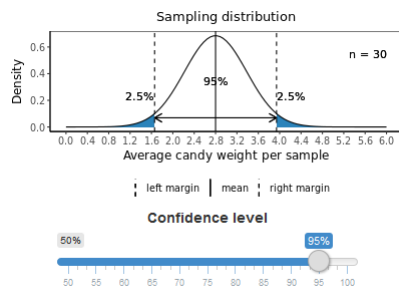


Figure 13: How does the confidence level affect the precision of an interval estimate?

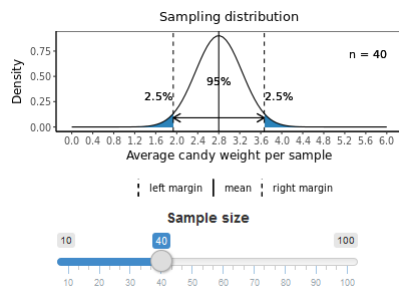


Figure 14: How does sample size affect the precision of an interval estimate?

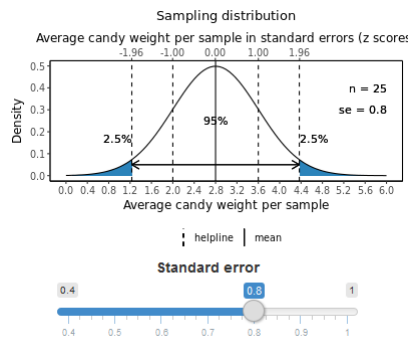


Figure 15: How do critical values relate to the standard error in a normal distribution?

Please draw a sample

Take single sample Take 100 samples Reset

Figure 16: The standard error: How wrong are point estimates?

```
# Two goals. First, remind student of the fact that a standard deviation represents deviations from the
# Use a normally distributed population with M = 2.8 and SD = 2 (candy weight) ; one button creates a r
knitr::include_app("http://82.196.4.233:3838/apps/se-point-est/", height="500px")
```

Chapter 4

```
# Compare app crit-values in Ch. 3.
# Draw a t distribution with mean 5.5, standard deviation 0.4, and degrees of freedom equal to selected
knitr::include_app("http://82.196.4.233:3838/apps/crit-df/", height="405px")
```

Chapter 5

```
#This Shiny app illustrates Type I and Type II Error. Interaction helps to understand how significance
#Source: Adapted from Tarik Gouhier, type1vs2-master, https://github.com/tgouhier/type1vs2
knitr::include_app("http://82.196.4.233:3838/apps/type1vs2/", height="735px")
```

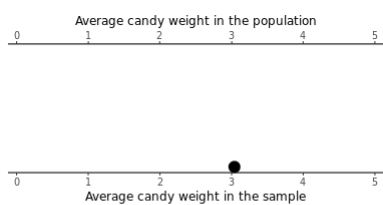


Figure 17: For which population means is our sample mean plausible?

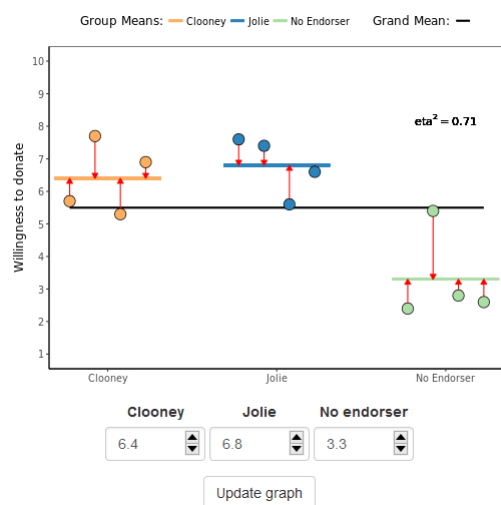


Figure 18: How do group level differences express association?

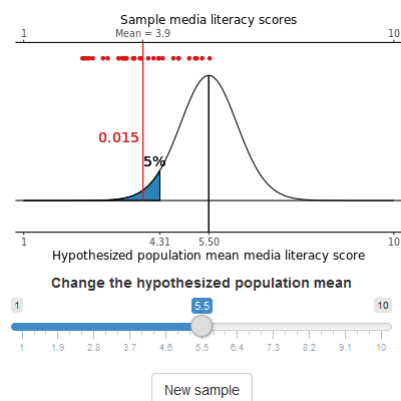


Figure 19: Sampling distribution of average media literacy.

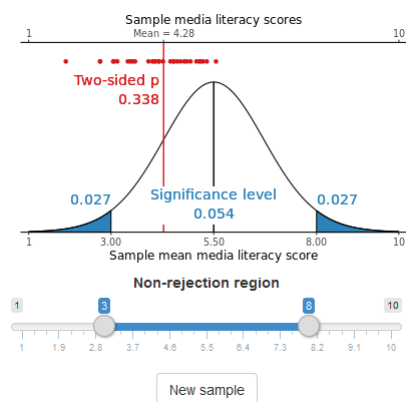


Figure 20: How do we obtain two-sided significance levels and p values?

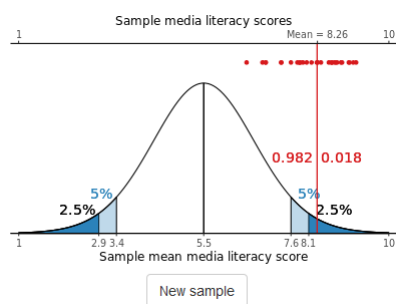


Figure 21: Is the test statistically significant?

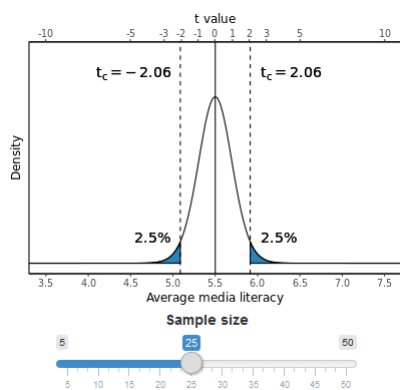


Figure 22: Sample size and critical values in a one-sample t test.

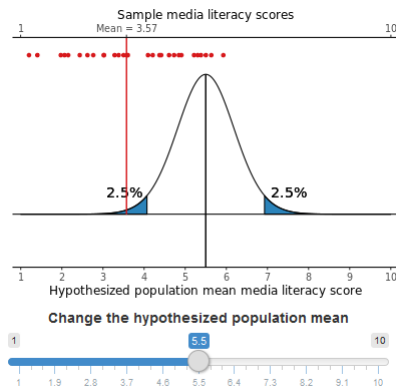


Figure 23: How does null hypothesis significance relate to confidence intervals?

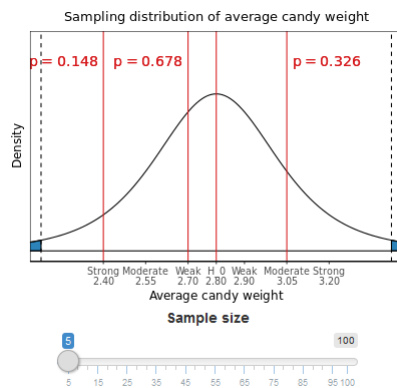
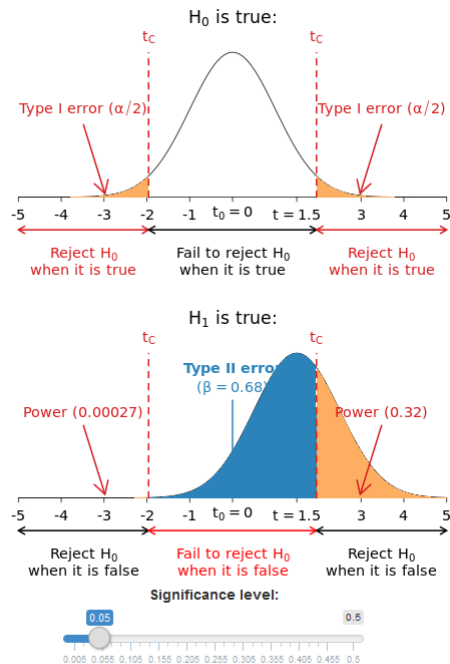


Figure 24: What is the minimum sample size required for a significant test result if the sample mean has a particular effect size?



Adapted from Tarik Gouhier, <https://github.com/tgouhier/type1vs2>

Figure 25: Simulation of Type I and Type II error.

```
#This Shiny app shows the relevance of effect size and sample size to the power of a test.
#Source: ShinyApps-spark (niet meer gevonden op GitHub)
knitr::include_app("http://82.196.4.233:3838/apps/ttest_simulation/", height=720)
```

Chapter 6

```
# (As in app tiny-effects), create a normal curve for the sampling distribution of average candy weight
knitr::include_app("http://82.196.4.233:3838/apps/sig-effect-power/", height="550px")
```

Chapter 7

```
# Goal: Illustrate that between groups variance represents differences between group means and the grand mean.
# App anova-means: Generate 4 random observations from a normally distributed population with mean 6.4,
# Extension/replacement: Add horizontal line for grand mean, vertical red solid double-sided arcs between group means and grand mean.
knitr::include_app("http://82.196.4.233:3838/apps/anova-between/", height="530px")
```

```
# Goals: Recognize effect size and statistical significance of interaction effects.
# Exactly the same app as anova-moderation but now add Eta^2 and the F value plus p value of the interaction.
# Initial means.
# d <- data.frame(endorser = factor(c("Nobody", "Clooney", "Jolie", "Nobody", "Clooney", "Jolie"), levels = c("Nobody", "Clooney", "Jolie")),
knitr::include_app("http://82.196.4.233:3838/apps/anova-interaction/", height="650px")
```

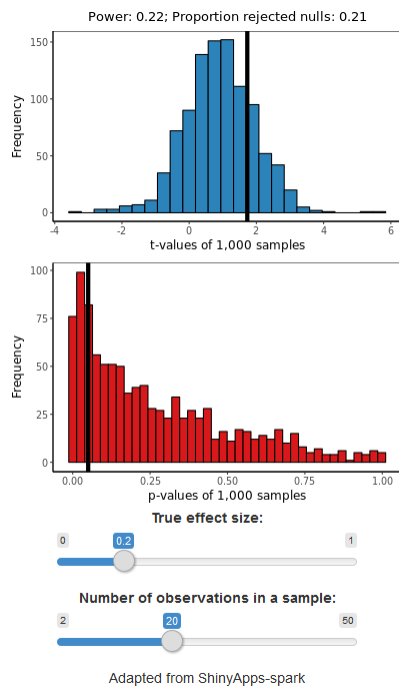


Figure 26: The relevance of effect size and sample size to test power for a right-sided test on one sample mean ($\alpha = 0.05$).

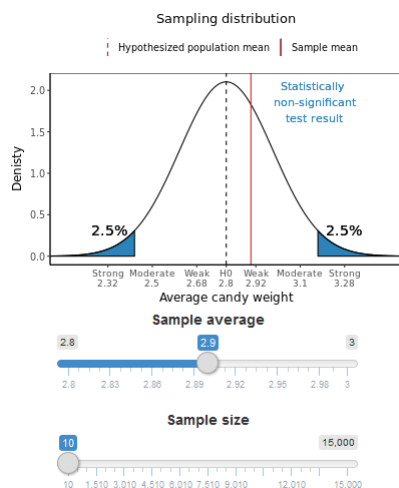


Figure 27: Any effect can be statistically significant.

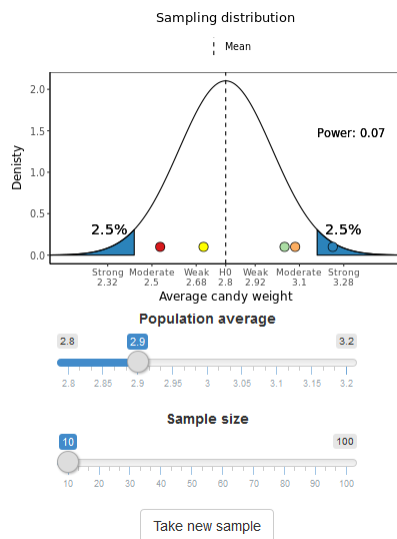


Figure 28: The relations between significance, effect size, sample size, and power.

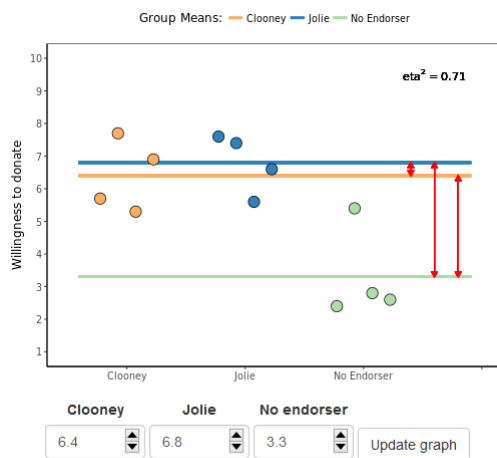


Figure 29: How do group means relate to effect size?

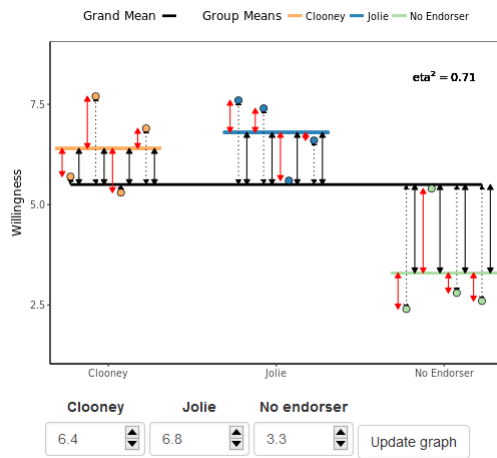


Figure 30: Which part of score differences tell us about the differences between groups?

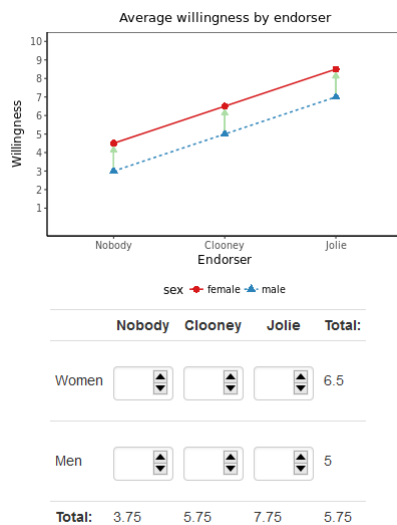


Figure 31: How can we recognize main effects and moderation in a means plot?

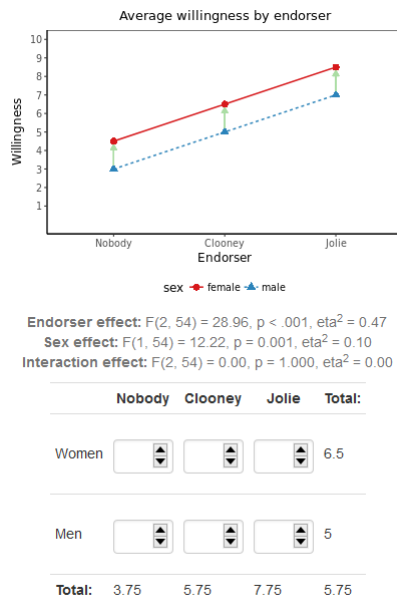


Figure 32: How can we recognize main effects and moderation in a means plot?

Chapter 8

```
# Goal: Understand the relation between linear model (scatterplot) and residuals plot by manipulating t
# Generate a sample (N = 20?) with a weak negative effect (-0.6) of exposure on attitude, with a sizabl
knitr::include_app("http://82.196.4.233:3838/apps/pred-linearity/", height="550px")
```

```
# Goal: Understand the relation between linear model (scatterplot) and residuals plot by manipulating h
# Generate a sample (N = 20) with a weak negative effect (-0.6) of exposure on attitude and exposure, w
knitr::include_app("http://82.196.4.233:3838/apps/pred-homoscedasticity/", height="550px")
```

```
# Use app continuous-moderator.
knitr::include_app("http://82.196.4.233:3838/apps/continuous-moderator/", height="550px")
```

```
# Goal: Understand that there is a conditional effect for each value of the moderator by gradually chan
# Generate a data set with a linear interaction (attitude ~ exposure*contact). Display a scattergram wi
# # Number of observations.
# n <- 85
# # Create predictor.
# set.seed(4932)
# exposure <- runif(n)*10
# # Create moderator.
# set.seed(4321)
# contact <- 0.12*(10 - exposure) + rnorm(n, mean = 4.5, sd = 2)
# # Create outcome.
# set.seed(390)
# attitude <- -0.26*exposure + 0.15*contact + 0.04*exposure*contact + rnorm(n, mean = 2, sd = 0.5)
```

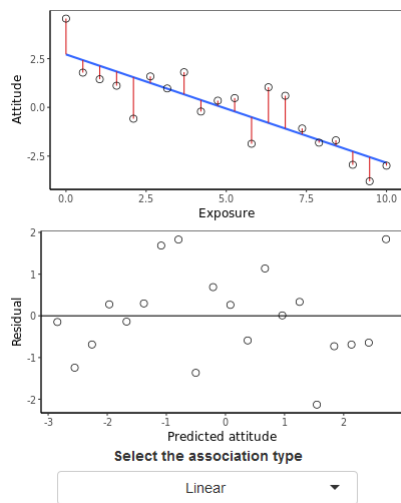


Figure 33: How do residuals tell us whether the relation is linear?

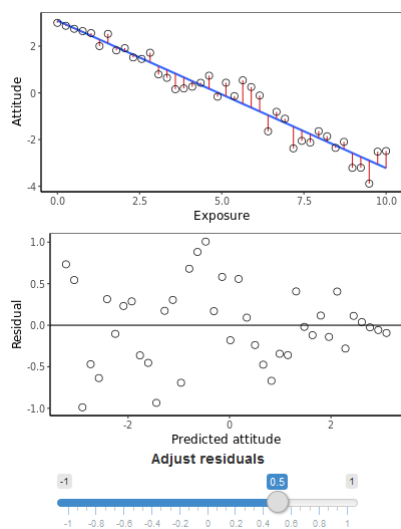


Figure 34: How do residuals tell us that we predict all values equally well?

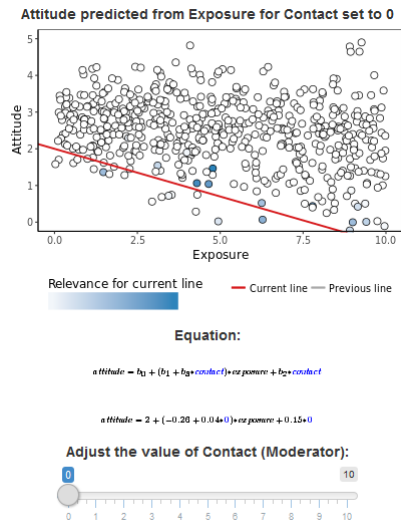


Figure 35: How do contact values affect the conditional effect of exposure on attitude?

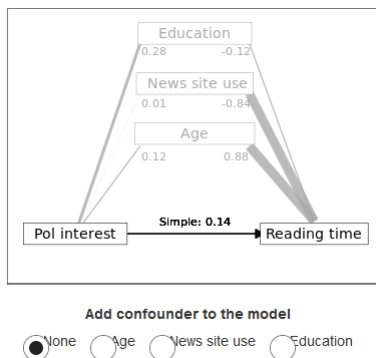


Figure 36: What happens to the regression coefficient if we add a confounder to the model? Numbers represent correlations (lines) or regression coefficients (arc).

Chapter 9

```
# Goal: Show that a regression coefficient changes more if the new predictor is more strongly correlate
# Display the simple (standardized) regression coefficient as a black arc from Pol.Interest to Reading
# Correlations and standardized coefficients that are in line with the example data file readers.sav:
# Pol. Interest - Age: 0.12
# Pol. Interest - Educ: 0.28
# Pol. Interest - News: 0.01
# Reading Time - Age: 0.88
# Reading Time - Educ: -0.12
# Reading Time - News: -0.84
# Pol. Interest -> Reading Time (simple): 0.14
# Pol. Interest -> Reading Time with Age: 0.04
# Pol. Interest -> Reading Time with Educ: 0.19
# Pol. Interest -> Reading Time with News: 0.15
knitr::include_app("http://82.196.4.233:3838/apps/mediation-indirectcorrelation/", height="370px")
```

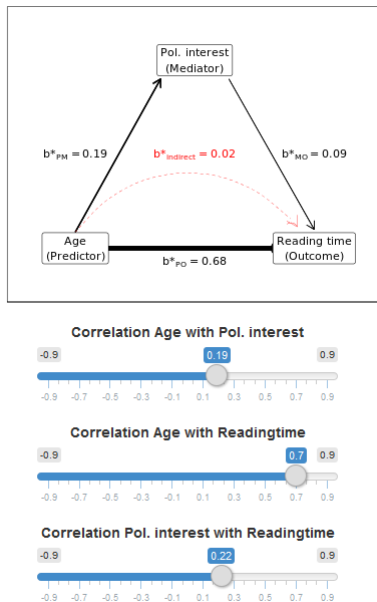


Figure 37: How does a common cause affect regression coefficients? The values in this path diagram represent standardized regression coefficients.

Goal: Sensitize students to the concept of a common cause creating a spurious effect and mediation as
 # Display causal diagram of age (predictor), political interest (mediator), and newspaper reading time
 knitr::include_app("http://82.196.4.233:3838/apps/mediation-commoncause/", height="625px")

```
# # Initial correlations.
# #correlation between Predictor and mediator.
# r_PM <- round(runif(n = 1, min = -.7, max = .7), digits = 2)
# #correlation between mediator and Outcome.
# r_MO <- round(runif(n = 1, min = -.7, max = .7), digits = 2)
# #correlation between Predictor and Outcome.
# r_PO <- round(runif(n = 1, min = -.7, max = .7), digits = 2)
# # Partial standardized regression coefficients.
# b_PM <- r_PM
# b_PO <- r_PO
# b_MO <- round((r_MO - r_PM*r_PO)/(1 - r_PM^2), digits = 2)
# b_indirect <- round(b_PM * b_MO, digits = 2)
```