Meta-analysis for psychology researchers: A practical application of basic and advanced meta-analytic procedures

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Outline

1 Intro to `R` & `MA*` packages

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1. Intro to `R` & `MA*` packages
2. Introduction

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2. Introduction
3. Meta-analytic steps

What is R?

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- Program of choice for many statisticians around the world.
- Command line interface (although GUI options for menu-driven data analysis).
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Working with R

- R is command-driven (i.e., not "point-and-click").
- It is object-oriented (e.g., create and manipulates objects with commands).
- It can be used interactively by typing commands or by loading code scripts.
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- There are also numerous books on R.
- A *very* brief introduction will be provided today and then we will demonstrate computations for and conduct analyses relevant to meta-analytic research.

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Demonstrate command line

- At its most basic, R is a calculator

```
> 2 + 2
```

```
[1] 4
```

- It's object-oriented

```
> x <- 2
> x + x
```

```
[1] 4
```

```
> x*x + 1
```

```
[1] 5
```

- Can work with vectors

```
> mydata <- c(5, 4, 3, 2, 1)  # c is for concatenate
> mydata/2
```

```
[1] 2.5 2.0 1.5 1.0 0.5
```

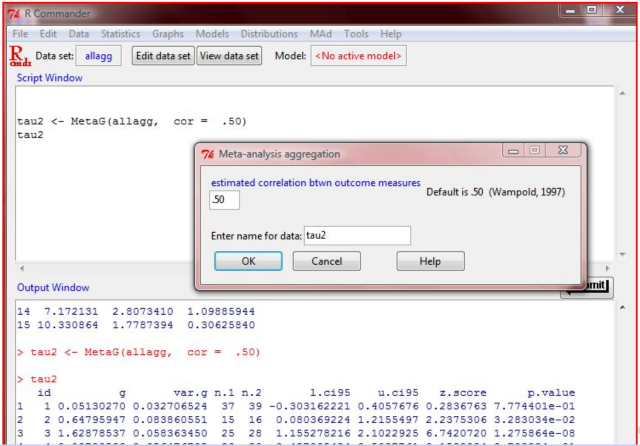
```
>
```

R practice!

- Go to DataCamp's free into to R course at https://www.datacamp.com/courses/free-introduction-to-r
- Take about 30-minutes and complete lesson one "Intro to Basics"

GUI

- Pic of R GUI (similar to menu-driven "point-and-click" SPSS program) for meta-analysis.



```
tau2 <- MetaG(allagg,  cor =  .50)
tau2
```

estimated correlation btwn outcome measures: .50

Default is .50 (Wampold, 1997)

Enter name for data: tau2

```
14  7.172131  2.8073410  1.09885944
15 10.330864  1.7787394  0.30625840

> tau2 <- MetaG(allagg,  cor =  .50)

> tau2
   id          g       var.g n.1 n.2        l.ci95    u.ci95   z.score      p.value
1   1 0.05130270 0.032706524  37  39 -0.303162221 0.4057676 0.2836763 7.774401e-01
2   2 0.64795947 0.083860551  15  16  0.080369224 1.2155497 2.2375306 3.283034e-02
3   3 1.62878537 0.058363450  25  28  1.155278216 2.1022925 6.7420720 1.275864e-08
```

GUI

- We will work with both the command line and GUI today.
- R code was provided (via email) for conducting analyses at the command line.
- For more information on the GUI or MA* packages:

  http://CRAN.R-project.org/package=MAd

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How do we draw conclusions from research findings?[1]

- Often with p-values (e.g., "likelihood of seeing a pattern of results this strong, if there were really nothing happening").
  - Single studies
    - $p < .05$?
  - Narrative reviews (discusses and summarises the literature on a particular topic, without generating any pooled summary values)
    - Why are some $ps < .05$ and others $>$?

- Quantitative research synthesis (meta-analysis)
  - "The statistical analysis of a large collection of analysis results from individual studies for the purpose of integrating the findings" (Glass, 1976; p. 3).
  - Focus on study effect sizes (ES)
  - It provides a quantitative summary of a body of research literature.

---

[1] Note: Many slides in this section are adapted from Dr William T. Hoyt's meta-analysis course at UW-Madison.

How do we draw conclusions from research findings?

Table 1: `Summary of procedures`

Research Context	**Basis for Conclusion**	**Explanation for BSDs**	**Conclusion**
Single Study	NHST ($p < .05$)	NA	IV → DV (or not)
N-Review	NHST ($p < .05$)	BSDs reveal boundary conditions for effect	IV → DV in some conditions, not in others
Q-Review	ES and CI	BSDs largely attributable to sampling error and different Ns	Quantifies str. of association (IV → DV) and may examine moderators

Note: NHST = null hypothesis significance testing; BSDs = between-study differences; ES = effect size; CI = confidence interval.

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   - Graphics

Example: Schmidt (1992) Table 1

Table 2: `21 validity studies (`$N = 68$` each)`

Study	$\hat{\rho}$	**Study**	$\hat{\rho}$	**Study**	$\hat{\rho}$
1	.04	8	.36*	15	.14
2	.14	9	.20	16	.29*
3	.31*	10	.02	17	.26*
4	.12	11	.23	18	.17
5	.38*	12	.11	19	.39*
6	.27*	13	.21	20	.22
7	.15	14	.37*	21	.21

Note: $\hat{\rho} = r =$ correlation coefficient; * $= p < .05$.

Narrative review (same 21 studies)

Table 3: `21 validity studies (`$N = 68$` each)`

Study	Concl	Study	Concl	Study	Concl
1	ns	8	*	15	ns
2	ns	9	ns	16	*
3	*	10	ns	17	*
4	ns	11	ns	18	ns
5	*	12	ns	19	*
6	*	13	ns	20	ns
7	ns	14	*	21	ns

Note: ns= not significant; * $= p < .05$.

Quantitative review (same 21 studies)

Table 4: `21 validity studies (`$N = 68$` each)`

Study	$\hat{\rho}[\sigma_{\hat{\rho}}]$	**Study**	$\hat{\rho}[\sigma_{\hat{\rho}}]$	**Study**	$\hat{\rho}[\sigma_{\hat{\rho}}]$
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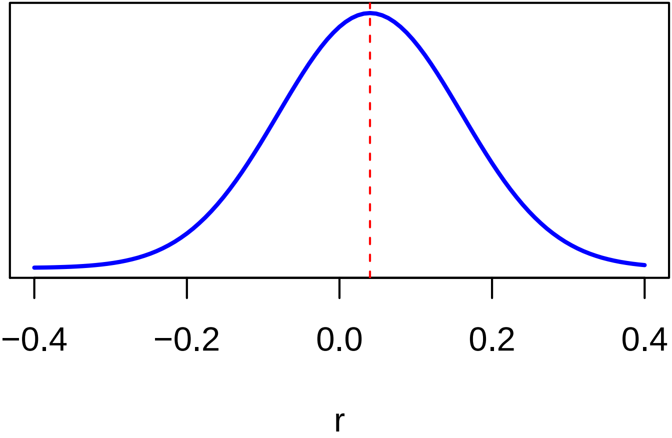
3	.31 [.11]	10	.02 [.12]	17	.26 [.11]
4	.12 [.12]	11	.23 [.12]	18	.17 [.12]
5	.38 [.10]	12	.11 [.12]	19	.39 [.10]
6	.27 [.11]	13	.21 [.12]	20	.22 [.12]
7	.15 [.12]	14	.37 [.11]	21	.21 [.12]

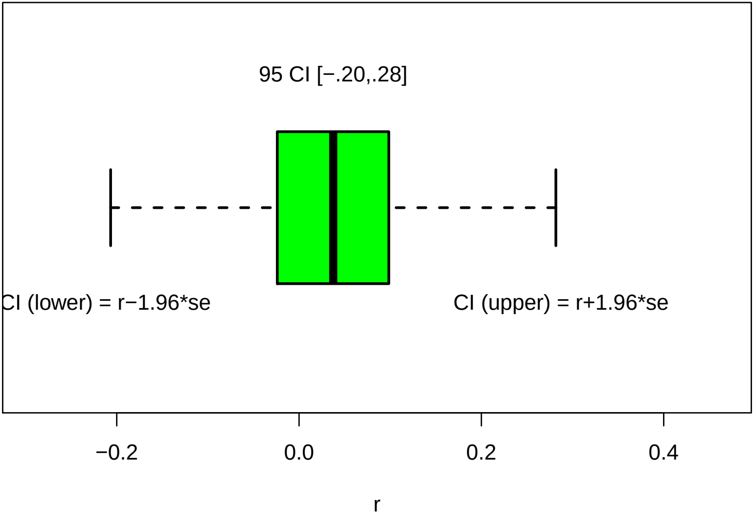
Note: $\hat{\rho} = r =$ correlation coefficient; $\sigma_{\hat{\rho}} =$ standard error for r which is computed as $\hat{\sigma}_i \sim \sqrt{(1 - \hat{\rho}_i^2)^2/(N_i - 1)}$.

What is the $\sigma_{\hat{\rho}}$ (standard error or SE)?

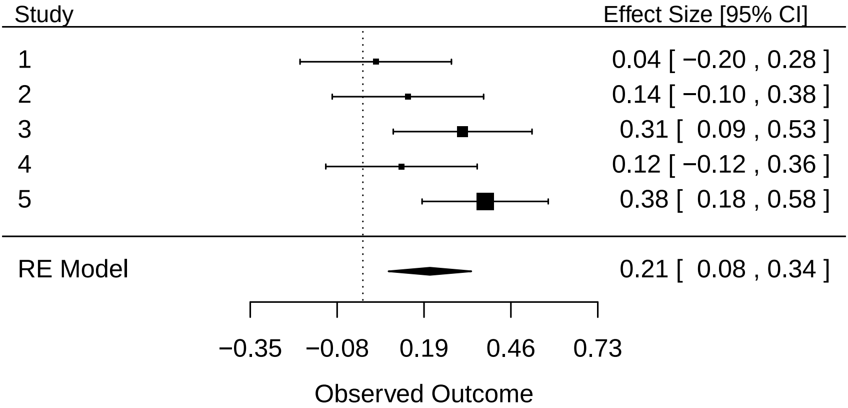
Expected sampling distribution ($\hat{\rho} = .04, \sigma_{\hat{\rho}} = .12, N = 68$)



Using $\sigma_{\hat{\rho}}$ (SE) to compute 95% CI



95% CI, first 5 studies (Schmidt, 1992)



Summary of approaches

- Narrative reviews and quantitative reviews differ in what between-study differences (BSDs) they attend to.

- Narrative reviews focus on BSDs in results of statistical significance tests ($p < .05$).

- Quantitative reviews focus on BSDs in the estimate of the population effect size (e.g., $\hat{\rho}$), and in the precision of these estimates (which is mostly a function of N).

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Advantages claimed for narrative reviews

- Able to give greater attention to high quality studies.
- Sensitive to ancillary findings, idiosyncracies in research design, other measures included.
- Ideal for telling nuanced story, taking all relevant findings into account

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- Looking at the wrong results (p versus effect size).
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- Statistically defensible summary of findings.
- Tests whether BSDs are greater than expected due to sampling error, before looking for moderators of the IV→DV relation
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- An effect size (ES) is a quantitative index of the strength of association between IV and DV.

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Intro to effect sizes

- An effect size (ES) is a quantitative index of the strength of association between IV and DV.
- The ES is the basic summary of a study's findings, and is the unit of analysis for the meta-analysis.
- Choice of ES for a meta-analysis depends on the research question (see Cooper et al., 2009[2])

---

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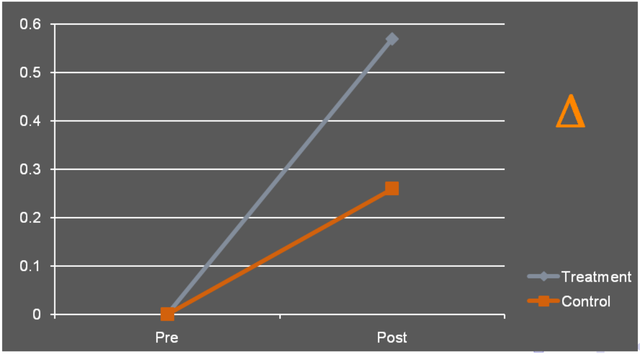
Research Qs, choice of ES

IV	**DV**	**Stats**	**ES**
Continuous	Continuous	MR/C	$\hat{\rho}$
Dichotomous	Continuous	ANOVA	$\hat{\delta}$
Dichotomous	Dichotomous	χ^2	Odds Ratio

Note: IV = independent variable (predictor or explanatory variable); DV = dependent variable (criterion, response, or outcome variable); ES = effect size; $\hat{\rho} = r =$ correlation coefficient; $\chi^2 =$ chi-squared statistic; $\hat{\delta} = d =$ mean difference.

ES for group comparisons: Cohen's δ

- Our focus today is on the standardized mean difference (δ) and Δ.



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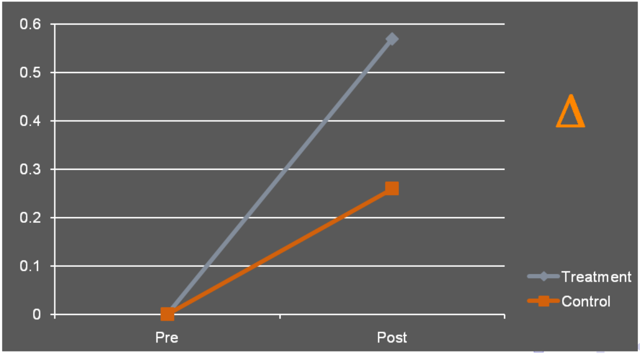

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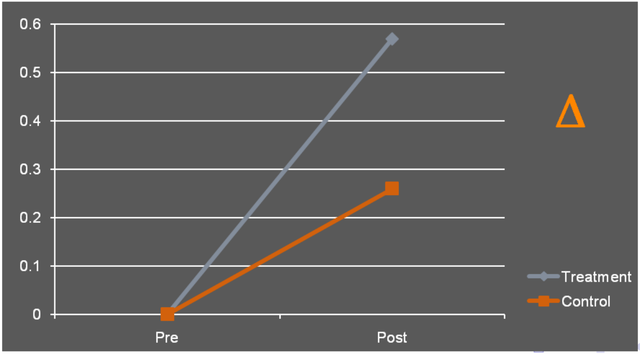

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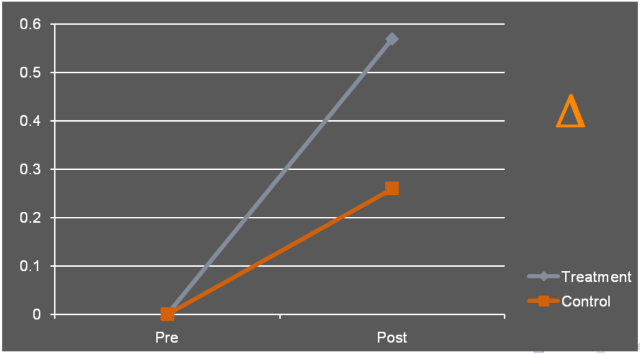
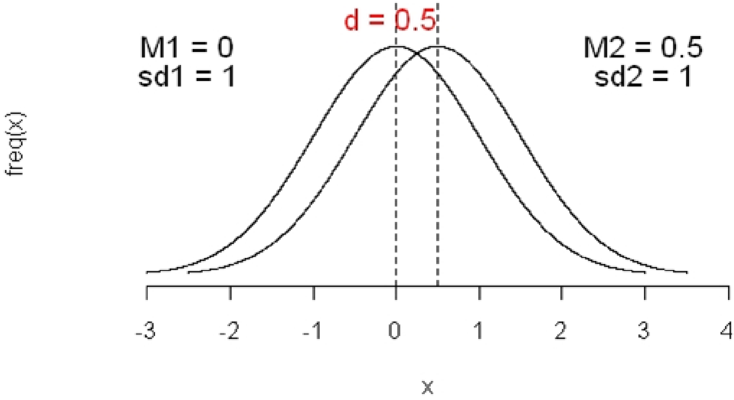
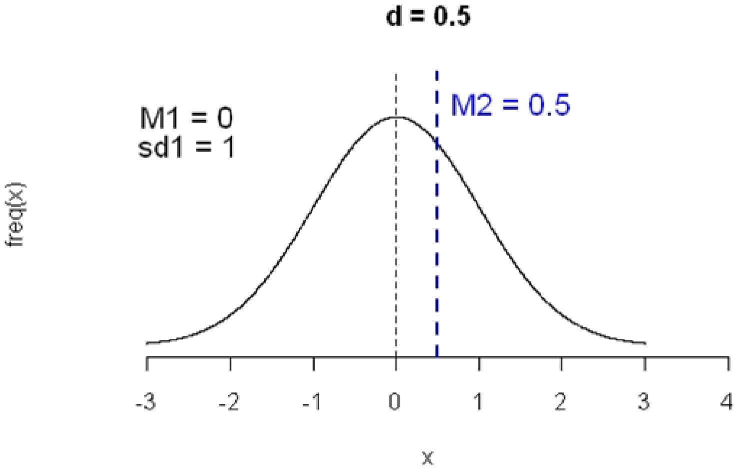
- How can we quantify the amount of improvement for the treatment group?
- Difference between two groups (e.g., treatment and control) and/or post and pre scores.
- Standardize, so that improvement can be compared across studies.




d = 0.5
M1 = 0
sd1 = 1
M2 = 0.5
sd2 = 1
freq(x)
-3
-2
-1
0
1
2
3
4
x

Interpreting δ



Interpreting δ

- Improvement in Tx group above what is observed in the absence of treatment.
- Cohen's (1988) rule of thumb (in the behavioral sciences):

$\delta = 0.2$ represents a small effect;
$\delta = 0.5$ represents a medium effect;
$\delta = 0.8$ represents a large effect.

▸ forward to es

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Null hypothesis significance tests (NHST)[3]

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Null hypothesis significance tests (NHST)[3]

- The goal of NHST is to avoid Type I errors (which is a worthy goal!).

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Null hypothesis significance tests (NHST)[3]

- The goal of NHST is to avoid Type I errors (which is a worthy goal!).
- Criticisms of NHST revolve around:
  - The optimal methods for achieving this goal
  - The relative importance of this goal, compared to other desirable goals (such as avoiding Type II errors)
  - The reporting conventions that have evolved to support this goal, but may obscure important information about study findings.

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- If $p > .05$, fail to reject H_0.

Possible Outcomes in NHST

Sample (observed) d	**Population (true)** δ	**Population (true)** δ
	$\delta = 0$	$\delta \neq 0$
Not significantly diff. from 0	Correctly fail to reject H_0	Incorrectly fail to reject H_0 **(Type II error)**
significantly diff. from 0	Incorrectly reject H_0 **(Type I error)**	Correctly reject H_0

Schmidt (1992) on sampling theory

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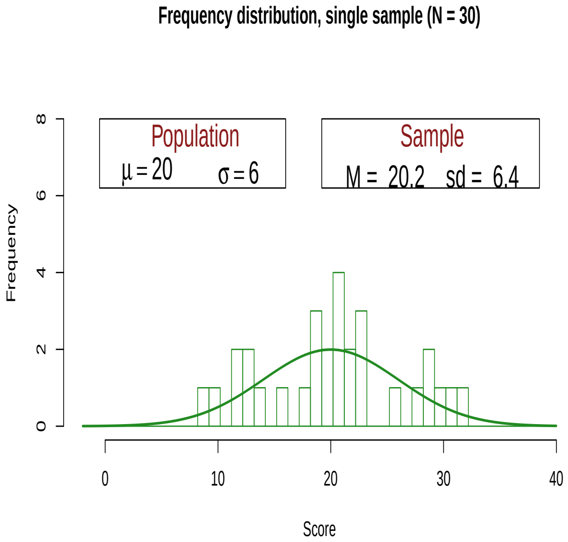
- Sampling distribution of d, under H_1
- If $p > .05$, fail to reject H_0.

Schmidt (1992) on sampling theory

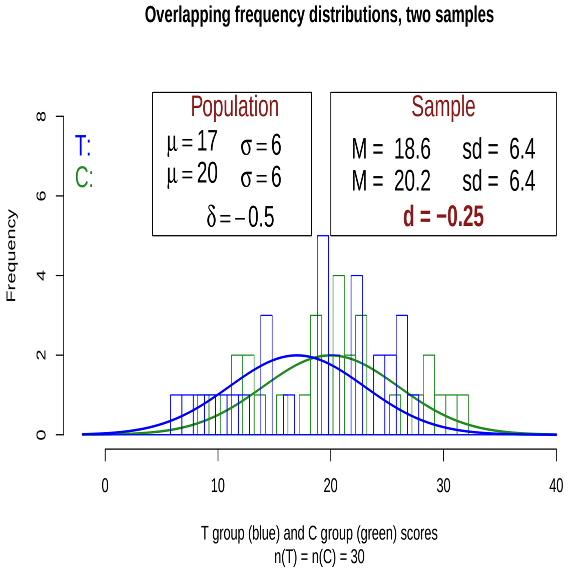
How to think about sampling error for studies of group differences:

- Sampling error for each group (M, sd).
- Sampling error is compounded when taking difference of independent variables
- Sampling distribution of d, under H_0
- Sampling distribution of d, under H_1
- If $p > .05$, fail to reject H_0.
- Type I and Type II errors under NHST.

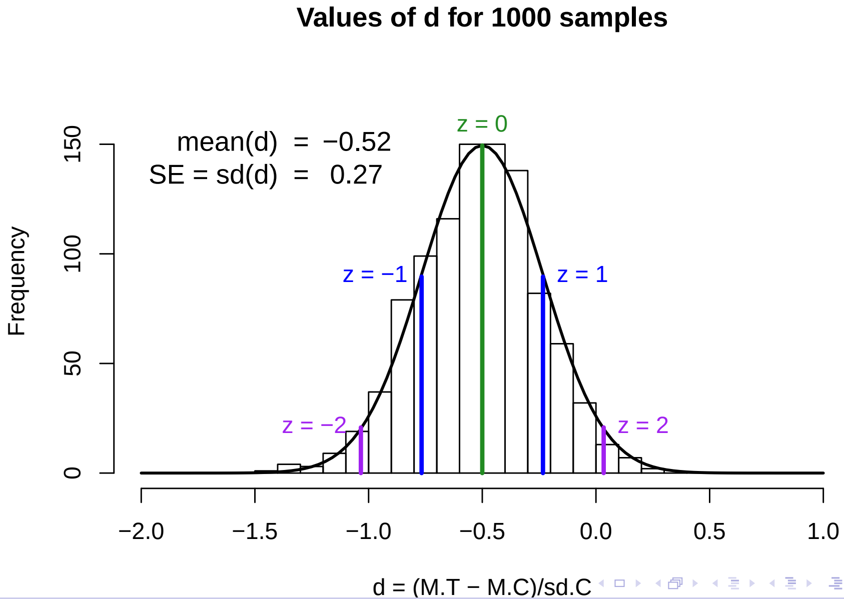
Sampling error for one group (M, sd)



Composite variables (e.g. d) compound sampling error



Sampling distribution of d (actual)



Sampling theory and NHST

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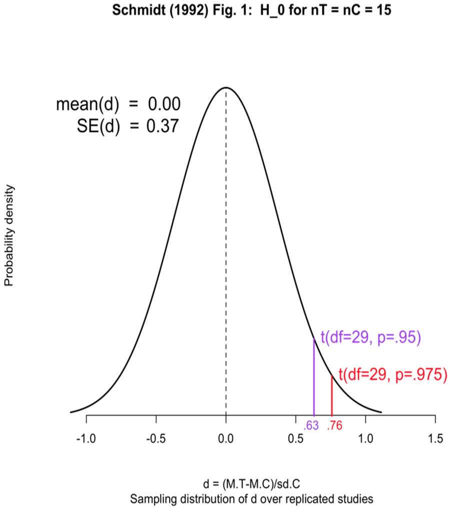
- Remember, in NHST, we assume that H_0 is true unless the evidence strongly suggests otherwise.

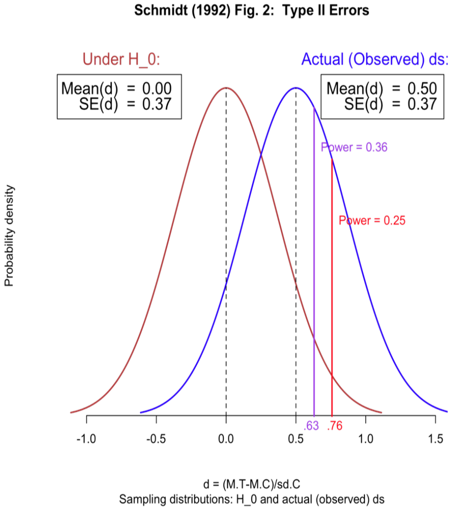
Sampling theory and NHST

- Remember, in NHST, we assume that H_0 is true unless the evidence strongly suggests otherwise.
- We use sample values to derive $\delta_{\hat{\sigma}}$, and evaluate the observed δ relative to the hypothetical sampling distribution under H_0.

Sampling distribution of d, under H_0 $(N_T = N_C = 15)$



Comparing sampling distributions under H_0 and H_1



Schmidt's (1992) conclusions

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- In most research areas, we are over-protecting against Type I errors.
- We act as though Type II errors (which are often the errors of greatest concern) are of no consequence.
- We adopt reporting conventions (dichotomous decisions, no specific p values or effect sizes) that obscure findings and make it difficult to summarize accurately what is known.

Overview of meta-analytic steps

- Initial stages (define theoretical relationship of interest, etc)

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- Display results graphically.
- All of these steps can be completed with the `MA*` meta-analysis packages in the `R` statistical software program (well, except the first! :).

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- Although all data can be entered directly into `R`, it is typically easier to use a spreadsheet interface program for data entry.

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- For mean differences meta-analyses, make sure to have columns:
  - study id
  - post-test mean for treatment group
  - treatment sample size
  - treatment standard deviation
  - post-test mean for control/comparison group
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  - control/comparison standard deviation
  - moderators

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  - treatment sample size
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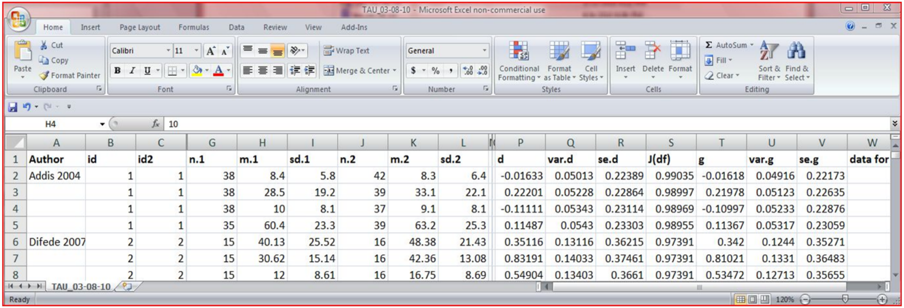
  - moderators

- Alternatively, columns for:
  - d and/or g (standardized mean difference)
  - variance of standardized mean difference
  - treatment sample size
  - control/comparison sample size

Prepare data for analyses

Visual of spreadsheat setup



	A	B	C	G	H	I	J	K	L	P	Q	R	S	T	U	V	W
1	**Author**	**id**	**id2**	**n.1**	**m.1**	**sd.1**	**n.2**	**m.2**	**sd.2**	**d**	**var.d**	**se.d**	**J(df)**	**g**	**var.g**	**se.g**	**data for**
2	Addis 2004	1	1	38	8.4	5.8	42	8.3	6.4	-0.01633	0.05013	0.22389	0.99035	-0.01618	0.04916	0.22173	
3		1	1	38	28.5	19.2	39	33.1	22.1	0.22201	0.05228	0.22864	0.98997	0.21978	0.05123	0.22635	
4		1	1	38	10	8.1	37	9.1	8.1	-0.11111	0.05343	0.23114	0.98969	-0.10997	0.05233	0.22876	
5		1	1	35	60.4	23.3	39	63.2	25.3	0.11487	0.0543	0.23303	0.98955	0.11367	0.05317	0.23059	
6	Difede 2007	2	2	15	40.13	25.52	16	48.38	21.43	0.35116	0.13116	0.36215	0.97391	0.342	0.1244	0.35271	
7		2	2	15	30.62	15.14	16	42.36	13.08	0.83191	0.14033	0.37461	0.97391	0.81021	0.1331	0.36483	
8		2	2	15	12	8.61	16	16.75	8.69	0.54904	0.13403	0.3661	0.97391	0.53472	0.12713	0.35655	

Importing data files

- Save main data file (spreadsheet) to a **.csv** file.

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- In `R`, set the working directory to the location of your **.csv** data file :
  - `R` menu: File → Change Dir → (location of **.csv** file)
- Use command to import the data:

  ```
  mydata <- read.csv('MetaData.csv', header=TRUE,
  na.strings= "")
  ```

  Where `mydata` is the name of the "object" the data file will be saved in and `MetaData.csv` = name of .csv file (you should change these names accordingly)

Example data from recent meta-analysis with δ

- Ideal to save seperate .csv files for ES and moderator data

```
> options(width = 60)
> # set working directory to location of .csv file
> #setwd()
>
> # import ES data
> grief <- read.csv('grief.csv', header=TRUE, sep=",", na.stri
> names(grief)

[1] "id"      "del"     "var.del" "n.1"     "n.2"
```

Example data from recent meta-analysis with δ

- Moderator data:

```
> options(width = 60)
> # import moderator data
> grief_mods <- read.csv('grief_mods.csv',
+ header=TRUE, na.strings= "")
> names(grief_mods)
```

```
[1] "id"      "risk"    "female" "n.sess"
```

Example data from recent meta-analysis with δ[4]

- This data is from a bereavement treatment meta-analysis recently submitted to Psych Bulletin.

◂ forward [grief omni]

---

[4] This slide adapted from Dr Dale Larson's presentation at ADEC, Miami, FL 2011.

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- A pessimistic view of grief treatment, and with it bereavement services in general, has emerged over the past 11 years.

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- This data is from a bereavement treatment meta-analysis recently submitted to Psych Bulletin.
- A pessimistic view of grief treatment, and with it bereavement services in general, has emerged over the past 11 years.
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Example data from recent meta-analysis with δ[4]

- This data is from a bereavement treatment meta-analysis recently submitted to Psych Bulletin.
- A pessimistic view of grief treatment, and with it bereavement services in general, has emerged over the past 11 years.
- Claims: often harmful, ineffective, only effective for the severely bereaved, no sustained gains over time.
- Grief treatment for normal bereavement classified as a "probably harmful treatment" by Lilienfeld (2007).

◂ forward [grief omni]

---

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- Recent meta-analysis by Currier et al (2008) further confirmed pessimistic views. They found:
    - Weak omnibus effect size.
    - Higher effect size only for clients assessed as severely bereaved.
    - Follow-up effect sizes homogeneous and not significantly different from zero.
    - Conclusion: grief treatment is not efficacious.

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- We conducted an updated meta-analysis with different criteria than Currier et al (2008).
    - Tighter definition of grief counseling.
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    - Unbiased inclusion of uncontrolled studies.
    - Post- and follow-up effect sizes computed from same subset of studies.

Example data from recent meta-analysis with δ

- We will return to this example later when conducting the omnibus analysis

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- To load the packages:

  `library(MAd)`

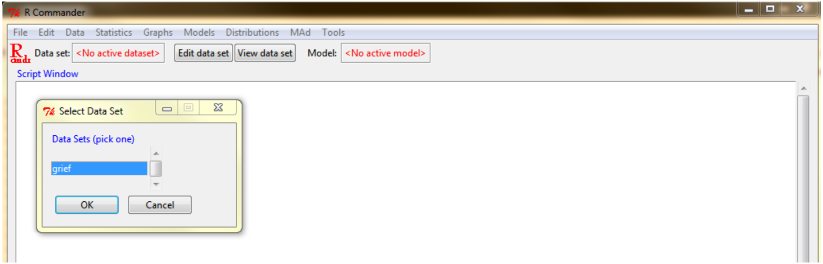
  - and/or:

  `library(RcmdrPlugin.MAd)`

MAd GUI

```
> # set working directory to location of .csv file
> library(RcmdrPlugin.MAd)
```

Then, load the data.frame that was just uploaded into current R session:



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Research Qs, choice of ES

ES	Preferred	Alternative
ρ	r	b or β and sd_β
δ	group n, M, sd	t or F and n
OR	cell frequencies or proportions	logistic regression b

Note: ES = effect size; ρ = population correlation coefficient; δ = population mean difference; OR = odds ratio; b = unstandardized beta coefficient; β = standardized beta coefficient; t = t-test; F = F-test.

▸ Interpreting δ

ES for group comparisons: Cohen's δ

- Standardized mean difference (δ):

$$\hat{\delta} = \frac{\bar{X}_1 - \bar{X}_2}{S_{within}}$$

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$$S_{within} = \sqrt{\frac{(n_1-1)S_1^2 + (n_2-1)S_2^2}{n_1+n_2-2}}$$

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- Variance of d:

$$\sigma_{\delta}^2 = V_d = \frac{n_1 + n_2}{n_1 n_2} + \frac{\hat{\delta}^2}{2(n_1 + n_2)}$$

Correct for bias in δ

- Correction factor J:

$$J = 1 - \frac{3}{4df - 1}$$

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- Variance of g:

$$V_g = J^2 V_d$$

- Standard error of g:

$$SE_g = \sqrt{V_g}$$

Working at the R command line

- Sample data to compute $\hat{\delta}$ and $\sigma^2_{\hat{\delta}}$

```
> # to fit code on screen
> options(width = 60)
> # Sample data (for computing d & g)
> n.1 <- 16
> m.1 <- 9.6
> sd.1 <- 4.82
> n.2 <- 13
> m.2 <- 12.3
> sd.2 <- 6.79
>
>
```

Working at the R command line

- Compute s_{within}

```
> options(width = 60)
> # various ways to calculate effect sizes
>
> # starting with standardized mean differences (Cohens d)
>
> # one way is to calc "by hand" (Formula 12.12)
> # s.within = pooled standard deviation of group 1 and 2
> s.within <- sqrt(((16-1)*4.82^2+(13-1)*6.79^2)/(16+13-2))
> s.within

[1] 5.779066

> # or similarly, using objects already created (also Formu
> s.within <- sqrt(((n.1-1)*sd.1^2+(n.2-1)*sd.2^2)/(n.1+n.
> s.within

[1] 5.779066

> # For complex formulas, you may use several steps:
```

Working at the R command line

- Compute δ & $\sigma^2_{\hat{\delta}}$

```
> options(width = 60)
> # std mean difference (control group st. dev)
> d <-(m.1-m.2)/sd.2
> d

[1] -0.3976436

> # std mean difference (pooled)
> d <-(m.1-m.2)/s.within    # (Formula 12.11)
> d

[1] -0.4672036

> # variance of d
> var.d <-(n.1+n.2)/(n.1*n.2)+ (d^2)/(2*(n.1+n.2))     # (
> var.d

[1] 0.1431865
```

Working at the R command line

- Compute g & $\sigma^2_{\hat{g}}$

```
> options(width = 60)
> # used to calculate j
> df <- (n.1+n.2)-2
> df

[1] 27

> # correction factor to biased d
> j<-1-(3/(4*df-1))                                        # (
> j

[1] 0.9719626

> # unbiased std mean difference (Hedges g)
> g <- j*d                                                 # (
> g

[1] -0.4541044
```

Working at the R command line

- Custom functions

```
> options(width = 60)
> # Another option:  Write a function to automate this proc
> # output all values simultaneously
>
> # sample function to demonstrate the mechanics of definin
> # and using functions.
>
> my.mean <- function(x) {
+   mean <- sum(x)/length(x)
+   return(mean)
+ }
> data <- 0:20
> my.mean(x=data)      # or just my.mean(data)

[1] 10
```

Working at the R command line

- Custom function for computing $\hat{\delta}$

```
> options(width = 60)
> # starting with mean differences
> mean_to_d <- function(n1, m1, sd1, n2, m2, sd2) {
+   s.within <- sqrt(((n1-1)*sd1^2+(n2-1)*sd2^2)/(n1+n2-2))
+   d <- (m1-m2)/s.within
+   var.d <- (n1+n2)/(n1*n2) + (d^2)/(2*(n1+n2))
+   df <- (n1+n2)-2
+   j <- 1-(3/(4*df-1))
+   g <- j*d
+   var.g <- j^2*var.d
+   out <- cbind(s.within, d, var.d, df, j , g, var.g)
+   return(out)
+ }
> mean_to_d(n.1,m.1, sd.1, n.2, m.2, sd.2)
```

```
     s.within          d     var.d df         j          g
[1,] 5.779066 -0.4672036 0.1431865 27 0.9719626 -0.4541044
         var.g
[1,] 0.1352699
```

Working at the R command line

- Vectorized capabilities for computing $\hat{\delta}$

```
> options(width = 60)
> # sample data of 20 studies
> id <- c(1,1,1,2,2:20)
> n.1 <- c(10,10,10,20,20,13,22,28,12,12,36,19,12,
+ 36,75,33,121,37,14,40,16,14,20)
> n.2 <- c(11,11,11,22,22,10,20,25,12,12,36,19,11,
+ 34,75,33,120,37,14,40,16,10,21)
> m.1 <- c(.68,.1,.3,.1,.56,.23,.64,.49,.4,1.49,
+ .53,.58,1.18,.11,1.27,.26,.40,.49,
+         .51,.40,.34,.42,.66)
> m.2 <- c(.38,.6,.3,.1,.36,.23,.34,.29,.4,1.9,
+ .33,.28,1.1,.111,.27,.21,.140,.149,
+         .51,.140,.134,.42,.16)
> sd.1 <- c(.28,.2,.2,.3,.26,.23,.44,.49,.34,.39,
+ .33,.58,.38,.31,.27,.26,.40,
+          .49,.51,.140,.134,.42,.46)
> sd.2 <- c(.28,.2,.2,.3,.26,.23,.44,.49,.44,.39,
+ .33,.58,.38,.51,.27,.26,.40,
```

Working at the R command line

- Vectorized capabilities for computing $\hat{\hat{\delta}}$

```
> options(width = 60)
> # sample data of 20 studies (continued)
>
> sd.2 <- c(.28,.2,.2,.3,.26,.23,.44,.49,.44,.39,
+ .33,.58,.38,.51,.27,.26,.40,
+           .49,.51,.140,.134,.142,.36)
> dfs <- data.frame(id, n.1,m.1, sd.1,
+ n.2, m.2, sd.2)
> # sample moderator data
> id_mods <- 1:20
> mod1 <- c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,
+ 3,2,3,5,7,1)
> mod2 <- factor(rep(c(1,2,3,4),5))
> dfs_mods <- data.frame(id=id_mods, mod1, mod2)
>
> # after aggregating sample ES data, then the meta-analyis
> # moderator and ES data, e.g., at the command line: merge
```

Working at the R command line

- Vectorized R functions for calculating $\hat{\delta}$

```
> options(width = 65)
> # function in the ’MAd’ package for calculating a vector
> # of ds and gs. Can either copy and paste function to us
> # or install the MAd package [install.packages(’MAd’)],
> # it up [library(MAd)], and use the function w/o having
> # copy and paste. Also, you do not have to use ’with’ fu
> # to calculate values. Finally, there are 2 options:
> # ’pooled.sd’ (pooled st dev) or ’control.sd’ (for contr
>
> # Example
>
> # using same function we created for computing a vector
> with(dfs, mean_to_d(n.1, m.1, sd.1, n.2, m.2, sd.2))

      s.within           d      var.d df         j           g
 [1,] 0.2800000  1.07142857 0.21824145 19 0.9600000  1.02857143
 [2,] 0.2000000 -2.50000000 0.33971861 19 0.9600000 -2.40000000
 [3,] 0.2000000  0.00000000 0.19090909 19 0.9600000  0.00000000
 [4,] 0.3000000  0.00000000 0.09545455 40 0.9811321  0.00000000
```

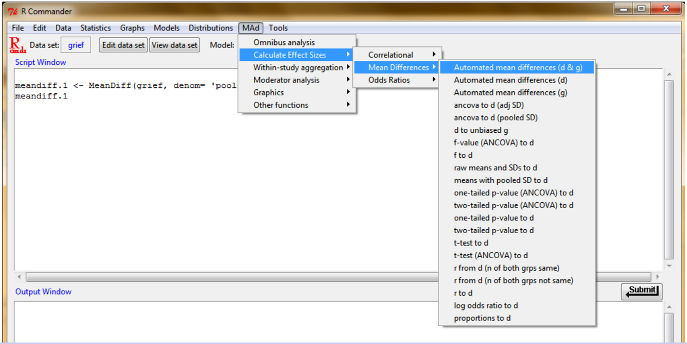
Working at the R command line

- The inner workings of the function

```
> # The inner workings of the function
>
> compute_dgs <- function(n.1, m.1, sd.1, n.2, m.2, sd.2,
+                             denom = "pooled.sd") {
+     call <- match.call()
+     mf <- match.call(expand.dots = FALSE)
+     args <- match(c("n.1", "m.1", "sd.1", "n.2", "m.2",
+     names(mf), 0)
+     mf <- mf[c(1, args)]
+     mf$drop.unused.levels <- TRUE
+     mf[[1]] <- as.name("model.frame")
+     meta <- data
+     mf.n.1 <- mf[[match("n.1", names(mf))]]
+     n.1 <- eval(mf.n.1, data, enclos = sys.frame(sys.pare
+     mf.m.1 <- mf[[match("m.1", names(mf))]]
+     m.1 <- eval(mf.m.1, data, enclos = sys.frame(sys.pare
+     mf.sd.1 <- mf[[match("sd.1", names(mf))]]
+     sd.1 <- eval(mf.sd.1, data, enclos = sys.frame(sys.pa
```

Computing $\hat{\delta}$ with the `MAd` `GUI`

- Click on `MAd` menu (in the GUI) → Calculate Effect Sizes → Mean Differences → Automated mean difference (d & g).
- Notice the values are the same as the command line version. The GUI is simply a menu-driven interface for the functions in the `MAd` package.



```
meandiff.1 <- MeanDiff(grief, denom= 'pool
meandiff.1
```

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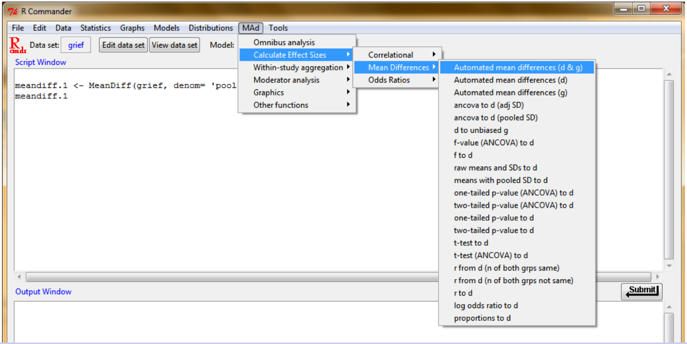

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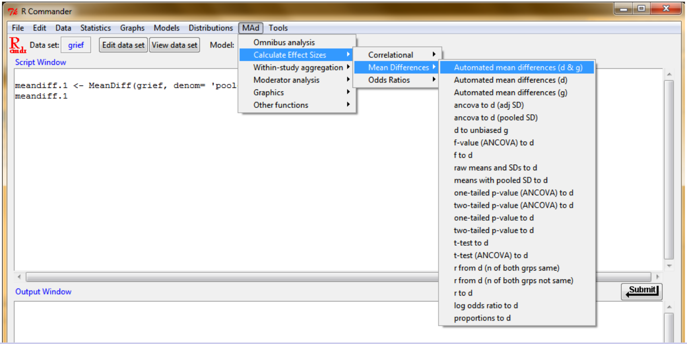

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- Some studies will not report M, sd, etc. to calculate $\hat{\delta}$.
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Working at the R command line: deriving $\hat{\delta}$

- For example, suppose a primary study does not report Ms and sds but reports a t-test and Ns

```
> # For example, suppose the primary study reported Ns and
> # between 2 groups. Then, running:
>
> t_to_d(1.5, 30, 30)

             d      var_d
[1,] 0.3872983 0.06791667

> # reported t-test = 1.5 and N.1 = N.2 = 30 will output t
> # standardized mean difference (d) and its variance (var
> # the meta-analysis.
>
> # to see the inner workings of the function
> t_to_d

function (t, n.1, n.2)
{
    d <- t * sqrt((n.1 + n.2)/(n.1 * n.2))
```

Working at the R command line: compute.es

- Similarly, one can download the compute.es package and run the same function:

```
> # Again, suppose the primary study reported Ns and a t-te
> # between 2 groups. This time using the compute.es packag
>
> library(compute.es)
> tes(1.5, 30, 30)

$MeanDifference
         d      var.d          g      var.g
0.38729833 0.06791667 0.38226849 0.06616405

$Correlation
         r      var.r
0.19324699 0.01570688

$Log_Odds
    log_odds var.log_odds
   0.7024815    0.2234369

$Fishers_z
```

Working at the R command line: `compute.es`

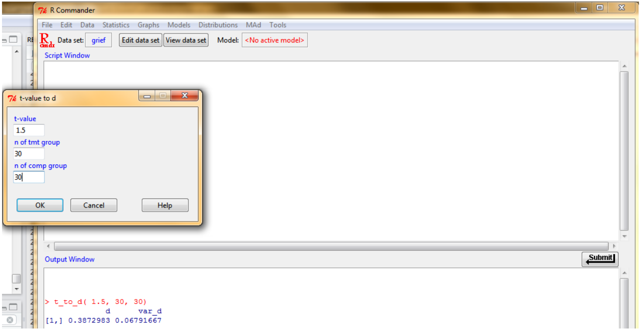
- Inner workings of the function

```
> library(compute.es)
> # to see the inner workings of the function
> tes

function (t, n.1, n.2)
{
    d <- t * sqrt((n.1 + n.2)/(n.1 * n.2))
    var.d <- (n.1 + n.2)/(n.1 * n.2) + (d^2)/(2 * (n.1 + n.2))
    df <- (n.1 + n.2) - 2
    j <- 1 - (3/(4 * df - 1))
    g <- j * d
    var.g <- j^2 * var.d
    n <- n.1 + n.2
    r <- sqrt((t^2)/(t^2 + n - 2))
    var.r <- ((1 - r^2)^2)/(n - 1)
    lor <- pi * d/sqrt(3)
    var.lor <- pi^2 * var.d/3
    z <- 0.5 * log((1 + r)/(1 - r))
    var.z <- 1/(n - 3)
```

Now with the `MAd` GUI

- Click on `MAd` menu (in the GUI) → Calculate Effect Sizes → Mean Differences → t-test to d.
- Notice there are several additional computational options



t-value: 1.5

n of tmt group: 30

n of comp group: 30

```
> t_to_d( 1.5, 30, 30)
             d      var_d
[1,] 0.3872983 0.06791667
```

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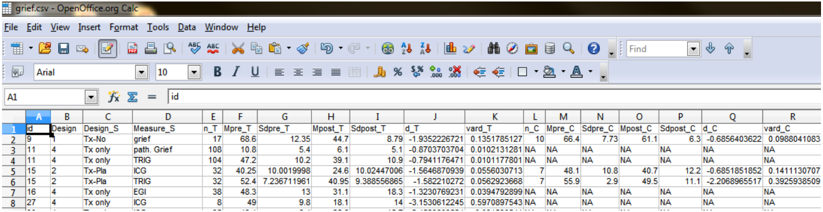
Within-study Aggregation of ESs

- How does one handle studies that report multiple outcome measures? e.g.:



id	Design	Design_S	Measure_S	n_T	Mpre_T	Sdpre_T	Mpost_T	Sdpost_T	d_T	vard_T	n_C	Mpre_C	Sdpre_C	Mpost_C	Sdpost_C	d_C	vard_C
9	1	Tx-No	grief	17	68.6	12.35	44.7	8.79	-1.9352226721	0.1351785127	10	66.4	7.73	61.1	6.3	-0.6856403622	0.0988041083
11	4	Tx only	path. Grief	108	10.8	5.4	6.1	5.1	-0.8703703704	0.0102131281	NA	NA	NA	NA	NA	NA	NA
11	4	Tx only	TRIG	104	47.2	10.2	39.1	10.9	-0.7941176471	0.0101177801	NA	NA	NA	NA	NA	NA	NA
15	2	Tx-Pla	ICG	32	40.25	10.0019998	24.6	10.02447006	-1.5646870939	0.0556030713	7	48.1	10.8	40.7	12.2	-0.6851851852	0.1411130707
15	2	Tx-Pla	TRIG	32	52.4	7.236711961	40.95	9.388556865	-1.582210272	0.0562923668	7	55.9	2.9	49.5	11.1	-2.2068965517	0.3925938509
16	4	Tx only	EGI	38	48.3	13	31.1	18.3	-1.3230769231	0.0394792899	NA	NA	NA	NA	NA	NA	NA
27	4	Tx only	ICG	8	49	9.8	18.1	14	-3.1530612245	0.5970897543	NA	NA	NA	NA	NA	NA	NA

Within-study Aggregation of ESs

- It is crucial to combine these ESs prior to conducting further analyses.

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- Why?

Within-study Aggregation of ESs

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- Why?
- If not, it violates the assumption of independence, giving greater weight to those studies reporting more outcome measures.

Within-study Aggregation of ESs

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Within-study Aggregation of ESs

- There are a couple procedures for combining ESs
  - Mean
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- Using the mean (or weighted mean) ES is problematic. Why?

- Fails to account for ρ (correlation) between measures.

- Gleser & Olkin's procedure computes a weighted average (using $\sigma^2_{\hat{\delta}}$) that accounts for ρ between measures.

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- Assume we are conducting a meta-analysis and the primary studies are generally reporting 3 measures (dep, anx, phy), which is not uncommon.

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- Comparison of each procedure with simulated data
- Assume we are conducting a meta-analysis and the primary studies are generally reporting 3 measures (dep, anx, phy), which is not uncommon.
- We would then aggregate these measures within each study to derive an independent data set (latent variable being "outcome" broadly-defined in this case).
- In this simulation, population values ("true values") were $\mu = x$, $\sigma = y$, with 3 measures correlated at $\rho = .5$

Working at the R command line: agg function

- Using agg function (in `MAd` package) and then merging with moderator data:

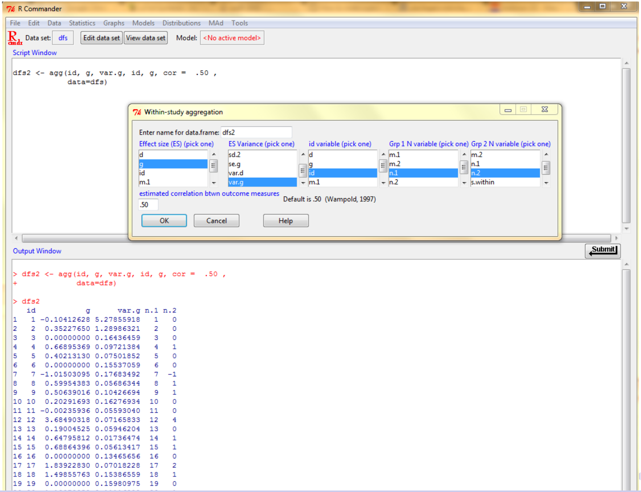
```
> library(MAd) # This package only needs to be loaded 1x in an
> # using the sample data.frame
>
> dfs2 <- agg(id = id, g = g, var = var.g, n.1 = n.1, n.2 =
n.2, cor = 0.5,
+                  data = dfs)
> dfs <- merge(dfs2, dfs_mods)
> # to see the first few rows [head()] of the merged data.fram
> head(dfs)

  id          g      var.g n.1 n.2 mod1 mod2
1  1 -0.1041263 0.13645255  10  11    1    1
2  2  0.3522765 0.07301113  20  22    2    2
3  3  0.0000000 0.16436459  13  10    3    3
4  4  0.6689537 0.09721384  22  20    4    4
5  5  0.4021313 0.07501852  28  25    1    1
6  6  0.0000000 0.15537059  12  12    2    2

>
```

Now with the `MAd GUI`: agg function

- Click on `MAd` menu (in the GUI) → Within-Study Aggregation → Aggregate effect size.



```
dfs2 <- agg(id, g, var.g, id, g, cor =  .50 ,
             data=dfs)
```

Enter name for data.frame: dfs2

Effect size (ES) (pick one): g

ES Variance (pick one): var.g

id variable (pick one): id

Grp 1 N variable (pick one): n.1

Grp 2 N variable (pick one): n.2

estimated correlation btwn outcome measures: .50

Default is .50 (Wampold, 1997)

```
> dfs2 <- agg(id, g, var.g, id, g, cor =  .50 ,
+              data=dfs)

> dfs2
   id           g     var.g n.1 n.2
1   1 -0.10412628 5.27855918   1   0
2   2  0.35227650 1.28986321   2   0
3   3  0.00000000 0.16436459   3   0
4   4  0.66895369 0.09721384   4   1
5   5  0.40213130 0.07501852   5   0
6   6  0.00000000 0.15537059   6   0
7   7 -1.01503095 0.17683492   7  -1
8   8  0.59954383 0.05686344   8   1
9   9  0.50639016 0.10426694   9   1
10 10  0.20291693 0.16276934  10   0
11 11 -0.00235936 0.05593040  11   0
12 12  3.68490318 0.07165833  12   4
13 13  0.19004525 0.05946204  13   0
14 14  0.64795812 0.01736474  14   1
15 15  0.68864396 0.05613417  15   1
16 16  0.00000000 0.13465656  16   0
17 17  1.83922830 0.07018228  17   2
18 18  1.49855763 0.15386559  18   1
19 19  0.00000000 0.15980975  19   0
```

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- General meta-analytic models begins with $i = 1, \ldots, k$ independent ESs (each estimating a “true” effect) and follow:

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- where y_i is the estimated effect size for study i, θ_i is the true effect for study i, e_i is the within-study sampling error, and $e_i \sim N(0, \tau^2)$.

Fixed and random effects models

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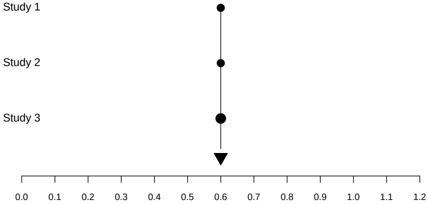
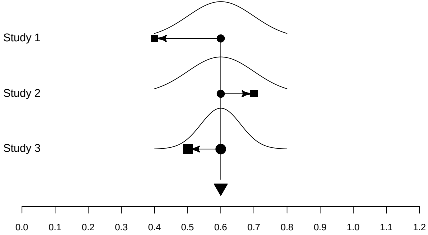
Fixed effects models: graphical representation



True effect sizes for three studies, fixed effect model



Observed effect sizes for three studies, fixed effect model

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- θ_i is the true effect for study i, μ is the average true effect, and $v_i^* = v_i + \tau^2$ is the total heterogeneity among ESs, where the variance of the within-study errors, v_i, are known and the between-study errors, τ^2 , are unknown and estimated based on the studies included in the analysis.

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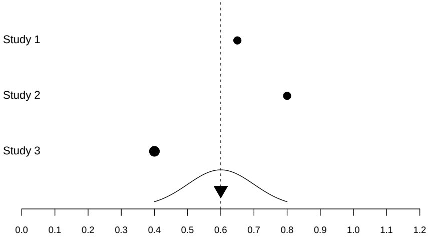

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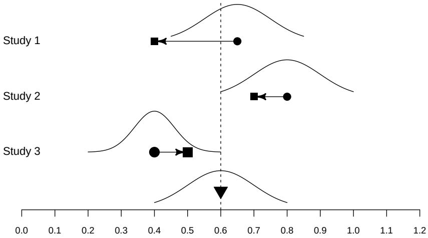

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Mixed effects models

- Models that include moderators (study-level variables) are called mixed effect or conditional models.

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  - θ_i is the true effect
  - x_{ij} is the value of the j-th moderator variable for the i-th study

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$$\theta_i = \beta_0 + \beta_1 x_{ij} + \ldots + \beta_{p\prime} x_{ip\prime} + v_i^*$$

- Assuming $v^* \sim N(0, \tau^2)$ and where
  - θ_i is the true effect
  - x_{ij} is the value of the j-th moderator variable for the i-th study
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▸ forward

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  - τ^2 is the residual heterogeneity among ESs (i.e., variability not accounted for by moderators included in the model) (Viechtbauer, 2010).
- The goal is to determine how much the included moderators influence the magnitude of $\bar{\theta}$ (average true ES).

forward

Heterogenity estimators

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---

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    - μ (or $\beta_0 \ldots \beta_{p\prime}$) is estimated with weighted least squares where $w_i = 1/v^*$

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Omnibus analysis (unconditional models)

- We will utilize a restricted-maximum likelihood estimator for both omnibus (i.e., $\theta_i = \mu + v_i^*$) and mixed-effect models
- Load the `grief2.csv`[8] file into the R session:

```
> options(width = 60)
> # import ES data
> # (Note: this is a cleaned up dataset with 1 ES per stud
> # already merged):
> g.dfd <- read.csv('grief2.csv', header=TRUE, na.strings=
> names(g.dfd)

[1] "id"      "del"     "var.del" "n.1"     "n.2"
[6] "risk"    "female"  "n.sess"
```

---

[8] Note: del $= \Delta = g_T - g_C$ which is the difference between the standardized mean change scores (corrected for bias) for the treatment (g_T) and control groups (g_C); var.del $= V_\Delta$ which is the variance of Δ; `n.1` and `n.2` are the T and C sample size respectively; and the remaining variables (minus `id`) are moderator variables.

Examine data structure

- Important to examine the data structure for proper output from data analysis.
- Looks OK but reference level needs to be changed.

```
> options(width = 65)
> # examine the data structure
> str(g.dfd)
```

```
'data.frame':         45 obs. of  8 variables:
 $ id      : Factor w/ 45 levels "11","113","118",..: 31 36 1 6 14 19 20 21
 $ del     : num  0.689 1.216 0.566 0.226 1.036 ...
 $ var.del: num  0.179 0.2052 0.0108 0.1573 0.0424 ...
 $ n.1     : int  17 12 143 10 54 8 34 49 39 52 ...
 $ n.2     : int  9 12 143 10 54 8 34 49 39 52 ...
 $ risk    : Factor w/ 3 levels "at-risk","complicated",..: 3 3 2 2 2 2 2 2
 $ female : int  46 100 79 74 69 56 88 88 50 36 ...
 $ n.sess : int  8 3 12 12 12 24 16 16 16 12 ...
```

```
> # risk needs to have reference level as "normal"
> g.dfd$risk <-relevel(g.dfd$risk, ref="normal")
```

Omnibus analysis (unconditional models)

- `grief2.csv` is a cleaned up version of the bereavement meta-analysis data discussed earlier.
- How do we conduct the overall omnibus ES (under a REML model, i.e., random effects)?

▸ substantive

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Omnibus analysis (unconditional models)

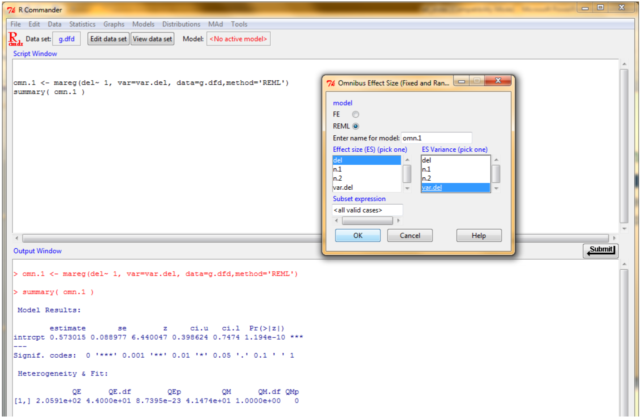
```
> options(width = 65)
> # load meta-analysis package:
> library(MAd)
> # omnibus analysis with grief data.frame
> # The formula: del ~ 1 with the ’del’ value to the left bein
> # criterion variable (del = mean diff effect size) predicted
> # by (’~’) 1 (which indicates intercept).
> # the argument’var’ is calling for the variance of del and t
> # method ’REML’ =  restricted maximum likelihood (random eff
> # g.dfd = grief data.frame
>
> omn.1 <- mareg(del ~ 1, var = var.del, method = "REML", data
> # lets examine the output object ’omn.1’
> summary(omn.1)

 Model Results:

        estimate    se     z  ci.l  ci.u p
intrcpt    0.573 0.089 6.440 0.399 0.747 0
```

Now with the MAd GUI: omnibus

- Click on `MAd` menu (in the GUI) → Omnibus.
- Then the dialogue box will have several options:



```
omn.1 <- mareg(del~ 1, var=var.del, data=g.dfd,method='REML')
summary( omn.1 )
```

model
FE ○
REML ●
Enter name for model: omn.1
Effect size (ES) (pick one): del (n.1, n.2, var.del)
ES Variance (pick one): var.del (del, n.1, n.2)
Subset expression: <all valid cases>

```
> omn.1 <- mareg(del~ 1, var=var.del, data=g.dfd,method='REML')

> summary( omn.1 )

 Model Results:

        estimate       se         z      ci.u    ci.l  Pr(>|z|)
intrcpt 0.573015 0.088977 6.440047 0.398624 0.7474 1.194e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Heterogeneity & Fit:

            QE       QE.df          QEp          QM       QM.df QMp
[1,] 2.0591e+02 4.4000e+01 8.7395e-23 4.1474e+01 1.0000e+00   0
```

Omnibus analysis: interpreting output

```
> # lets examine tau^2 and I^2 for 'omn.1'
> omn.1$I2  #notice no summary command around the model object

[1] 86.07395

> summary(omn.1)$tau2

[1] 0.2671543

>
```

- tau2 $= \hat{\tau}^2$ is amount of true heterogeneity in the omnibus ES.
- I2 $= I^2$ which is the percent of how much of total variability in the ES estimate (between-study heterogeneity and sampling variability) is attributed to differences among the true ES

Omnibus analysis: interpreting output

```
> options(width = 60)
> # lets examine the coefficients  for 'omn.1'
> summary(omn.1)$coef

        estimate    se    z  ci.l  ci.u p
intrcpt    0.573 0.089 6.44 0.399 0.747 0
```

- `estimate` $= \hat{\mu} =$ overall omnibus ES (β_0).
- `se` $=$ standard error of omnibus ES.
- `z` $=$ z-value.
- `ci.u` $=$ Upper confidence interval.
- `ci.l` $=$ Lower confidence interval.
- `Pr(>|z|)` $=$ p-value.

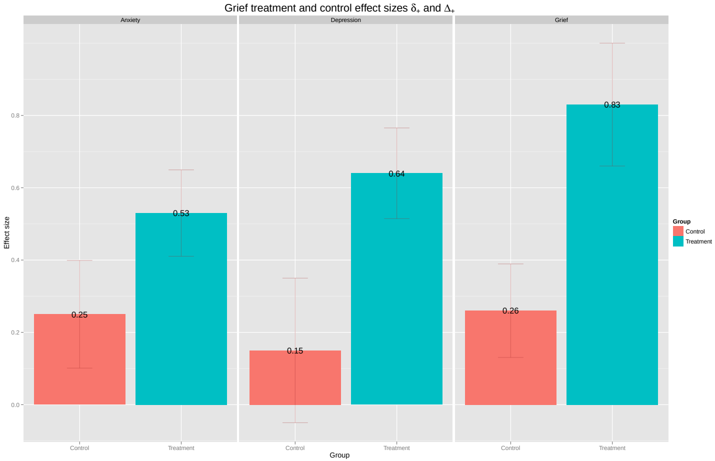
Omnibus analysis: interpreting output

```
> # lets examine  model fit for 'omn.1'
>
> summary(omn.1)$fit

          QE QE.df QEp     QM QM.df QMp
[1,] 205.914    44   0 41.474     1   0
```

- These values relate to model fit.
- `QE` = Q-error which is the measure of error in the model.
- `QE.df` = Degrees of freedom for Q-error.
- `QEp` = Q-error p-value (for homogeneity).
- `QM` = Q-model which is the measure of model fit.
- `QM.df` = Degrees of freedom for Q-model.
- `QMp` = Q-between p-value.

Omnibus: graphical representation



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Case Diagnostics

- A single outlying trial could be the source of substantial heterogeneity and or influence.

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- To identify potential studies, leave-one-out method can be used where meta-analysis is rerun, iteratively removing studies.

Publication Bias

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- Null studies relegated to the file-drawer could bias the summary effect in the direction of efficacy.

Detecting Publication Bias

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- Asymmetry in the funnel may be indicative of publication bias, although some consider this plot subjective.
- Less subjective procedures include Trim-and-Fill and Fail Safe N

Trim and Fill

- The trim and fill method estimates the number of missing null studies from meta-analysis.

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- trimfill() function for trim and fill method

Fail Safe N

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- Number of null studies that have to be added for the overall effect to be reduced to NS.

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Moderator analyses

- Notice there was a significant Q-statistic, indicating there are substantial between-study differences ($I^2 = .86$)

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- Therefore, interpretation of the omnibus is difficult (the average effect is not very telling).
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- For demonstrative purposes we will examine two potential moderators of treatment effects (number of sessions & risk level)

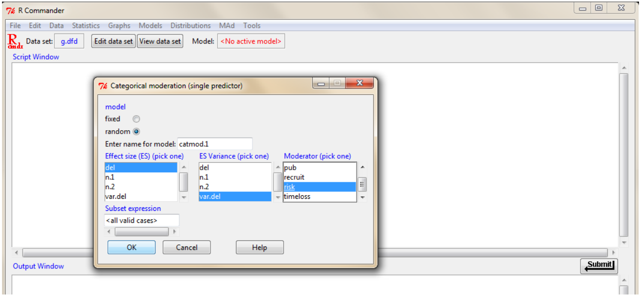
▸ $\theta_i = \beta_0 + \beta_{1xi} + \ldots$

Working at the R command line: macat

```
> options(width = 70)
> # single predictor moderator analyses (categorical variable)
>
> mod.risk <- macat(del, var=var.del, mod=risk, data=g.dfd,me
> mod.risk

 Model Results:


          mod  k estimate   var    se   ci.l  ci.u     z     p
1     at-risk 14    0.223 0.013 0.114 -0.001 0.447 1.950 0.051
2 complicated 10    0.916 0.018 0.136  0.650 1.182 6.748 0.000
3      normal 21    0.568 0.010 0.101  0.370 0.766 5.617 0.000
4     Overall 45    0.535 0.004 0.066  0.405 0.664 8.089 0.000
        Q df  p.h  I2
1  24.082 13 0.03 46%
2  46.281  9 0.00 81%
3  80.768 20 0.00 75%
4 205.914 44 0.00 79%

 Heterogeneity:
```

Now with the `MAd` GUI

- Click on `MAd` menu (in the GUI) → Moderator analysis → Categorical moderation
- Notice there are several additional moderator options



Data set: g.dfd

Model: <No active model>

model

fixed ○

random ●

Enter name for model: catmod.1

Effect size (ES) (pick one)	ES Variance (pick one)	Moderator (pick one)
del (selected)	del	pub
n.1	n.1	recruit
n.2	n.2	risk (selected)
var.del	var.del (selected)	timeloss

Subset expression

<all valid cases>

Moderator analysis: interpreting output

```
> options(width = 65)
> # lets examine the model fit  for 'mod.risk'
> mod.risk$Model

          mod  k  estimate         se         var         ci.l
1     at-risk 14 0.2227130 0.11418647 0.013038549 -0.001092516
2 complicated 10 0.9162415 0.13577125 0.018433831  0.650129866
3      normal 21 0.5680614 0.10112449 0.010226161  0.369857422
4     Overall 45 0.5348408 0.06612054 0.004371926  0.405244540
       ci.u        z            p         Q df          p.h  I2
1 0.4465184 1.950432 5.112463e-02  24.08248 13 3.037976e-02 46%
2 1.1823531 6.748421 1.494629e-11  46.28083  9 5.340628e-07 81%
3 0.7662654 5.617447 1.937998e-08  80.76838 20 2.906314e-09 75%
4 0.6644371 8.088875 6.021833e-16 205.91422 44 8.739541e-23 79%
```

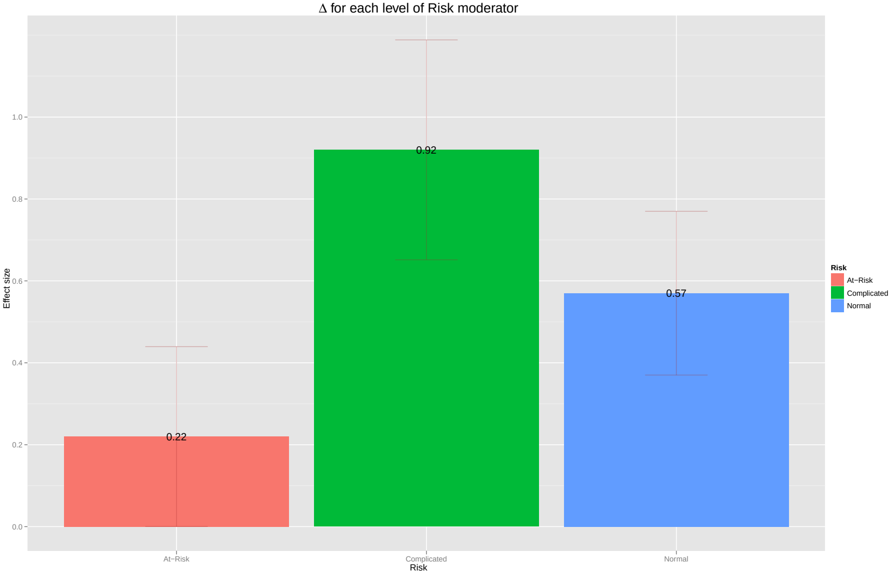
- `estimate` $= \hat{\mu} =$ mean ES for each moderator factor level.
- `se` $=$ standard error of ES.
- `var` $= \sigma^2 =$ variance of ES.
- `ci.l` & `ci.u` $=$ 95% confidence level.
- `p.h` $= p$-value for heterogeneity.

Moderator analysis: interpreting output

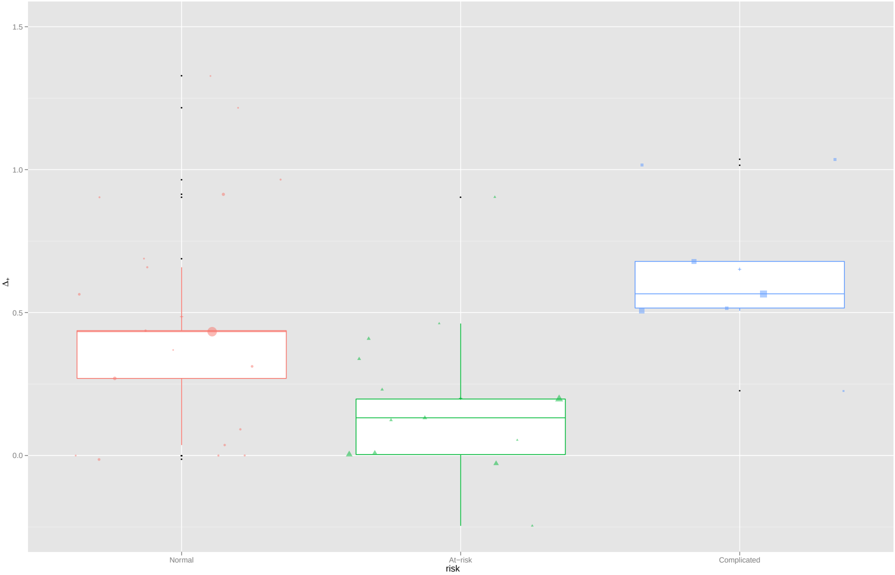
```
> # lets examine  model fit for 'omn.1'
>
> mod.risk$Hetero

         Q       Qw df.w          p.w       Qb df.b          p.b
1 205.9142 151.1317   42 3.119727e-14 15.47118    2 0.0004369946
```

- These values relate to model fit.
- `Qw` = Q-error which is the measure of error in the model.
- `df.w` = Degrees of freedom for Q-error.
- `p.w` = Q-error p-value (for homogeneity).
- `Qb` = Q-model which is the measure of model fit.
- `df.b` = Degrees of freedom for Q-model.
- `p.b` = Q-between p-value.

Graphical depiction of categorical moderator analysis



Better graphical depiction of categorical moderator analysis



Moderator analyses (continuous variable)

- Now we will examine number of sessions (`n.sess`)
- This is a continuous moderator so we will use a different function to conduct the analysis.

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Working at the R command line: mareg

```
> options(width = 65)
> #
>
> # single predictor moderator analyses with grief data.frame
> # The formula: del ~ mod with the ’del’ value to the left be
> # criterion variable (del = mean diff effect size) predicted
> # by (’~’)  (which indicates the modderator variable risk).
> # the argument’var’ is calling for the variance of del and t
> # method ’REML’ =  restricted maximum likelihood (random eff
> # g.dfd = grief data.frame
>
> mod.sess <- mareg(del~n.sess,  var=var.del,  data=g.dfd,meth
> # model coefficients, or to see both coefficients and fits s
> # just summary(mod.sess)
> summary(mod.sess)$coef

        estimate    se      z   ci.l  ci.u     p
intrcpt   -0.201 0.217 -0.925 -0.627 0.225 0.355
mods       0.075 0.020  3.817  0.036 0.113 0.000
```

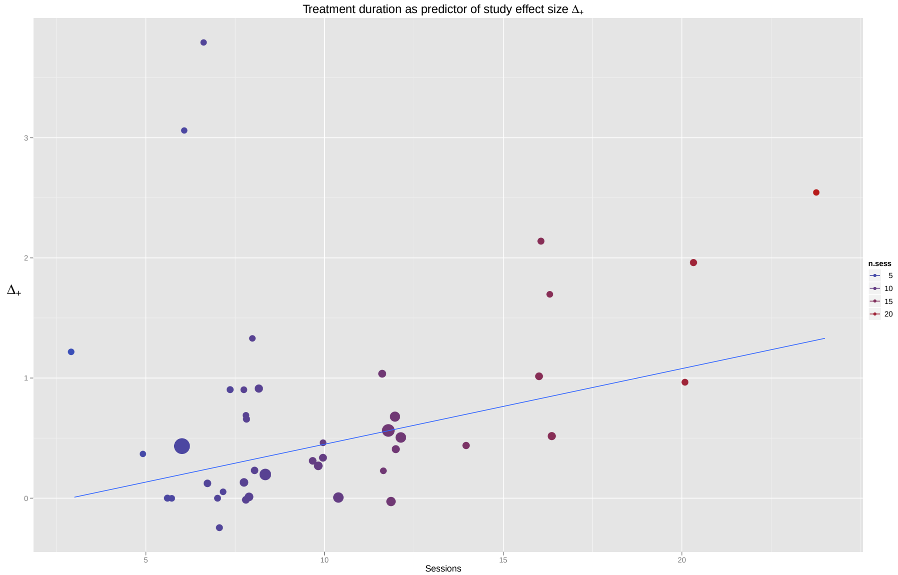
Working at the R command line: `mareg`

```
> options(width = 65)
> # model fit, or to see both coefficients and fits stats use
> # just summary(mod.sess)
> summary(mod.sess)$fit

          QE QE.df QEp     QM QM.df QMp
[1,] 158.681    40   0 14.567     1   0

>
```

Graphical depiction of continuous moderator analysis



Moderator analyses: confounding

- Both moderators are significant.
- However, what about potential confounds or covariates of these significant moderators?
- In this case, what if the two moderators are correlated?
- We first need to determine if the variables are correlated. We can do this visually or by conducting a correlational analysis.
- If they co-vary then we need to assess for the unique variance of each predictor. How?
- Lets begin by examining this visually with boxplots.

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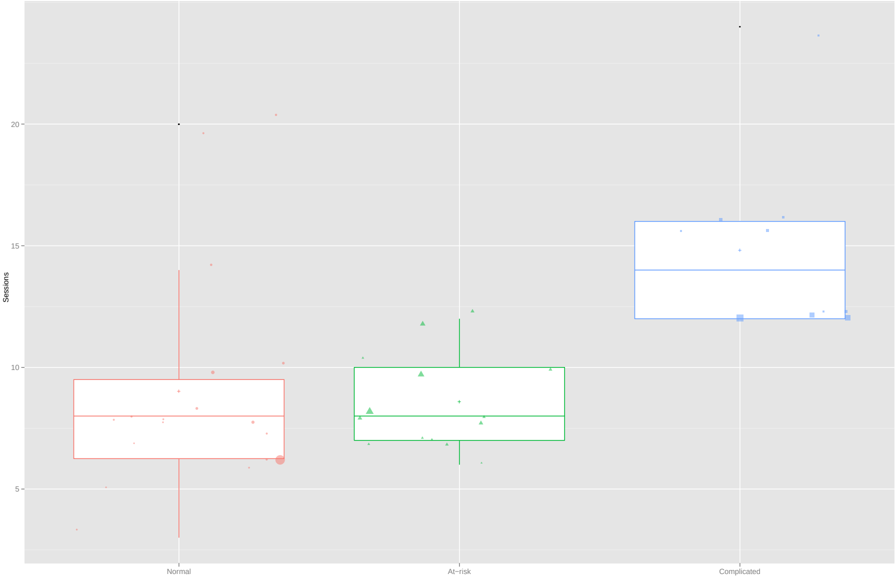
Graphical depiction of confounding moderators



Moderator analyses: confounding

- Clearly these two moderators co-vary.
- Therefore, it is *crucial* that we test these moderators together in a multi-predictor meta-regression.
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Working at the R command line: multi-predictor mareg

```
> options(width = 65)
> # multi-predictor moderator analyses with grief data.frame
> # The formula: del ~ mod with the ’del’ value to the left be
> # criterion variable (del = mean diff effect size) predicted
> # by (’~’)  (which indicates the moderator variables risk, n
> # the argument’var’ is calling for the variance of del and t
> # method ’REML’ =  restricted maximum likelihood (random eff
> # g.dfd = grief data.frame
>
> mod.multi <- mareg(del~risk+n.sess+female,  var=var.del,  dat
> # model coefficients, or to see both coefficients and fits s
> # just summary(mod.sess)
> summary(mod.multi)$coef
```

```
                estimate    se      z   ci.l   ci.u     p
intrcpt           -0.646 0.298 -2.169 -1.229 -0.062 0.030
riskat-risk       -0.263 0.169 -1.560 -0.594  0.067 0.119
riskcomplicated   -0.064 0.194 -0.332 -0.443  0.315 0.740
n.sess             0.071 0.021  3.431  0.030  0.111 0.001
female             0.008 0.003  2.705  0.002  0.014 0.007
```

Working at the R command line: multi-predictor `mareg`

```
> options(width = 65)
> # model fit, or to see both coefficients and fits stats use
> # just summary(mod.multi)
> summary(mod.multi)$fit

         QE QE.df QEp     QM QM.df QMp
[1,] 75.412    28   0 31.591     4   0

>
```

Outline

1 Intro to `R` & `MA*` packages
2 Introduction
- Schmidt (1992)
- NHST

3 Meta-analytic steps
- Initial stages
- Inclusion and exclusion criteria
- Data prep
- Calculate ESs
- Aggregation
- Models
- Omnibus
- Sensitivity Analysis
- Moderator
- Diagnostics
- Graphics

Diagnostics: Check assumptions, outliers, influential studies

- Prior to running omnibus test, assess ESs for normality and outliers ($z > 2$).
- Less than 5% of ES values should be greater or lesser than 2.
- Then, test the omnibus analysis for normally distributed residual values and outlier data.
- These procedures are implemented in the `metafor` package in `R` (and can be run using the `MAd` package but not the GUI).

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Graphics

- A pictures speaks a thousand words. . .
- We have utilized boxplots and scatterplots for moderator variables up until this point. There are several additional plots for visualizing data and results.
- For example, the most common are funnel, residual, and forest plots.
- The forest plot will be discussed briefly.

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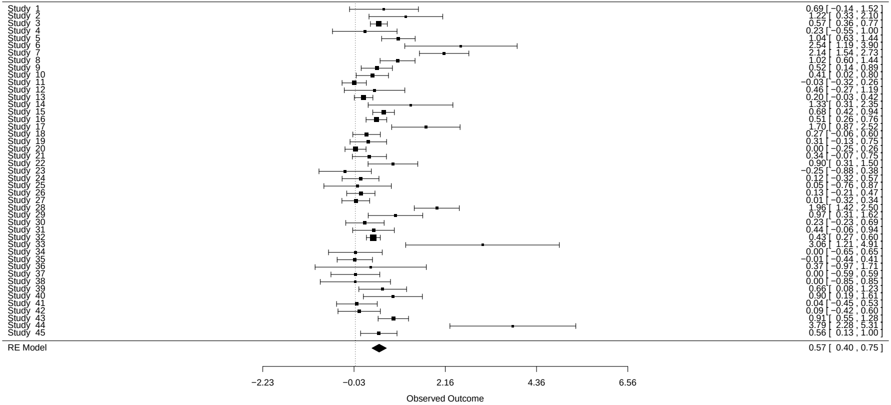
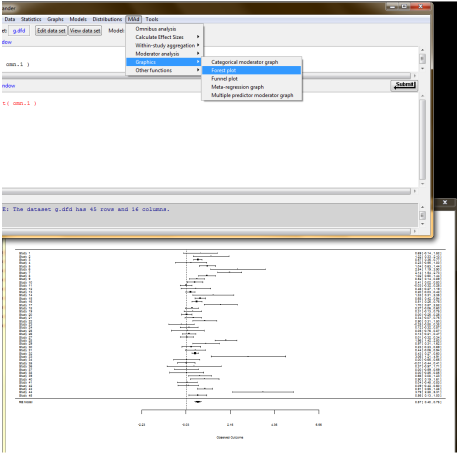
Graphical depiction of confounding moderators



Now with the `MAd` GUI

- Click on `MAd` menu (in the GUI) → Graphics → Forest Plot.
- Default option is not elegant but useful for visualization.

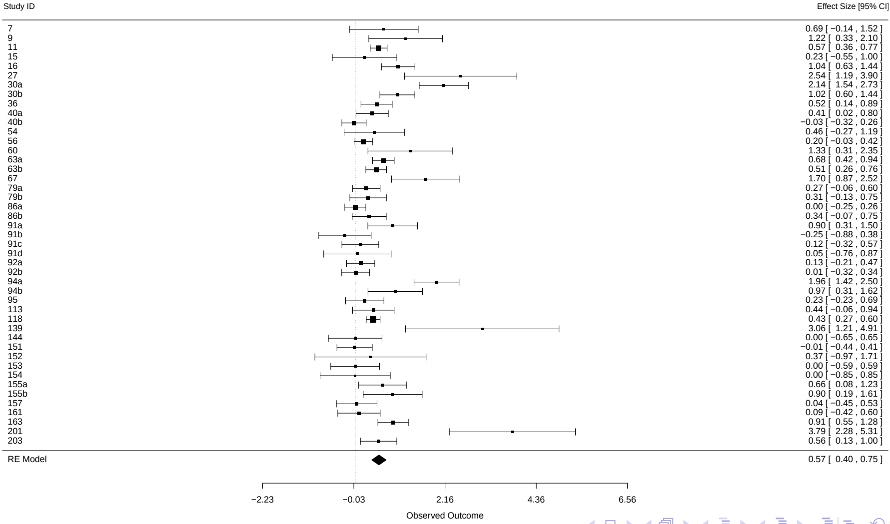


```
omn.1 )
```

```
t( omn.1 )
```

```
E: The dataset g.dfd has 45 rows and 16 columns.
```

Graphical depiction of confounding moderators



Study ID	Effect Size [95% CI]
7	0.69 [−0.14 , 1.52]
9	1.22 [0.33 , 2.10]
11	0.57 [0.36 , 0.77]
15	0.23 [−0.55 , 1.00]
16	1.04 [0.63 , 1.44]
27	2.54 [1.19 , 3.90]
30a	2.14 [1.54 , 2.73]
30b	1.02 [0.60 , 1.44]
36	0.52 [0.14 , 0.89]
40a	0.41 [0.02 , 0.80]
40b	−0.03 [−0.32 , 0.26]
54	0.46 [−0.27 , 1.19]
56	0.20 [−0.03 , 0.42]
60	1.33 [0.31 , 2.35]
63a	0.68 [0.42 , 0.94]
63b	0.51 [0.26 , 0.76]
67	1.70 [0.87 , 2.52]
79a	0.27 [−0.06 , 0.60]
79b	0.31 [−0.13 , 0.75]
86a	0.00 [−0.25 , 0.26]
86b	0.34 [−0.07 , 0.75]
91a	0.90 [0.31 , 1.50]
91b	−0.25 [−0.88 , 0.38]
91c	0.12 [−0.32 , 0.57]
91d	0.05 [−0.76 , 0.87]
92a	0.13 [−0.21 , 0.47]
92b	0.01 [−0.32 , 0.34]
94a	1.96 [1.42 , 2.50]
94b	0.97 [0.31 , 1.62]
95	0.23 [−0.23 , 0.69]
113	0.44 [−0.06 , 0.94]
118	0.43 [0.27 , 0.60]
139	3.06 [1.21 , 4.91]
144	0.00 [−0.65 , 0.65]
151	−0.01 [−0.44 , 0.41]
152	0.37 [−0.97 , 1.71]
153	0.00 [−0.59 , 0.59]
154	0.00 [−0.85 , 0.85]
155a	0.66 [0.08 , 1.23]
155b	0.90 [0.19 , 1.61]
157	0.04 [−0.45 , 0.53]
161	0.09 [−0.42 , 0.60]
163	0.91 [0.55 , 1.28]
201	3.79 [2.28 , 5.31]
203	0.56 [0.13 , 1.00]
RE Model	0.57 [0.40 , 0.75]

Outline

4 Appendix A
- R session info
- Source code

- R version 2.15.3 (2013-03-01), `x86_64-w64-mingw32`

- Locale: `LC_COLLATE=English_United States.1252`, `LC_CTYPE=English_United States.1252`, `LC_MONETARY=English_United States.1252`, `LC_NUMERIC=C`, `LC_TIME=English_United States.1252`

- Base packages: base, datasets, graphics, grDevices, methods, stats, utils

- Other packages: compute.es 0.2.1, Formula 1.1-0, ggplot2 0.9.3.1, MAd 0.9, metafor 1.7-0, quantreg 4.96, RcmdrPlugin.MAd 0.6.3, shape 1.4.0, SparseM 0.96

- Loaded via a namespace (and not attached): colorspace 1.2-1, dichromat 2.0-0, digest 0.6.3, grid 2.15.3, gtable 0.1.2, labeling 0.1, MASS 7.3-23, munsell 0.4, plyr 1.8, proto 0.3-10, Rcmdr 1.9-6, RColorBrewer 1.0-5, reshape2 1.2.2, scales 0.2.3, stringr 0.6.2, tcltk 2.15.3, tools 2.15.3

Outline

4 Appendix A
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```
Writing to file wkshp_meta.R

###################################################
### chunk number 1: calculator
###################################################
#line 200 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w

2 + 2


###################################################
### chunk number 2: object_oriented
###################################################
#line 207 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w

x <- 2
x + x

x*x + 1


###################################################
### chunk number 3: vectors
```

```
###################################################
#line 217 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w

mydata <- c(5, 4, 3, 2, 1)  # c is for concatenate

mydata/2




###################################################
### chunk number 4: schmidt
###################################################
#line 261 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w
Study <- c(1:21)
r <- c(.04,.14,.31,.12,.38,.27,.15,.36,.20,.02,.23,.11,.21,.37,.14,.29,.26,
se <- c(.12,.12,.11,.12,.10,.11,.12,.11,.12,.12,.12,.12,.12,.11,.12,.11,.11
schmidt <- data.frame(Study,r,se)
rm(Study, r, se)


###################################################
### chunk number 5: one
```

```
###################################################
#line 489 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w
curve(dnorm(x,mean=.04, sd=.12),from=-.4,to=.4, col="blue",ylab="", xlab="r
lwd=2, yaxt="n" )
abline(v=.04,  lty=2,col="red")


###################################################
### chunk number 6: two
###################################################
#line 519 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w
temp <- boxplot(split(rnorm(n=10000,mean=.04, sd=.09), gl(1,10000)), col="g
lwd=2, yaxt="n", horizontal=T, outpch=NA )
text(temp$stats[3, ],seq(along = temp$n)+.4,
     labels = c("95 CI [-.20,.28]"), pos = 1)
text(temp$stats[3, ]-.25,seq(along = temp$n)-.20,  #expression(CI(lower) ==
     labels = c("CI (lower) = r-1.96*se"), pos = 1)
text(temp$stats[3, ]+.25,seq(along = temp$n)-.20,  #expression(CI(upper) ==
     labels = c("CI (upper) = r+1.96*se"), pos = 1)
```

```
###################################################
### chunk number 7: three
###################################################
#line 546 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w
library(metafor)
omn <- rma(r, vi=se^2, data=schmidt, subset=Study==c(1:5))

forest(omn, slab=paste(1:5))
text(-1.13,6.3, "Study",    pos=4, cex=.9)
text( .7, 6.3, "Effect Size [95% CI]", pos=4, cex=.9)



###################################################
### chunk number 8: four
###################################################
#line 911 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w
# Coutesy of William T. Hoyt, PhD
# Draws single sample from one population.
# Draws histogram, computes M and sd.
set.seed(121465)
# Population mean and sd:
```

```
mu1 <- 20
sig1 <- 6

# Random sample:
y1 <- rnorm(n = 30, mean = mu1, sd = sig1)

# Depicting results graphically:
cl = colors()
hist(y1, border = cl[139], xlim = c(-2,40), ylim = c(0,9),
     breaks = seq(-1.8, 39.2, by = 1),
     main = 'Frequency distribution, single sample (N = 30)',
     xlab = 'Score')
curve(30*dnorm(x, mean=20, sd=6), col=cl[139], lwd = 2, add=T)

Samp <- paste("M = ", round(mean(y1),1),"  ",
              "sd = ", round(sd(y1),1))

text(8, 7.5, "Population", cex = 1.5, col = cl[137])
text(8, 6.5, expression(mu == 20), cex = 1.5, pos=2, offset = 1.5)
text(8, 6.5, expression(sigma == 6), cex = 1.5, pos=4, offset = 1.5)
rect(-0.5,6.2,16,8)
```

```
text(29, 7.5, "Sample", cex = 1.5, col=cl[137])
text(29, 6.5, Samp, cex = 1.5)
rect(19.2,6.2,38.5,8)


###################################################
### chunk number 9: five
###################################################
#line 958 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/w
# Coutesy of William T. Hoyt, PhD
# Draws single sample from each of two populations.
# Draws histogram of both samples, computes d.
set.seed(121465)
# Population means and sds:
mu1 <- 20
sig1 <- 6
mu2 <- 17
sig2 <- 6

# Random samples:
y1 <- rnorm(n = 30, mean = mu1, sd = sig1)
y2 <- rnorm(n = 30, mean = mu2, sd = sig2)
```

```
# Depicting results graphically:
cl = colors()
hist(y1, border = cl[139], xlim = c(-2,40), ylim = c(0,9),
     breaks = seq(-0.8, 37.2, by = 1),
     main = ’Overlapping frequency distributions, two samples’,
     sub = ’n(T) = n(C) = 30’,
     xlab = ’T group (blue) and C group (green) scores’)
curve(30*dnorm(x, mean=20, sd=6), col = cl[139], lwd = 2, add=T)
hist(y2, border = 4, breaks = seq(-1.2, 36.8, by = 1), add = T)
curve(30*dnorm(x, mean=17, sd=6), col = 4, lwd = 2, add=T)

delta <- (mu2 - mu1)/sig1
d <- (mean(y2) - mean(y1))/sd(y1)

text(11.5, 8.2, "Population", cex = 1.5, col=cl[137])
text(-2, 7.2, "T:", pos = 4, offset = -0.5, cex = 1.5, col=4)
text(10, 7.2, expression(mu == 17), cex = 1.5, pos=2, offset = 0)
text(10, 7.2, expression(sigma == 6), cex = 1.5, pos=4, offset = 1.5)

text(-2, 6.4, "C:", pos = 4, offset = -0.5, cex = 1.5, col=cl[139])
text(10, 6.4, expression(mu == 20), cex = 1.5, pos=2, offset = 0)
```

```
text(10, 6.4, expression(sigma == 6), cex = 1.5, pos=4, offset = 1.5)

SampT <- paste("M = ", round(mean(y2),1),"     ",
              "sd = ", round(sd(y2),1))
SampC <- paste("M = ", round(mean(y1),1),"     ",
              "sd = ", round(sd(y1),1))

text(30, 8.2, "Sample", cex = 1.5, col=cl[137])
text(30, 7.2, SampT, cex = 1.5)
text(30, 6.4, SampC, cex = 1.5)

d.text <- paste("d =", round(d,2))

text(12, 5.5, expression(delta == -0.5), cex = 1.5)
text(30,5.5, d.text, cex = 1.5, col=cl[137], font=2)

rect(4.2,5,18.3,8.6)
rect(20,5,40,8.6)


###################################################
```

```
### chunk number 10: six
###################################################
#line 1025 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# Coutesy of William T. Hoyt, PhD
# Draws 1000 independent samples from each of two populations.
# Computes and saves d for each pair of samples (T vs. C)
set.seed(121465)
# Population means and sds:
mu1 <- 20        # Control group
sig1 <- 6
mu2 <- 17        # Treatment group
sig2 <- 6
n <- 30
nsamp <- 1000

# out is a data frame to store results, one row per sample.

out = data.frame(M.T = rep(NA,nsamp),
                 sd.T = rep(NA,nsamp),
                 M.C = rep(NA,nsamp),
                 sd.C = rep(NA,nsamp),
                 sd.within = rep(NA,nsamp),
```

```
                 d1 = rep(NA,nsamp),
                 d2 = rep(NA,nsamp))

for(iii in 1:nsamp)    {

  # Random samples:
  y1 <- rnorm(n = 30, mean = mu1, sd = sig1)  # Control grp
  y2 <- rnorm(n = 30, mean = mu2, sd = sig2)  # Treatment grp

  out$M.T[iii] <- mean(y2)
  out$M.C[iii] <- mean(y1)
  out$sd.T[iii] <- sd(y2)
  out$sd.C[iii] <- sd(y1)
  out$sd.within[iii] <- sqrt((var(y1)+var(y2))/2)
  out$d1[iii] <- (mean(y2)-mean(y1))/sd(y1)
  out$d2[iii] <- (mean(y2)-mean(y1))/out$sd.within[iii]
  }

out2 <- data.frame(means = colMeans(out),
                   sds = sd(out[,1:7]))

# Depicting results graphically:
```

```
cl <- colors()
hist(out$d1, xlim = c(-2,1), ylim = c(0,175),
     breaks = seq(-2, 1, by = .1),
     main = "Values of d for 1000 samples",
     sub = "(n_T = n_C = 30, delta = 0.5)",
     xlab = "d = (M.T - M.C)/sd.C")
curve(100*dnorm(x, mean=-.5, sd=out2$sds[6]), lwd = 2, add=T)

text(-1.2, 150, "mean(d)  =", pos = 2, cex=1.2)
text(-1.17, 150, round(out2$means[6], 2), pos = 4, offset = -.26, cex=1.2)
text(-1.2, 135, "SE = sd(d)  =", pos = 2, cex=1.2)
text(-1.17, 135, round(out2$sds[6], 2), pos = 4, offset = -.001, cex=1.2)

# Vertical lines at z = {-2, -1, 0, 1, 2}
sd.d <- out2$sds[6]
pts <- seq(0,3,by =.01) - 2
crv <- 100*dnorm(pts, mean = -.5, sd = sd.d)
crv2 <- data.frame(x = pts, y = crv)

xco <- c(-.5, -.5,
        -.5 - sd.d, -.5 - sd.d,
        -.5 + sd.d, -.5 + sd.d,
```

```
        -.5 - 2*sd.d, -.5 - 2*sd.d,
        -.5 + 2*sd.d, -.5 + 2*sd.d)
yco <- rep(0,10)
for(ii in 1:5*2) {
yco[ii] <- crv2$y[round(crv2$x,2)==round(xco[ii],2)]   }

lines(xco[1:2], yco[1:2], col = cl[139], lwd = 3)
lines(xco[3:4], yco[3:4], col = "blue", lwd = 3)
lines(xco[5:6], yco[5:6], col = "blue", lwd = 3)
lines(xco[7:8], yco[7:8], col = "purple", lwd = 3)
lines(xco[9:10], yco[9:10], col = "purple", lwd = 3)

text(xco[2], yco[2], "z = 0", col = cl[139], pos = 3)
text(xco[4], yco[4], "z = -1", col = "blue", pos = 2)
text(xco[6], yco[6], "z = 1", col = "blue", pos = 4)
text(xco[8], yco[8], "z = -2", col = "purple", pos = 2)
text(xco[10], yco[10], "z = 2", col = "purple", pos = 4)


###################################################
### chunk number 11: seven
###################################################
```

```
#line 1139 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# Coutesy of William T. Hoyt, PhD
set.seed(121465)
# Adaptation of Schmidt (1992) Figure 1.

n <- 15                            # n per group
delta <- 0.5                       # d between groups (pop)
SE.d <- sqrt(2/n + delta^2/(4*n))  # SE of sempling distr

x1 <- seq(-3,3, by=.01)            # z-scores for sampling distr
y1 <- SE.d*dnorm(x1)

plot(x1*SE.d, y1, xlim = c(-3*SE.d, 4*SE.d), ylim = c(0,max(y1)*1.1),
     type = "l", axes = FALSE, frame.plot = FALSE, lwd=2,
     main = "Schmidt (1992) Fig. 1",
     xlab = "d = (M.T-M.C)/sd.C",
     ylab = "Probability density",
     sub = "Sampling distribution of d over replicated studies",
     cex.lab=0.75)
# lines(x1*SE.d + delta, y1)
axis(1, line=-1)                     # x-axis at y=0
lines(c(0,0),c(0,max(y1)), lty=2)    # vertical line at mean
```

```
t1 <- qt(.95,29)*SE.d
t2 <- qt(.975,29)*SE.d
yt1 <- y1[round(x1,2)==round(t1/SE.d,2)]  # height of curve at t1
yt2 <- y1[round(x1,2)==round(t2/SE.d,2)]  # height of curve at t2

# (For greater color varieties:)
cl <- colors()

lines(c(t1,t1), c(0, yt1), col = cl[31], lwd=2)
lines(c(t2,t2), c(0, yt2), col = "red", lwd=2)
text(t1,yt1, "t(df=29, p=.95)", col=cl[31], pos=4, cex=0.75)
text(t2,yt2, "t(df=29, p=.975)", col="red", pos=4, cex=0.75)
text(t1-.02, 0, ".63", col=cl[31], pos=1,  offset=.4,cex=0.4)
text(t2+.02, 0, ".76", col="red", pos=1,  offset=.4,cex=0.4)

text(-0.77, .140, "mean(d)  =  0.00", cex=0.75)
text(-0.57, .130, "SE(d)  =", pos = 2, cex=0.75)
text(-0.57, .130, round(SE.d, 2), pos = 4, offset = 0, cex=0.75)

# optional:  box()
```

```
###################################################
### chunk number 12: eight
###################################################
#line 1196 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# Coutesy of William T. Hoyt, PhD
set.seed(121465)

# Draws two normal curves, displaced by a specified amount (d)

n <- 15                            # n per group
delta <- 0.5                       # d between groups (pop)
SE.d <- sqrt(2/n + delta^2/(4*n))  # SE of sempling distr
rSE = round(SE.d, 3)

x1 <- seq(-3,3, by=.01)            # z-scores for sampling distr
y1 <- SE.d*dnorm(x1)

cl <- colors()

plot(x1*SE.d, y1, xlim = c(-3*SE.d, 4*SE.d), ylim = c(0,max(y1)*1.1),
     type = "l", col = cl[32], axes = FALSE, frame.plot = FALSE, lwd = 2,
```

```
     main = "Schmidt (1992) Fig. 2:  Type II Errors",
     xlab = "d = (M.T-M.C)/sd.C",
     ylab = "Probability density",
     sub = "Sampling distributions: H_0 and actual (observed) ds")
lines(x1*SE.d + delta, y1, col = "blue", lwd = 2)
axis(1, line=-1)                        # x-axis at y=0
lines(c(0,0),c(0,max(y1)), lty=2)     # vertical line at mean
lines(c(delta, delta),c(0,max(y1)), lty=2)

t1 <- qt(.95,29)*SE.d
t2 <- qt(.975,29)*SE.d
yt1 <- y1[round(x1,2)==round((t1-.5)/SE.d,2)]  # height of distr at t1
yt2 <- y1[round(x1,2)==round((t2-.5)/SE.d,2)]  # height of distr at t2

lines(c(t1,t1), c(0, yt1), col = cl[31], lwd=2)
lines(c(t2,t2), c(0, yt2), col = "red", lwd=2)
# text(t1,yt1, "t(df=29, p=.95)", col=cl[31], pos=4)
# text(t2,yt2, "t(df=29, p=.975)", col="red", pos=4)
text(t1-.02, 0, ".63", col=cl[31], pos=1, cex=1, offset=.4)
text(t2+.02, 0, ".76", col="red", pos=1, cex=1, offset=.4)

# Function paste() is useful for creating labels to add to graphics.
```

```
P1 <- paste("Power =", 1 - round(pt((t1-.5)/SE.d, 29), 2))
P2 <- paste("Power =", 1 - round(pt((t2-.5)/SE.d, 29), 2))
text(t1, yt2 + .005, P1, col=cl[31], pos=4)
text(t2, yt2 - .028, P2, col="red", pos=4)

text(-0.75, .155, "Under H_0:", pos = 3, col = cl[32], cex=1.35)
text(-0.6, .147, "Mean(d)  =", pos = 2, cex=1.35)
text(-0.6, .147, "0.00", pos = 4, offset = 0, cex=1.35)
text(-0.6, .140, "SE(d)  =", pos = 2, cex=1.35)
text(-0.6, .140, round(SE.d, 2), pos = 4, offset = 0, cex=1.35)

text(1.07, .155, "Actual (Observed) ds:", pos = 3, col = "blue", cex=1.35)
text(1.3, .147, "Mean(d)  =", pos = 2, cex=1.35)
text(1.3, .147, "0.50", pos = 4, offset = 0, cex=1.35)
text(1.3, .140, "SE(d)  =", pos = 2, cex=1.35)
text(1.3, .140, round(SE.d, 2), pos = 4, offset = 0, cex=1.35)

rect(-1.21, .134, -.32, .154)
rect(.68, .134, 1.56, .154)

# optional:  box()
```

```
###################################################
### chunk number 13: grief
###################################################
#line 1388 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)

# set working directory to location of .csv file
#setwd()

# import ES data
grief <- read.csv('grief.csv', header=TRUE, sep=",", na.strings= "")

names(grief)


###################################################
### chunk number 14: grief_mods
###################################################
#line 1407 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
```

```
# import moderator data
grief_mods <- read.csv('grief_mods.csv',
header=TRUE, na.strings= "")

names(grief_mods)



###################################################
### chunk number 15: MAd_GUI
###################################################
#line 1502 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# set working directory to location of .csv file
library(RcmdrPlugin.MAd)



###################################################
### chunk number 16: compute_d
###################################################
#line 1620 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# to fit code on screen
```

```
options(width = 60)

# Sample data (for computing d & g)
n.1 <- 16
m.1 <- 9.6
sd.1 <- 4.82
n.2 <- 13
m.2 <- 12.3
sd.2 <- 6.79



###################################################
### chunk number 17: compute_d
###################################################
#line 1646 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)

# various ways to calculate effect sizes

# starting with standardized mean differences (Cohens d)
```

```
# one way is to calc "by hand" (Formula 12.12)
# s.within = pooled standard deviation of group 1 and 2
s.within <- sqrt(((16-1)*4.82^2+(13-1)*6.79^2)/(16+13-2))
s.within

# or similarly, using objects already created (also Formula 12.12)
s.within <- sqrt(((n.1-1)*sd.1^2+(n.2-1)*sd.2^2)/(n.1+n.2-2))
s.within

# For complex formulas, you may use several steps:
num <- (n.1-1)*sd.1^2+(n.2-1)*sd.2^2
denom <- n.1+n.2-2
s.within <- sqrt(num/denom)



###################################################
### chunk number 18: compute_d
###################################################
#line 1679 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
```

```
# std mean difference (control group st. dev)
d <-(m.1-m.2)/sd.2
d

# std mean difference (pooled)
d <-(m.1-m.2)/s.within    # (Formula 12.11)
d

# variance of d
var.d <-(n.1+n.2)/(n.1*n.2)+ (d^2)/(2*(n.1+n.2))     # (12.13)
var.d

# standard error of d
sqrt(var.d)                                            # (12.14)



###################################################
### chunk number 19: compute_g
###################################################
```

```
#line 1710 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
# used to calculate j
df <- (n.1+n.2)-2
df

# correction factor to biased d
j<-1-(3/(4*df-1))                                    # (12.15)
j

# unbiased std mean difference (Hedges g)
g <- j*d                                             # (12.16)
g

# variance of g
var.g <- j^2*var.d                                   # (12.17)
var.g



###################################################
### chunk number 20: function_d
```

```
###################################################
#line 1741 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
# Another option:  Write a function to automate this process;
# output all values simultaneously

# sample function to demonstrate the mechanics of defining
# and using functions.

my.mean <- function(x) {
  mean <- sum(x)/length(x)
  return(mean)
}

data <- 0:20

my.mean(x=data)     # or just my.mean(data)


###################################################
### chunk number 21: function_d
###################################################
```

```
#line 1770 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
# starting with mean differences
mean_to_d <- function(n1, m1, sd1, n2, m2, sd2) {
  s.within <- sqrt(((n1-1)*sd1^2+(n2-1)*sd2^2)/(n1+n2-2))
  d <- (m1-m2)/s.within
  var.d <- (n1+n2)/(n1*n2) + (d^2)/(2*(n1+n2))
  df <- (n1+n2)-2
  j <- 1-(3/(4*df-1))
  g <- j*d
  var.g <- j^2*var.d
  out <- cbind(s.within, d, var.d, df, j , g, var.g)
  return(out)
}

mean_to_d(n.1,m.1, sd.1, n.2, m.2, sd.2)



###################################################
### chunk number 22: vector_d
###################################################
```

```
#line 1800 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
# sample data of 20 studies
id <- c(1,1,1,2,2:20)
n.1 <- c(10,10,10,20,20,13,22,28,12,12,36,19,12,
36,75,33,121,37,14,40,16,14,20)
n.2 <- c(11,11,11,22,22,10,20,25,12,12,36,19,11,
34,75,33,120,37,14,40,16,10,21)
m.1 <- c(.68,.1,.3,.1,.56,.23,.64,.49,.4,1.49,
.53,.58,1.18,.11,1.27,.26,.40,.49,
         .51,.40,.34,.42,.66)
m.2 <- c(.38,.6,.3,.1,.36,.23,.34,.29,.4,1.9,
.33,.28,1.1,.111,.27,.21,.140,.149,
         .51,.140,.134,.42,.16)
sd.1 <- c(.28,.2,.2,.3,.26,.23,.44,.49,.34,.39,
.33,.58,.38,.31,.27,.26,.40,
          .49,.51,.140,.134,.42,.46)
sd.2 <- c(.28,.2,.2,.3,.26,.23,.44,.49,.44,.39,
.33,.58,.38,.51,.27,.26,.40,
          .49,.51,.140,.134,.142,.36)

dfs <- data.frame(id, n.1,m.1, sd.1,
```

```
n.2, m.2, sd.2)

# sample moderator data
id_mods <- 1:20
mod1 <- c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,
3,2,3,5,7,1)
mod2 <- factor(rep(c(1,2,3,4),5))

dfs_mods <- data.frame(id=id_mods, mod1, mod2)

# after aggregating sample ES data, then the meta-analyist can merge
# moderator and ES data, e.g., at the command line: merge(dfs, dfs_mods)


###################################################
### chunk number 23: vector_d
###################################################
#line 1846 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
# sample data of 20 studies (continued)

sd.2 <- c(.28,.2,.2,.3,.26,.23,.44,.49,.44,.39,
```

```
.33,.58,.38,.51,.27,.26,.40,
          .49,.51,.140,.134,.142,.36)

dfs <- data.frame(id, n.1,m.1, sd.1,
n.2, m.2, sd.2)

# sample moderator data
id_mods <- 1:20
mod1 <- c(1,2,3,4,1,2,8,7,5,3,9,7,5,4,
3,2,3,5,7,1)
mod2 <- factor(rep(c(1,2,3,4),5))

dfs_mods <- data.frame(id=id_mods, mod1, mod2)

# after aggregating sample ES data, then the meta-analyist can merge
# moderator and ES data, e.g., at the command line: merge(dfs, dfs_mods)


###################################################
### chunk number 24: vector_d
###################################################
#line 1880 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
```

```
options(width = 65)
# function in the ’MAd’ package for calculating a vector
# of ds and gs. Can either copy and paste function to use
# or install the MAd package [install.packages(’MAd’)], load
# it up [library(MAd)], and use the function w/o having to
# copy and paste. Also, you do not have to use ’with’ function
# to calculate values. Finally, there are 2 options:
# ’pooled.sd’ (pooled st dev) or ’control.sd’ (for control grp st dev)

# Example

# using same function we created for computing a vector of values
with(dfs, mean_to_d(n.1, m.1, sd.1, n.2, m.2, sd.2))


# or use function from MAd package
# load the package
library(MAd)

dfs <-compute_dgs(n.1, m.1, sd.1, n.2, m.2, sd.2,
            data = dfs, denom="pooled.sd")
```

```
###################################################
### chunk number 25: function
###################################################
#line 1917 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/


# The inner workings of the function

compute_dgs <- function(n.1, m.1, sd.1, n.2, m.2, sd.2, data,
                       denom = "pooled.sd") {
    call <- match.call()
    mf <- match.call(expand.dots = FALSE)
    args <- match(c("n.1", "m.1", "sd.1", "n.2", "m.2", "sd.2", "data"),
    names(mf), 0)
    mf <- mf[c(1, args)]
    mf$drop.unused.levels <- TRUE
    mf[[1]] <- as.name("model.frame")
    meta <- data
    mf.n.1 <- mf[[match("n.1", names(mf))]]
```

```
    n.1 <- eval(mf.n.1, data, enclos = sys.frame(sys.parent()))
    mf.m.1 <- mf[[match("m.1", names(mf))]]
    m.1 <- eval(mf.m.1, data, enclos = sys.frame(sys.parent()))
    mf.sd.1 <- mf[[match("sd.1", names(mf))]]
    sd.1 <- eval(mf.sd.1, data, enclos = sys.frame(sys.parent()))
    mf.n.2 <- mf[[match("n.2", names(mf))]]
    n.2 <- eval(mf.n.2, data, enclos = sys.frame(sys.parent()))
    mf.m.2 <- mf[[match("m.2", names(mf))]]
    m.2 <- eval(mf.m.2, data, enclos = sys.frame(sys.parent()))
    mf.sd.2 <- mf[[match("sd.2", names(mf))]]
    sd.2 <- eval(mf.sd.2, data, enclos = sys.frame(sys.parent()))
  if(denom == "pooled.sd"){
    meta$s.within <- sqrt(((n.1-1)*sd.1^2+
                      (n.2-1)*sd.2^2)/(n.1+n.2-2))# pooled.sd
    meta$d <-(m.1-m.2)/meta$s.within
    meta$var.d <- ((n.1+n.2)/(n.1*n.2))+
                  ((meta$d^2)/(2*(n.1+n.2)))
    df <- n.1+n.2-2
    j <- 1-(3/(4*df-1))
    meta$g <- j*meta$d
    meta$var.g <- j^2*meta$var.d
    meta$se.g <- sqrt(meta$var.g)
```

```
  }
  if(denom == "control.sd") {
    meta$d <-(m.1-m.2)/sd.2  # control.sd in denominator
    meta$var.d <- (n.1+n.2)/(n.1*n.2)+
                  (meta$d^2)/(2*(n.1+n.2))
    df <- n.1+n.2-2
    j <- 1-(3/(4*df-1))
    meta$g <- j*meta$d
    meta$var.g <- j^2*meta$var.d
    meta$se.g <- sqrt(meta$var.g)
  }
  return(meta)
}


###################################################
### chunk number 26: compute_es
###################################################
#line 2021 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# For example, suppose the primary study reported Ns and a t-test for diffe
```

```
# between 2 groups. Then, running:

t_to_d(1.5, 30, 30)

# reported t-test = 1.5 and N.1 = N.2 = 30 will output the
# standardized mean difference (d) and its variance (var.d) for use in
# the meta-analysis.

# to see the inner workings of the function
t_to_d



###################################################
### chunk number 27: compute_es
###################################################
#line 2044 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# Again, suppose the primary study reported Ns and a t-test for differences
# between 2 groups. This time using the compute.es package:

library(compute.es)
```

```
tes(1.5, 30, 30)

# reported t-test = 1.5 and N.1 = N.2 = 30 will output the
# standardized mean difference (d) and its variance (var.d) for use in
# the meta-analysis.


###################################################
### chunk number 28: compute_es
###################################################
#line 2067 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
library(compute.es)

# to see the inner workings of the function
tes



###################################################
### chunk number 29: aggregated
###################################################
#line 2178 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
```

```
library(MAd) # This package only needs to be loaded 1x in an Rsession

# using the sample data.frame

dfs2 <- agg(id = id, g = g, var = var.g, n.1 = n.1, n.2 =  n.2, cor = 0.5,
            data = dfs)
dfs <- merge(dfs2, dfs_mods)

# to see the first few rows [head()] of the merged data.frame with mods and
head(dfs)



###################################################
### chunk number 30: FE_graph
###################################################
#line 2307 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# Courtest of William T. Hoyt, PhD
# Plots to recreate Fig 11.2 and Fig 12.3
# (fixed and random effects illustrations)
# in Borenstein et al. (2009)
```

```
library(shape)  # (for nicer arrowheads)
par(mfrow=c(2,1))

# Top plot = true effects only
plot.new()
plot.window(xlim=c(-0.05,1.2), ylim=c(-0.9,2.6))
axis(side=1, at=seq(0,1.2, by=0.1), cex.axis=0.8)
points(x=rep(0.6, 3), y=0:2, pch=19, cex=c(2, 1.5, 1.5))
points(x=0.6, y=-0.7, pch=25, cex=2, bg="black")
lines(x=c(0.6, 0.6), y=c(-0.55, 2))
text(x=rep(0,3), y=2:0, labels=c("Study 1", "Study 2", "Study 3"))
mtext("True effect sizes for three studies, fixed effect model",
      side=1, line=3, at=-0.06, adj=0, cex=0.85)


# Bottom plot = observed effect sizes
plot.new()
plot.window(xlim=c(-0.05,1.2), ylim=c(-0.9,2.6))
axis(side=1, at=seq(0,1.2, by=0.1), cex.axis=0.8)
points(x=rep(0.6, 3), y=0:2, pch=19, cex=c(2, 1.5, 1.5))
points(x=0.6, y=-0.7, pch=25, cex=2, bg="black")
lines(x=c(0.6, 0.6), y=c(-0.55, 2))
```

```
text(x=rep(0,3), y=2:0, labels=c("Study 1", "Study 2", "Study 3"))
mtext("Observed effect sizes for three studies, fixed effect model",
      side=1, line=3, at=-0.06, adj=0, cex=0.85)

points(x=c(0.4, 0.7, 0.5), y=2:0, pch=15, cex=c(1.5, 1.5, 2))

Arrows(x0=rep(0.6,3), y0=2:0, x1=c(0.42, 0.68, 0.52), y1=2:0,
       arr.type="curved", arr.length=0.3)

# Sampling distr's
x <- seq(-0.2, 0.2, by=.001)
lines(x+0.6, dnorm(x, 0, 0.1)/6 + 2)
lines(x+0.6, dnorm(x, 0, 0.1)/6 + 1)
lines(x+0.6, dnorm(x, 0, 0.06)/9 + 0)  # Study 3 large N



###################################################
### chunk number 31: RE_graph
###################################################
#line 2389 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
# Courtest of William T. Hoyt, PhD
```

```
# Plots to recreate Fig 11.2 and Fig 12.3
# (fixed and random effects illustrations)
# in Borenstein et al. (2009)

# library(shape)  # (for nicer arrowheads)
par(mfrow=c(2,1))

# Top plot = true effects only
plot.new()
plot.window(xlim=c(-0.05,1.2), ylim=c(-0.9,2.6))
axis(side=1, at=seq(0,1.2, by=0.1), cex.axis=0.8)
points(x=c(0.65, 0.8, 0.4), y=2:0, pch=19, cex=c(1.5, 1.5, 2))
points(x=0.6, y=-0.7, pch=25, cex=2, bg="black")
abline(v=0.6, lty=2)

x <- seq(-0.2, 0.2, by=.001)
lines(x+0.60, dnorm(x, 0, 0.1)/6 - 1) # Thetas have sampl distr

text(x=rep(0,3), y=2:0, labels=c("Study 1", "Study 2", "Study 3"))
mtext("True effect sizes for three studies, random effects model",
      side=1, line=3, at=-0.06, adj=0, cex=0.85)
```

```
# Bottom plot = observed effect sizes
plot.new()
plot.window(xlim=c(-0.05,1.2), ylim=c(-0.9,2.6))
axis(side=1, at=seq(0,1.2, by=0.1), cex.axis=0.8)
points(x=c(0.65, 0.8, 0.4), y=2:0, pch=19, cex=c(1.5, 1.5, 2))
points(x=0.6, y=-0.7, pch=25, cex=2, bg="black")
abline(v=0.6, lty=2)
text(x=rep(0,3), y=2:0, labels=c("Study 1", "Study 2", "Study 3"))
mtext("Observed effect sizes for three studies, random effects model",
      side=1, line=3, at=-0.06, adj=0, cex=0.85)

points(x=c(0.4, 0.7, 0.5), y=2:0, pch=15, cex=c(1.5, 1.5, 2))

Arrows(x0=c(0.65, 0.8, 0.4), y0=2:0, x1=c(0.42, 0.72, 0.48), y1=2:0,
       arr.type="curved", arr.length=0.3)

# Sampling distr's
x <- seq(-0.2, 0.2, by=.001)
lines(x+0.65, dnorm(x, 0, 0.1)/6 + 2)
lines(x+0.8, dnorm(x, 0, 0.1)/6 + 1)
lines(x+0.4, dnorm(x, 0, 0.06)/9 + 0)  # Study 3 large N
```

```
lines(x+0.60, dnorm(x, 0, 0.1)/6 - 1) # Thetas have sampl distr



###################################################
### chunk number 32: g.dfd
###################################################
#line 2596 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)

# import ES data
# (Note: this is a cleaned up dataset with 1 ES per study and moderators
# already merged):
g.dfd <- read.csv('grief2.csv', header=TRUE, na.strings= "")

names(g.dfd)



###################################################
### chunk number 33: g.dfd
###################################################
#line 2617 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
```

```
options(width = 65)

# examine the data structure
str(g.dfd)

# risk needs to have reference level as "normal"
g.dfd$risk <-relevel(g.dfd$risk, ref="normal")


###################################################
### chunk number 34: grief_omnibus
###################################################
#line 2647 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 65)

# load meta-analysis package:
library(MAd)

# omnibus analysis with grief data.frame
# The formula: del ˜ 1 with the ’del’ value to the left being the
# criterion variable (del = mean diff effect size) predicted
# by (’˜’) 1 (which indicates intercept).
```

```
# the argument’var’ is calling for the variance of del and the
# method ’REML’ =  restricted maximum likelihood (random effects) and
# g.dfd = grief data.frame

omn.1 <- mareg(del ~ 1, var = var.del, method = "REML", data = g.dfd)

# lets examine the output object ’omn.1’
summary(omn.1)


###################################################
### chunk number 35: omni_hetero
###################################################
#line 2687 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# lets examine tau^2 and I^2 for ’omn.1’
omn.1$I2  #notice no summary command around the model object
summary(omn.1)$tau2



###################################################
```

```
### chunk number 36: omni_coef
###################################################
#line 2709 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)

# lets examine the coefficients  for ’omn.1’
summary(omn.1)$coef


###################################################
### chunk number 37: omni_hetero
###################################################
#line 2731 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# lets examine  model fit for ’omn.1’

summary(omn.1)$fit


###################################################
### chunk number 38: es_bar
###################################################
```

```
#line 2757 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# # using base graphics
# #produces bar graph of omni ESs (Courtesy of William Hoyt, PhD)
#
# ht=c(0.83, 0.26, 0.64, 0.15, 0.53, 0.25)
# barplot(height=ht, space=rep(c(1,0),3), ylim=c(0,1),
#         xlim=c(0,10),main="Omnibus analysis",
#         col=rep(c(rgb(0,0.75,0.7, alpha=0.5),"gray"),3),
#         names.arg=rep(c("T","C"),3), ylab="Effect size" )
#
# text(x=c(1.5,2.5,4.5,5.5,7.5,8.5), y=0.03+ht,
#      labels=as.character(ht), cex=0.7)
# mtext(text=c("Grief","Depr","Anx"),side=1,
#       line=0, at=c(2,5,8),)
# text(x=c(3,6,9), y=c(1.09/2, 0.79/2, 0.78/2),
#      labels=c("D=0.57","D=0.49","D=0.28"),
#      font=c(5), col="blue")


# or using ggplot2:
# # es g for each grp and dv
```

```
d <- c(.83,.26,.64,.15,.53,.25)
se <- c(0.0867,0.066,0.064, 0.102, 0.061,0.076)
Group <- rep(c("Treatment", "Control"), 3)
dv <-c("Grief", "Grief","Depression", "Depression","Anxiety",
       "Anxiety")
df <- data.frame(d, dv,Group)
df$se <- se

library(ggplot2)

# set the CI limits for plot:
limits <- aes(ymax = d + 1.96*se, ymin=d - 1.96*se)

p <- ggplot(data=df, aes(x=Group,y=d, fill=Group )) +
    ylab("Effect size")+
    opts(title=expression("Grief treatment and control effect sizes "*delta
    plot.title=theme_text(size=17.5,face="bold"))+ #
    geom_bar( stat="identity")+
    facet_grid(.~ dv)+
    geom_text(aes(label=d))+
    geom_errorbar(limits, width=0.25, color=’brown’, alpha=.3)
```

```
show(p)


###################################################
### chunk number 39: mod_risk
###################################################
#line 2836 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 70)

# single predictor moderator analyses (categorical variable) with grief dat

mod.risk <- macat(del,  var=var.del,  mod=risk, data=g.dfd,method='random')


mod.risk



###################################################
### chunk number 40: mod_risk
###################################################
#line 2866 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
```

```
options(width = 65)

# lets examine the model fit  for 'mod.risk'
mod.risk$Model



###################################################
### chunk number 41: mod_risk_hetero
###################################################
#line 2889 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# lets examine  model fit for 'omn.1'

mod.risk$Hetero



###################################################
### chunk number 42: barplot_cat
###################################################
#line 2912 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
```

```
# # es g for each grp and dv
d <- c(.57,.22,.92)
se <- c(0.102,0.112,0.137)
Risk <- c("Normal","At-Risk", "Complicated")

df <- data.frame(d,se, Risk)

library(ggplot2)

# set the CI limits for plot:
limits <- aes(ymax = d + 1.96*se, ymin=d - 1.96*se)

p2 <- ggplot(data=df, aes(x=Risk,y=d, fill=Risk )) +
    ylab("Effect size")+
    opts(title=expression(""*Delta*" for each level of Risk moderator"),
    plot.title=theme_text(size=17.5,face="bold"))+ #
    geom_bar( stat="identity")+
    geom_text(aes(label=d))+
    geom_errorbar(limits, width=0.25, color=’brown’, alpha=.3)

show(p2)
```

```
###################################################
### chunk number 43: boxplot_cat
###################################################
#line 2942 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

#function to add mean to boxplot
stat_sum_single <- function(fun, geom="point", weight=1/var.del,...) {
stat_summary(fun.y=fun, shape="+", geom=geom, size = 3, ...)
}
# boxplots of risk levels
q<-ggplot(g.dfd, aes(factor(risk), color=risk, del,weight=1/var.del))
qq<-q+geom_boxplot(outlier.size=1)+
geom_jitter(aes(shape=risk,size=1/var.del),alpha=.5)+
scale_x_discrete("risk",labels=c("Normal","At-risk","Complicated"),
breaks=c("normal","at-risk","complicated"))+
ylab(expression(Delta["+"]))+
opts(legend.position = "none")+
ylim(-0.25,1.5)+
stat_sum_single(mean)
```

```
show(qq)


###################################################
### chunk number 44: mod_sess_coef
###################################################
#line 2979 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 65)

#

# single predictor moderator analyses with grief data.frame
# The formula: del ~ mod with the ’del’ value to the left being the
# criterion variable (del = mean diff effect size) predicted
# by (’~’)  (which indicates the modderator variable risk).
# the argument’var’ is calling for the variance of del and the
# method ’REML’ =  restricted maximum likelihood (random effects) and
# g.dfd = grief data.frame

mod.sess <- mareg(del~n.sess,  var=var.del,  data=g.dfd,method=’REML’)

# model coefficients, or to see both coefficients and fits stats use
```

```
# just summary(mod.sess)
summary(mod.sess)$coef


###################################################
### chunk number 45: mod_sess_fit
###################################################
#line 3004 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 65)

# model fit, or to see both coefficients and fits stats use
# just summary(mod.sess)
summary(mod.sess)$fit




###################################################
### chunk number 46: scatter_con
###################################################
#line 3017 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# scatter for n sess
```

```
p<-qplot(n.sess,del,data=g.dfd, weight=1/var.del,size=1/var.del,
  geom="jitter", color=n.sess)
pp<-p + geom_smooth(aes(group=1),method = lm, se = F)+
xlab("Sessions")+
ylab(expression(Delta["+"]))+
scale_size(to = c(4, 10), legend=F)+
opts(title=expression("Treatment duration as predictor of study effect size
plot.title=theme_text(size=15.5,face="bold"),
axis.title.y=theme_text(size=19))
pp
show(pp)


###################################################
### chunk number 47: confounding
###################################################
#line 3051 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# confounding among moderator variables?
r<-ggplot(g.dfd, aes(factor(risk), color=risk,n.sess))
rr<-r+geom_boxplot(outlier.size=1)+
geom_jitter(aes(shape=risk,size=1/var.del),solid=TRUE,alpha=.5)+
```

```
scale_x_discrete("Risk",labels=c("Normal","At-risk","Complicated"),
breaks=c("normal","at-risk","complicated"))+
ylab("Sessions")+
opts(legend.position = "none",
axis.title.y=theme_text(angle=90),
axis.title.x = theme_blank())+
stat_sum_single(mean)

show(rr)



###################################################
### chunk number 48: multipred_coef
###################################################
#line 3082 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 65)

# multi-predictor moderator analyses with grief data.frame
# The formula: del ~ mod with the 'del' value to the left being the
# criterion variable (del = mean diff effect size) predicted
# by ('~')  (which indicates the moderator variables risk, n.sess, and % fe
# the argument'var' is calling for the variance of del and the
```

```
# method ’REML’ =  restricted maximum likelihood (random effects) and
# g.dfd = grief data.frame

mod.multi <- mareg(del˜risk+n.sess+female,  var=var.del,  data=g.dfd,method

# model coefficients, or to see both coefficients and fits stats use
# just summary(mod.sess)
summary(mod.multi)$coef


###################################################
### chunk number 49: multipred_fit
###################################################
#line 3105 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 65)

# model fit, or to see both coefficients and fits stats use
# just summary(mod.multi)
summary(mod.multi)$fit
```

```
###################################################
### chunk number 50: multipred_plot
###################################################
#line 3119 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# rename risk for plotting purposes
g.dfd$Risk <- g.dfd$risk
levels(g.dfd$Risk)<- c("Normal", "At-risk",  "Complicated")

# multi-predictor graph
p<-qplot(n.sess,del,data=g.dfd, weight=1/var.del,size=1/var.del,shape=facto
color=Risk,  geom="jitter", alpha = I(0.62))
pp<-p + geom_smooth(aes(group=1),method = lm, se = F)+
scale_discrete(aes(color=risk),name="Risk Level", breaks = c("normal",
"at-risk", "complicated"), labels = c("Normal", "At-risk",  "Complicated"),
legend=F)+
xlab("Sessions")+
ylab(expression(Delta["+"]))+
scale_shape(solid = T, name="Risk",
breaks = c("normal", "at-risk", "complicated"), labels = c("Normal", "At-ri
"Complicated"))+
scale_size(to = c(4, 10), legend=F)+
```

```
opts(title=expression("Treatment duration & risk status as joint predictors
plot.title=theme_text(size=13.5,face="bold"))+
ylim(-2.25, 3.9)+
xlim(2,28)

#function to add mean to boxplot
stat_sum_single <- function(fun, geom="point", weight=1/var.del,...) {
stat_summary(fun.y=fun, shape="+", geom=geom, size = 3, ...)
}

#subplot 1
q<-ggplot(g.dfd, aes(factor(risk), color=risk, del,weight=1/var.del))
qq<-q+geom_boxplot(outlier.size=1)+
geom_jitter(aes(shape=risk,size=1/var.del),alpha=.3)+
theme_bw()+
scale_x_discrete("risk",labels=c("Normal","At-risk","Complicated"),
breaks=c("normal","at-risk","complicated"))+
ylab(expression(Delta["+"]))+
opts(legend.position = "none", title="(b)",
axis.text.y=theme_text(size=6),
axis.title.y=theme_text(size=7, vjust=.6,angle=90),
axis.title.x = theme_blank(),
```

```
axis.text.x=theme_text(size=6,vjust=1))+
stat_sum_single(mean)+
scale_size(to = c(1.2, 2.7))

#subplot 2
r<-ggplot(g.dfd, aes(factor(risk), color=risk,n.sess))
rr<-r+geom_boxplot(outlier.size=1)+
geom_jitter(aes(shape=risk,size=1/var.del),solid=TRUE,alpha=.3)+
theme_bw()+
scale_x_discrete("Risk",labels=c("Normal","At-risk","Complicated"),
breaks=c("normal","at-risk","complicated"))+
ylab("Sessions")+
opts(legend.position = "none", title="(a)",
axis.text.y=theme_text(size=6),
axis.title.y=theme_text(size=7,vjust=.6,angle=90),
axis.title.x = theme_blank(),
axis.text.x=theme_text(size=6,vjust=1))+
stat_sum_single(mean)+
scale_size(to = c(1.2, 2.7))


#graphing plots!
```

```
subvp <- viewport(width = 0.25, height = 0.4,  x = 0.764377, y = 0.27)
subvp2 <- viewport(width = 0.25, height = 0.4,  x = 0.537, y = 0.27)

show(pp)
print(qq, vp = subvp)
print(rr,vp=subvp2)



###################################################
### chunk number 51: forest_plot
###################################################
#line 3215 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/

# This function was created by W. Viechtbauer
forest(omn.1)  # recall omn.1 is the omnibus analysis


###################################################
### chunk number 52: forest_custom
###################################################
#line 3238 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
```

```
# This function was created by W. Viechtbauer

forest(omn.1, slab=paste(g.dfd$id))
text(-8.6, 47.4, "Study ID",    pos=4, cex=.9)
text( 11, 47.4, "Effect Size [95% CI]", pos=4, cex=.9)


###################################################
### chunk number 53: SessionInformtaion
###################################################
#line 3255 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
toLatex(sessionInfo())


###################################################
### chunk number 54: SourceCode
###################################################
#line 3261 "C:/Users/AC Del Re/Desktop/AC/presentations/2011-9-13_wkshp_ma/
options(width = 60)
Stangle(file.path("C:\\Users\\AC Del Re\\Desktop\\AC\\presentations\\2011-9
```

```
SourceCode <- readLines(file.path("C:\\Users\\AC Del Re\\Desktop\\AC\\prese
writeLines(SourceCode)
```