

Meta-Analytic Visualizations

15 April 2020

Modern Research Methods

Logistics

- Complete coding of 5 papers by Friday at 5pm
- I have office hours today and Friday (10:30-12:30)
- Sign up on spreadsheet on website for a slot
- No class Friday

INSTRUCTOR

 Dr. Molly Lewis

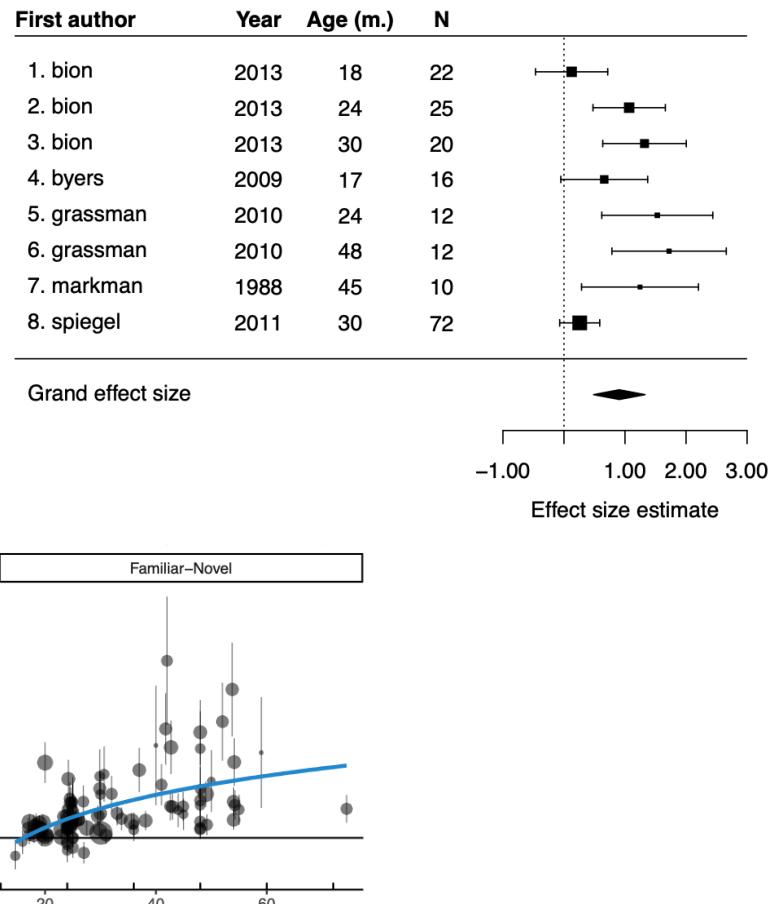
 mollylewis@cmu.edu

 **ZOOM OFFICE**

 Office Hours: W 4:30-6:30pm

 Signup: [signup sheet](#)

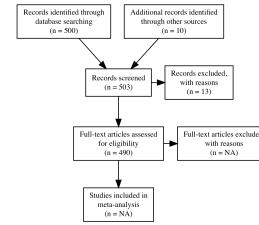
Conducting a Meta-analysis



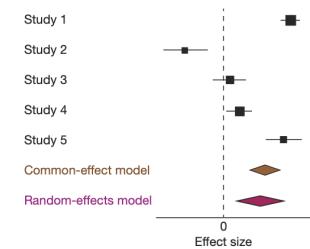
1. Identify Topic
2. Conduct literature search
3. Code studies and calculate ES
4. Plot and analyze data
5. Report and discuss results

Four meta-analytic visualizations

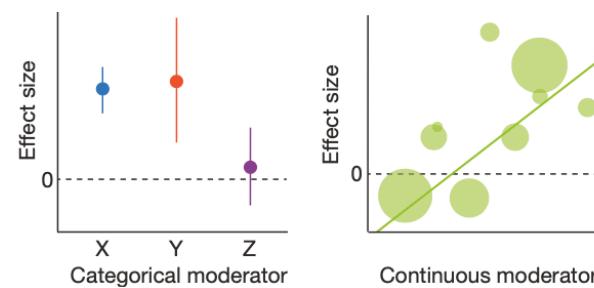
1. PRISMA flow diagram



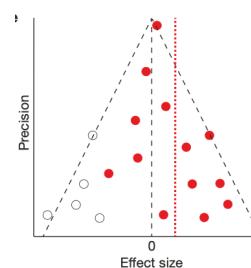
2. Forest plot



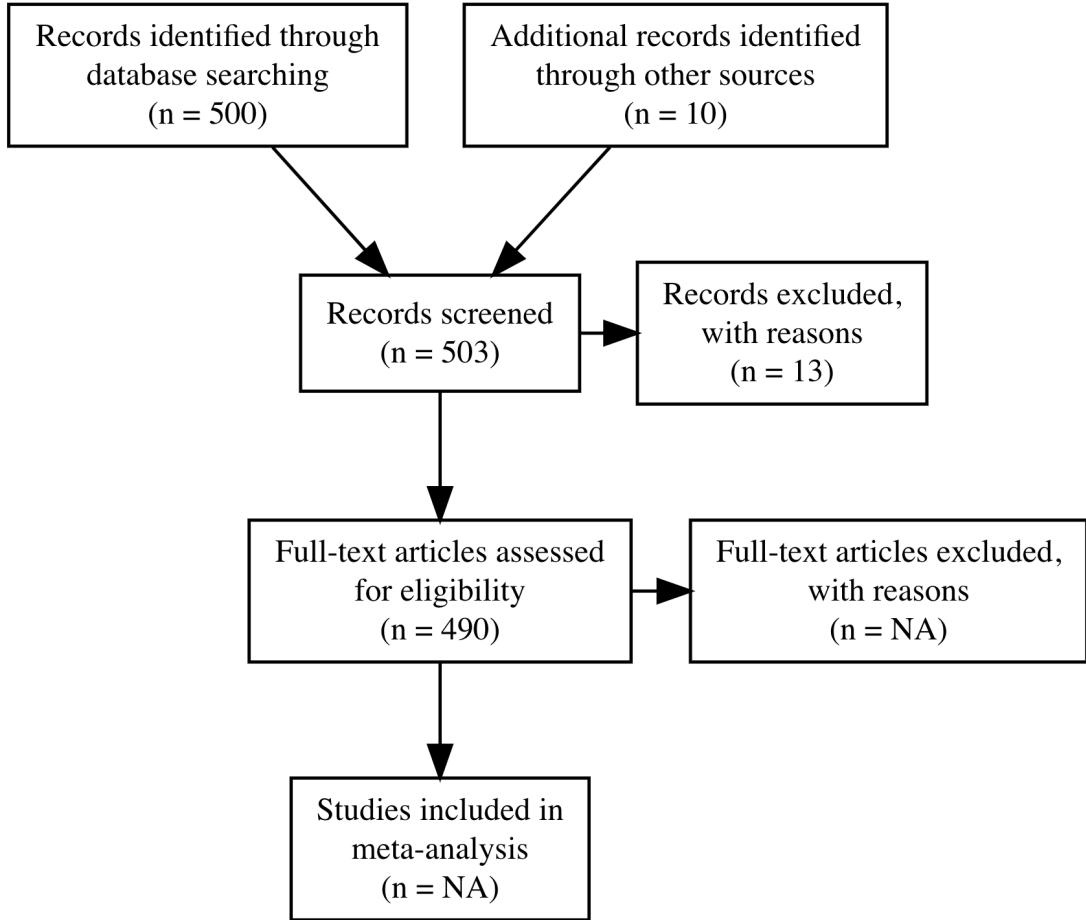
3. Moderator plots



4. Funnel plot



PRISMA flow diagram

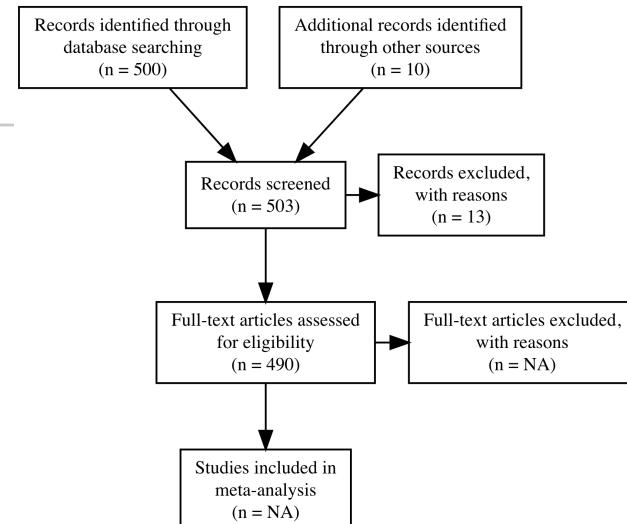


- Questions addressed:
 - What is the scope of the literature on topic X?
 - What was your method for identifying papers for a meta-analysis on topic X?
- Standardized diagram for reporting paper selection process for meta-analytic review
- Describes 4 stages: Identification, Screening, Eligibility, Excluded

Making your own PRISMA diagram

```
my_prisma_plot <- prisma2(found = 500, # how many unique papers did you find through database searches (good)
  found_other = 10, # how many papers did you find through other sources?
  screened = 503, # how many of those papers did you screen by looking at the title/abstract?
  screen_exclusions = 400, # how many of those papers that you screened did you exclude?
  full_text = 103, # how many papers did you look at the full text for?
  full_text_exclusions = NA, # how many papers did you exclude after looking at the full text?
  quantitative = NA, # how many papers went in your final meta-analysis
  width = 800, height = 800)

my_prisma_plot
```



Forest Plots

Study 1

Study 2

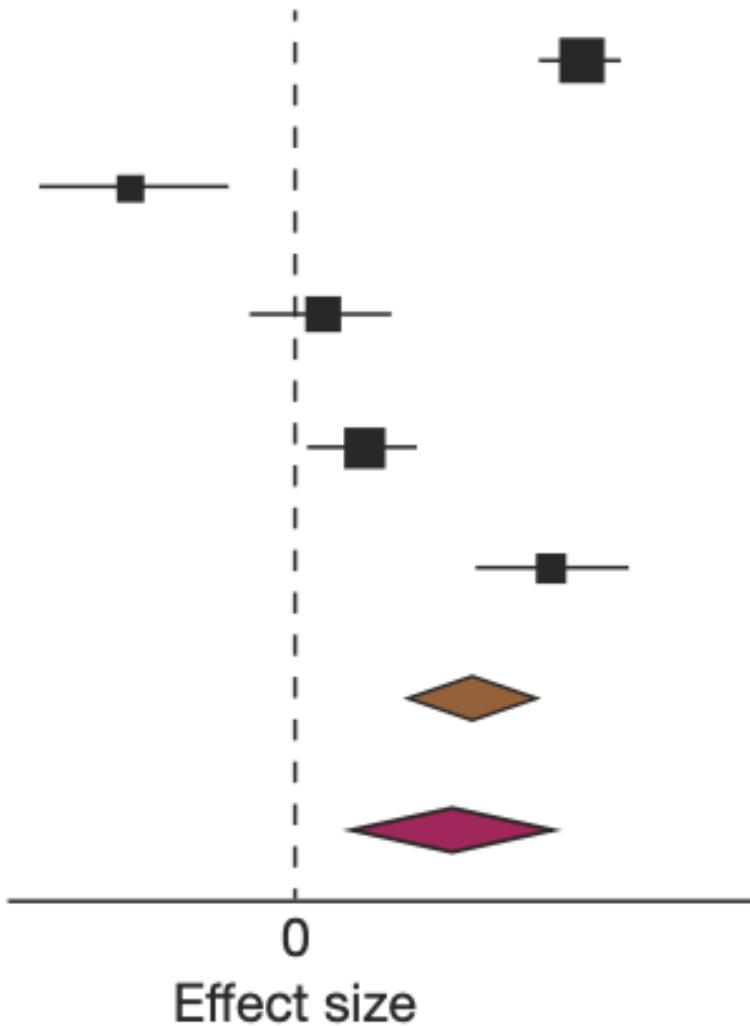
Study 3

Study 4

Study 5

Common-effect model

Random-effects model



- Point = study
- Size of square = weight
- Length 'arms' = individual confidence intervals (uncertainty)
- Diamond = weighted mean
- Dashed line = ES of 0
- If diamond overlap with dashed line the overall effect sizes does not differ from zero

(Text adapted from slide from A. Cristia;
Fig. from Gurevitch et al, 2018)

Forest Plots: Questions addressed

1. What is the overall effect size for phenomenon X?
 - Because this estimate reflects data from many more participants than a single study, it should be more accurate than the effect size from a single study.
 - How big is this effect relative to other effects in psychology?
2. Does the effect significantly differ from zero?
 - If it does not, this suggest there may be no effect (even though individual studies may show an effect).
3. How much variability is there?
 - Are the effects of individual studies roughly the same, or is there a lot of variability?
 - If there's a lot of variability, this suggests there might be an important moderator

We'll calculate these two columns once you have all the raw data entered for your MA

ma_data for mutual exclusivity MA

study_ID	short_cite	expt_num	n	d_calc	d_var_calc	mean_age	response_mode
bedford2013	Beford et al (2013)	1	31	4.0000000	0.2903226	748.7471	behavior
bedford2013	Beford et al (2013)	1	31	3.0000000	0.1774194	739.6161	behavior
beverly2003	Beverly & Estis (2003)	1	5	2.5862069	0.8688466	1765.3390	behavior
beverly2003	Beverly & Estis (2003)	1	5	4.5000000	2.2250000	1795.7760	behavior
beverly2003	Beverly & Estis (2003)	1	5	4.8780488	2.5795360	1217.4750	behavior
bion2013	Bion, Borovsky, & Fernald (2013)	2	22	0.1428571	0.0459184	547.5600	eye-tracking
bion2013	Bion, Borovsky, & Fernald (2013)	2	25	1.1538462	0.0666272	730.0800	eye-tracking
bion2013	Bion, Borovsky, & Fernald (2013)	2	20	1.2857143	0.0913265	912.6000	eye-tracking
byers2009	Byers-Heinlein & Werker (2009)	1	16	0.4210526	0.0680402	517.4270	eye-tracking
byers2009	Byers-Heinlein & Werker (2009)	1	16	-0.1250000	0.0629883	547.8638	eye-tracking

N = 50 effect sizes

Making your own forest plot

- To make a forest plot, we need to calculate the grand mean (pooled effect size estimate)
- To do that, we use a package called *metafor* in R
- The `rma()` function fits a model that estimates the grand mean effect size taking into account study size
- It's actually a random effect model – happy to talk more about the details offline
- The syntax:
`model <- rma(effect_size, effect_size_variances)`

Fitting the meta-analytic model

study_ID	short_cite	expt_num	n	d_calc	d_var_calc	mean_age	response_mode
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```
ma_model <- rma(ma_data$d_calc, ma_data$d_var_calc)  
ma_model
```

```
##  
## Random-Effects Model (k = 50; tau^2 estimator: REML)  
##  
## tau^2 (estimated amount of total heterogeneity): 1.2903 (SE = 0.3021)  
## tau (square root of estimated tau^2 value): 1.1359  
## I^2 (total heterogeneity / total variability): 92.95%  
## H^2 (total variability / sampling variability): 14.19  
##  
## Test for Heterogeneity:  
## Q(df = 49) = 340.9223, p-val < .0001  
##  
## Model Results:  
##  
## estimate se zval pval ci.lb ci.upper ***  
## 1.4065 0.1748 8.0452 <.0001 1.0638 1.7491 ***  
## ---  
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Grand meta-analytic effect size

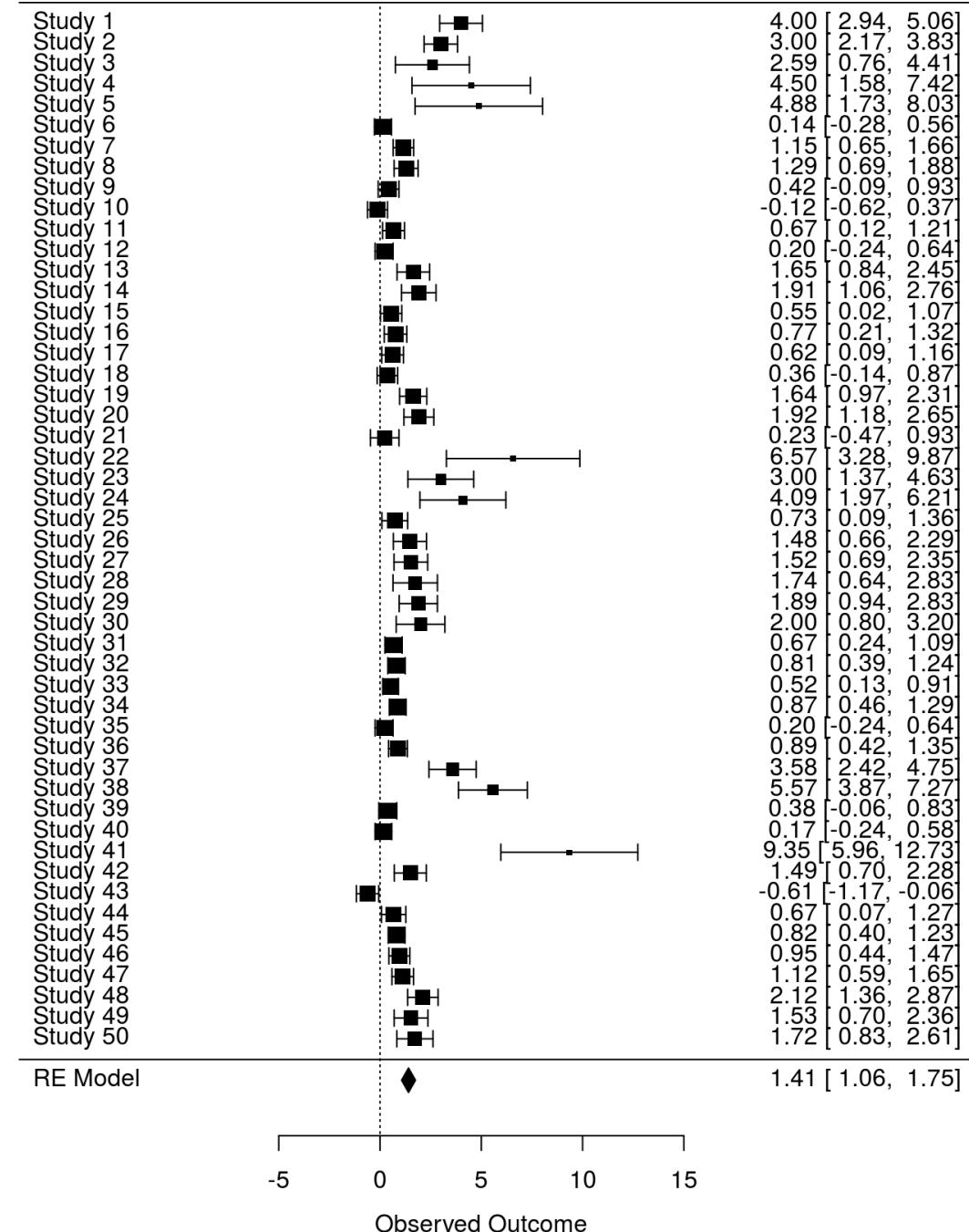
Is the grand effect size significantly different from zero?

Grand meta-analytic effect size confidence interval

Making the forest plot

Use a function in metafor to make forest plot (unfortunately there doesn't exist a good forest plot ggplot function (yet!)

```
forest(ma_model)
```

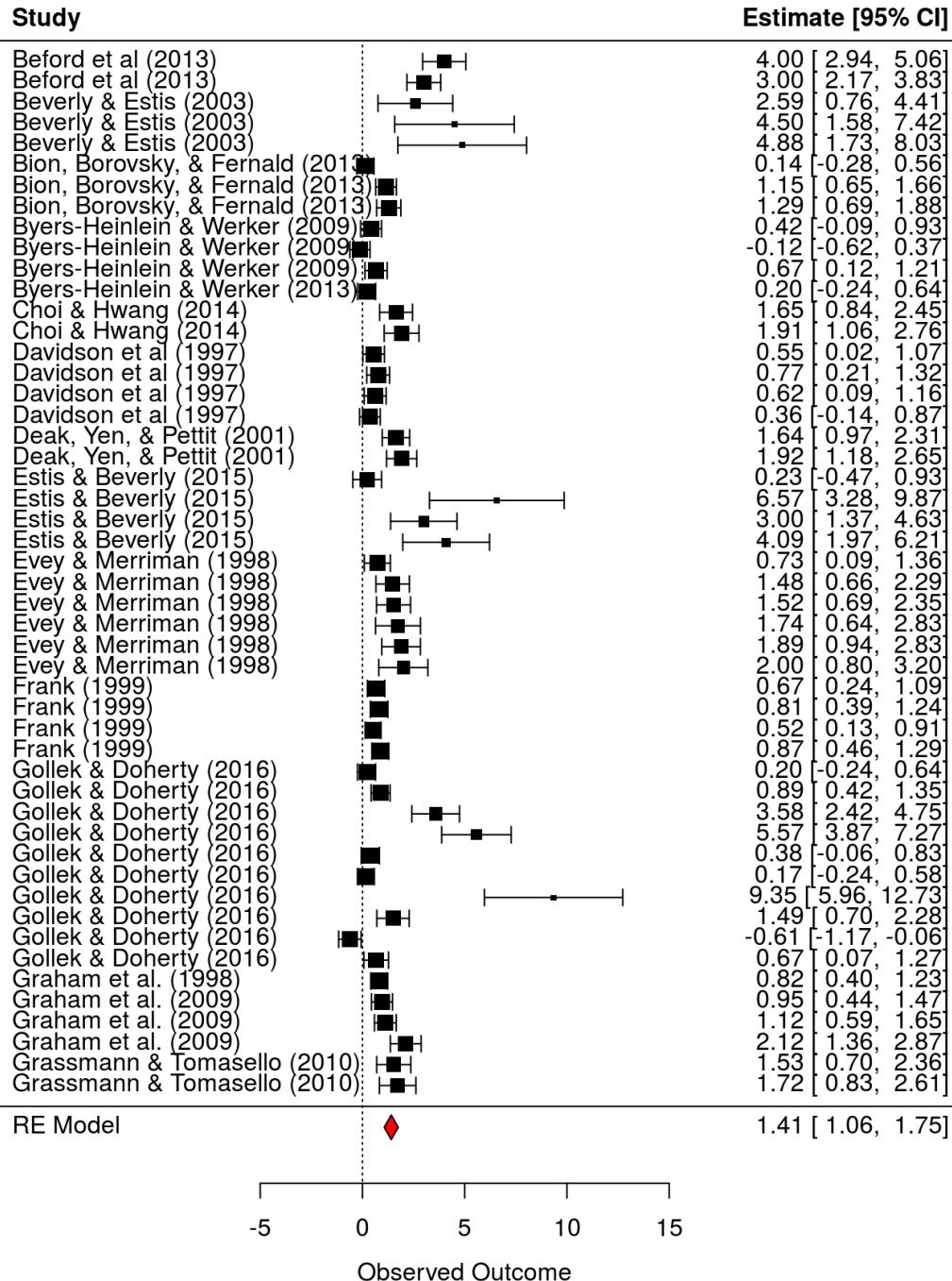


Making a better forest plot

```
forest(ma_model,  
       header = T,  
       slab = ma_data$short_cite,  
       col = "red")
```

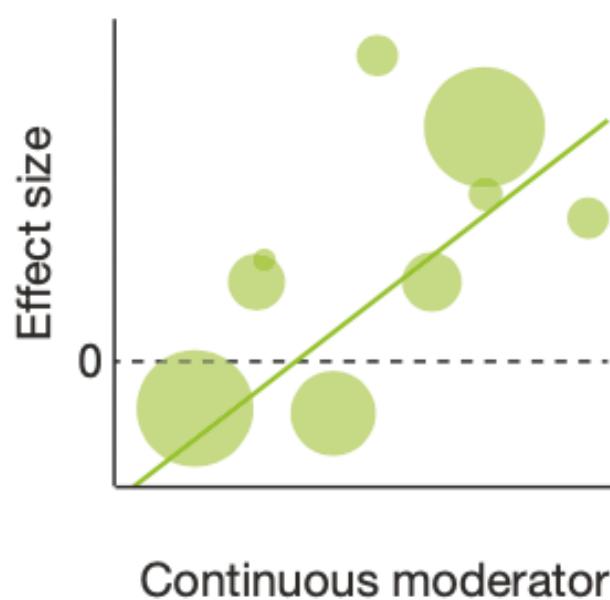
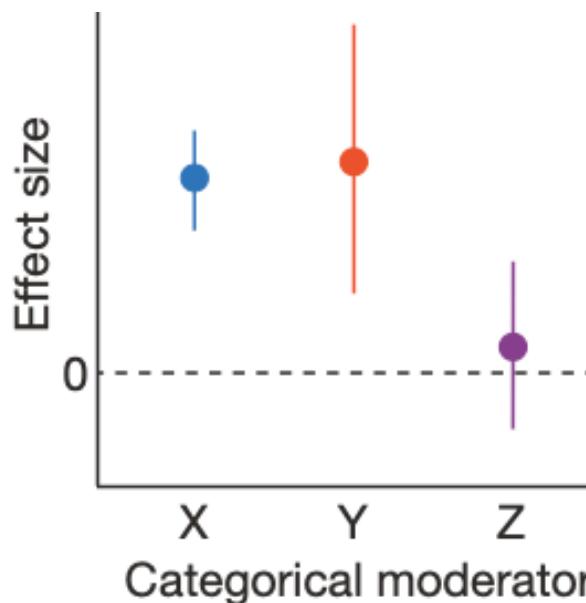
There are lots of modifications you can make to this plot to make it more informative.

You can see all the options here:
<https://www.rdocumentation.org/packages/metafor VERSIONS 2.4-0/topics/forest.rma>.



Moderator plots

- Question addressed: Does the effect size vary by different features of the experiment?
- Two kinds of moderators: Categorical and Continuous



(Fig. from Gurevitch et al, 2018)

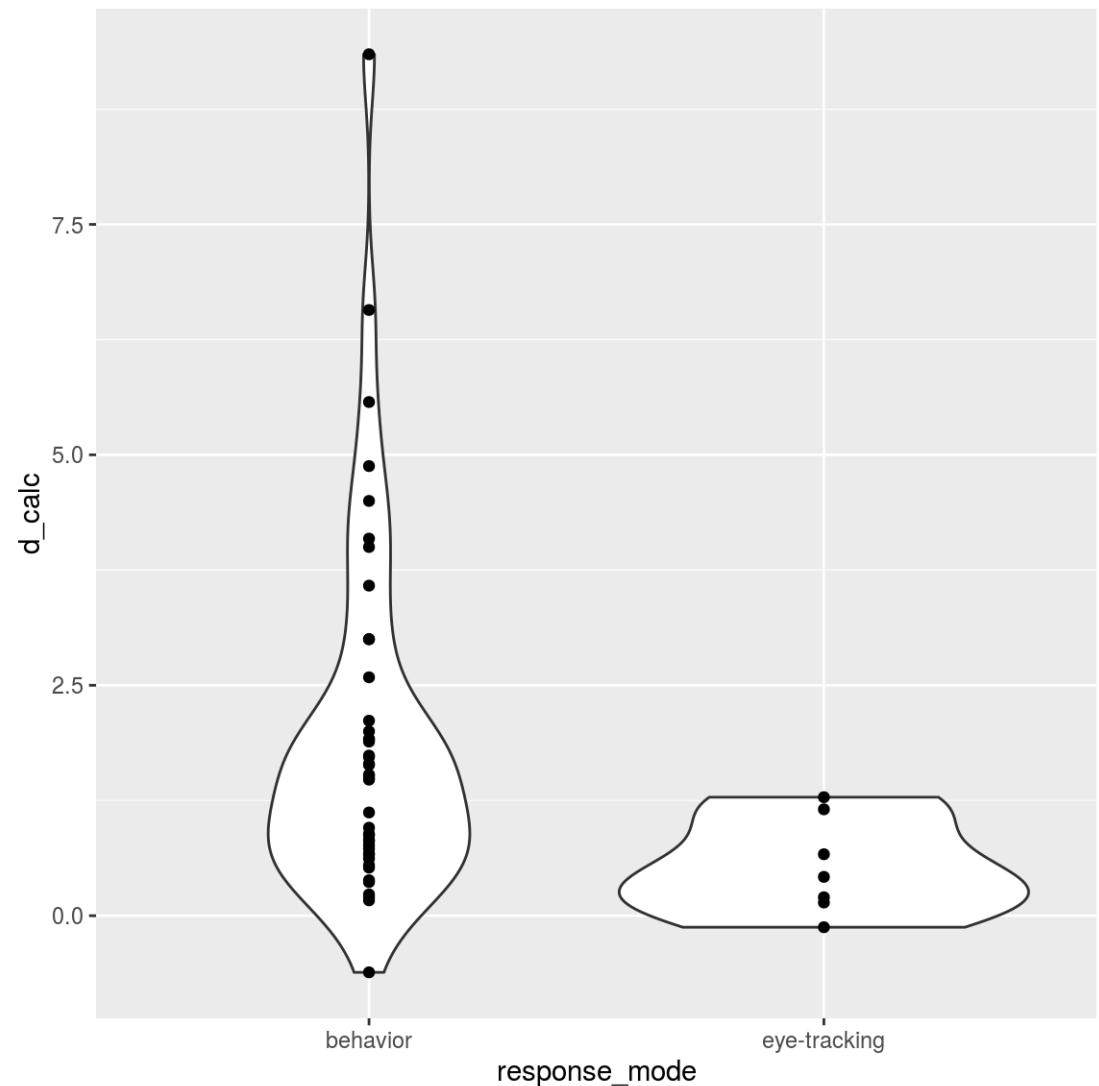
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N = 50 effect sizes

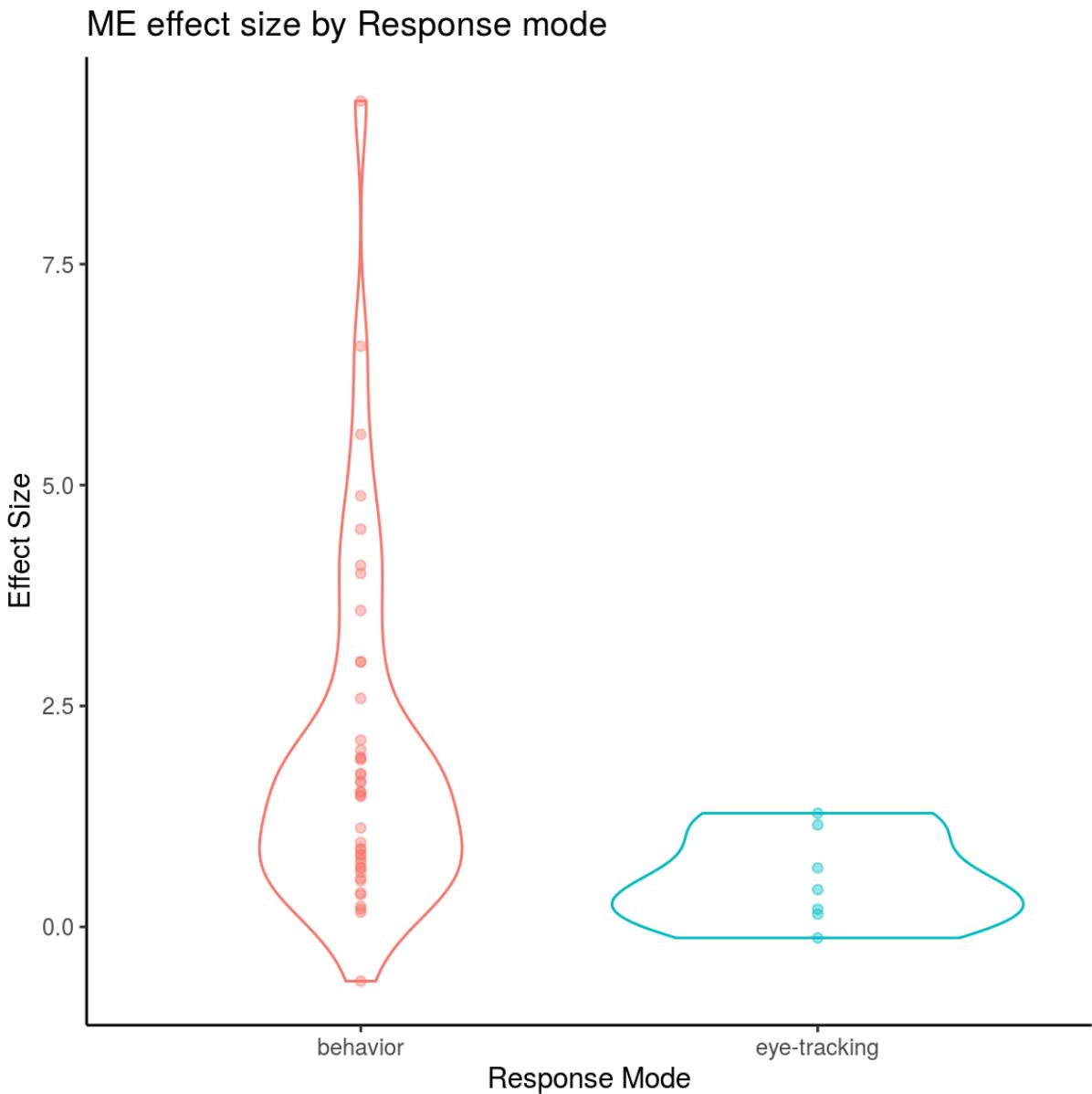
Making a categorical moderator plot

```
ggplot(ma_data, aes(x = response_mode, y = d_calc)) +  
  geom_violin() +  
  geom_point()
```



Making a better categorical moderator plot

```
ggplot(ma_data, aes(x = response_mode,  
                    y = d_calc,  
                    color = response_mode)) +  
  geom_violin() +  
  geom_point(alpha = .4) +  
  ylab("Effect Size") +  
  xlab("Response Mode") +  
  ggtitle("ME effect size by Response mode") +  
  theme_classic() +  
  theme(legend.position = "none")
```

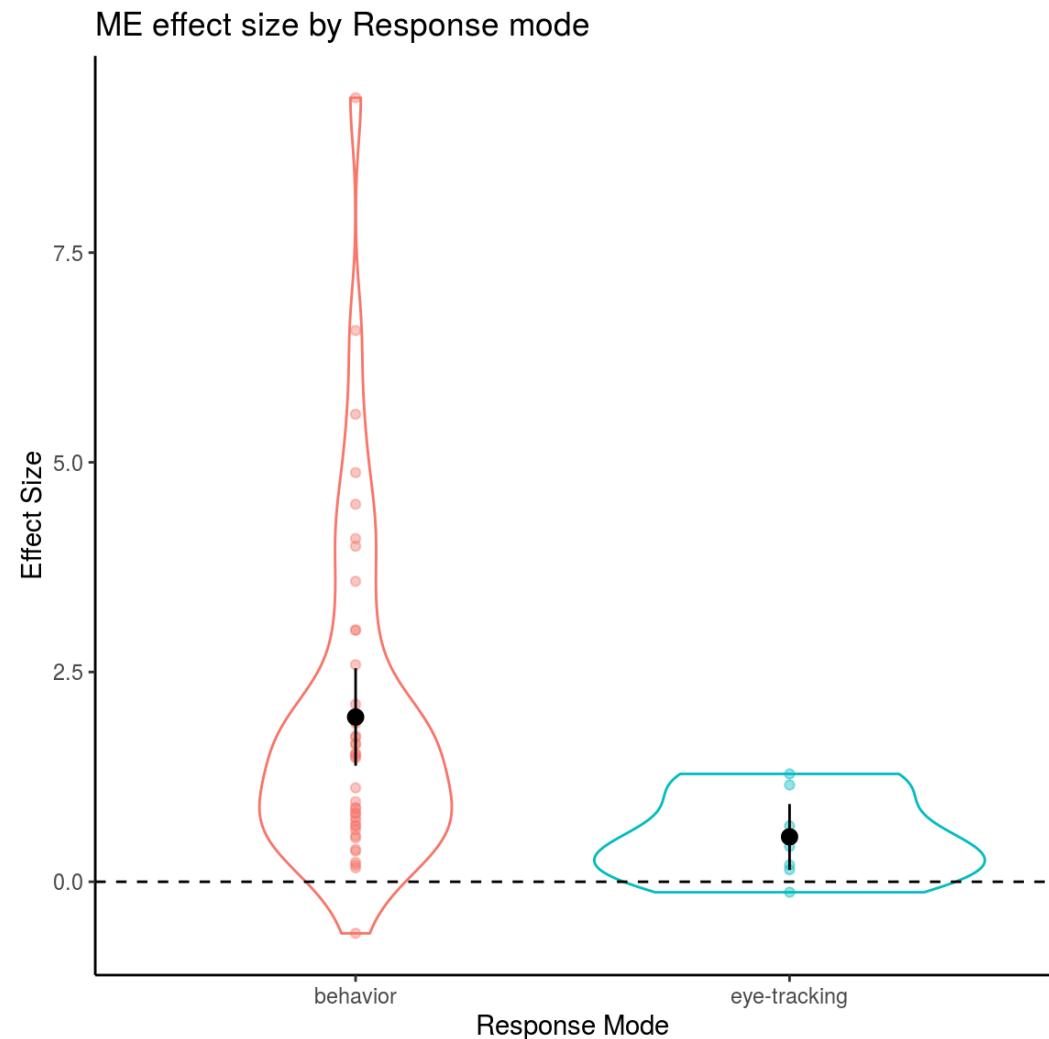


```

cis_by_response_mode <- ma_data %>%
  group_by(response_mode) %>%
  summarize(mean = mean(d_calc),
            sd = sd(d_calc),
            n = n()) %>%
  mutate(ci_range_95 = 1.96 * (sd/sqrt(n)),
        ci_lower = mean - ci_range_95,
        ci_upper = mean + ci_range_95)

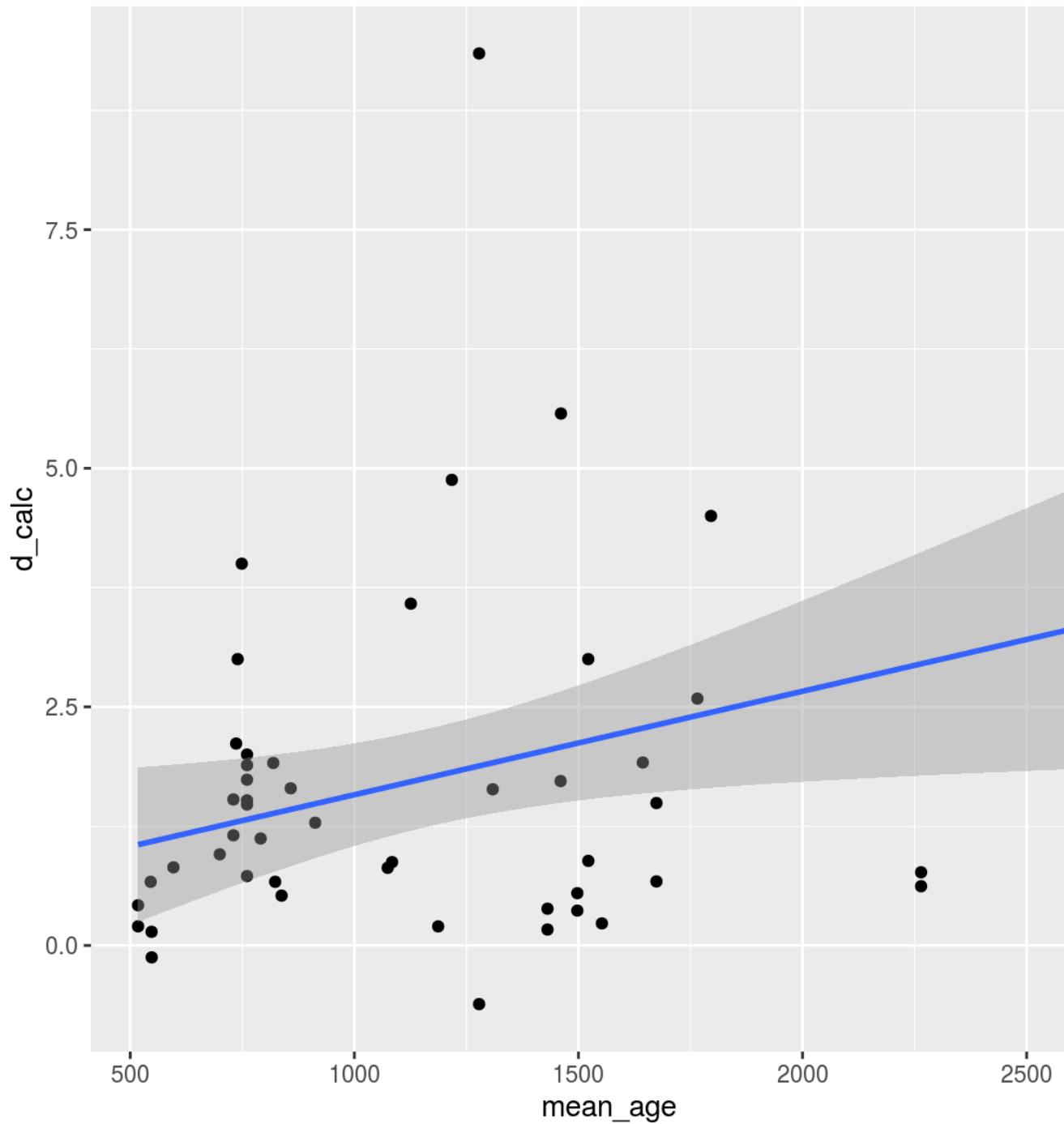
ggplot(ma_data, aes(x = response_mode,
                     y = d_calc,
                     color = response_mode)) +
  geom_violin() +
  geom_point(alpha = .4) +
  ylab("Effect Size") +
  xlab("Response Mode") +
  ggtitle("ME effect size by Response mode") +
  geom_pointrange(data = cis_by_response_mode,
                  aes(x = response_mode,
                      y = mean, ymin = ci_lower,
                      ymax = ci_upper),
                  color = "black") +
  geom_hline(aes(yintercept = 0), linetype = 2) +
  theme_classic() +
  theme(legend.position = "none")

```



Making a continuous moderator plot

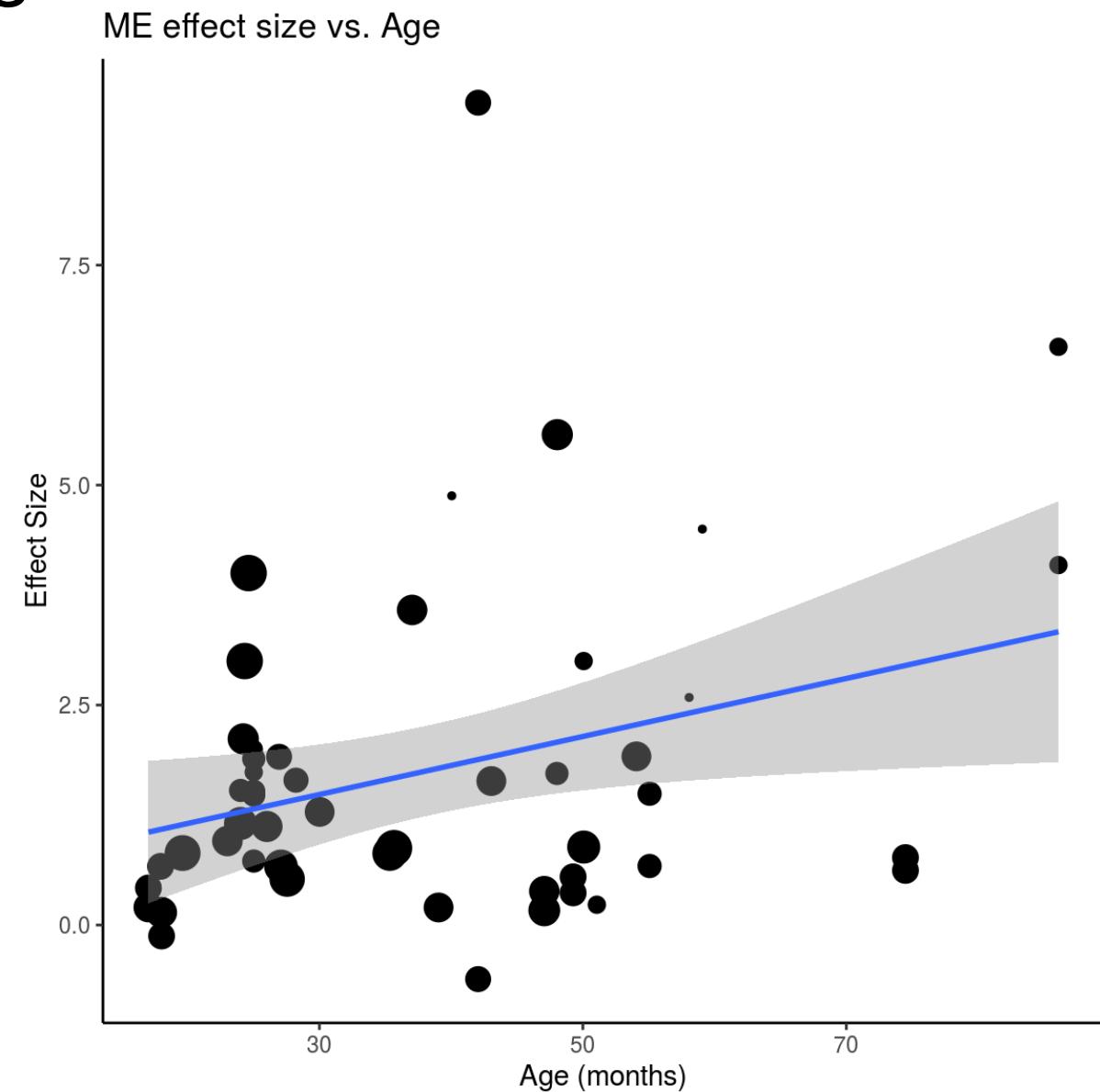
```
ggplot(ma_data, aes(x = mean_age, y = d_calc)) +  
  geom_point() +  
  geom_smooth(method = "lm")
```



Making a better continuous moderator plot

```
ma_data_for_age_plot <- ma_data %>%
  mutate(age_months = mean_age/30.4)

ggplot(ma_data_for_age_plot, aes(x = age_months,
                                  y = d_calc,
                                  size = n)) +
  geom_point() +
  geom_smooth(method = "lm") +
  ylab("Effect Size") +
  xlab("Age (months)") +
  ggtitle("ME effect size vs. Age") +
  theme_classic() +
  theme(legend.position = "none")
```



Coding for MA plots on Rstudio Cloud

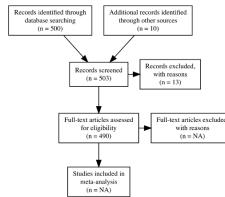
Final Project Analyses

The screenshot shows the RStudio Cloud interface. The top navigation bar includes 'Cumulative_science_2020 / Final Project Analyses', a user profile for 'Molly Lewis', and an R version dropdown ('R 3.6.0'). The main area features a code editor with the file 'final_project_analyses.Rmd' open. The code includes R Markdown syntax, such as code chunks and a PRISMA diagram section. Below the code editor are tabs for 'Console', 'Terminal', and 'Jobs'. To the right of the code editor is the 'Environment' pane, which is currently empty. At the bottom is the 'Files' pane, displaying a list of project files:

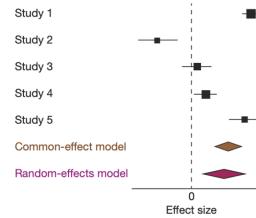
Name	Size	Modified
final_project_analyses.Rmd	4.3 KB	Apr 15, 2020, 9:58 AM
helpers		
mutual_exclusivity_sample_MA_data.csv	4.3 KB	Apr 14, 2020, 7:03 PM
plots		
prisma_diagram.R	4 KB	Apr 14, 2020, 7:28 PM
project.Rproj	205 B	Apr 15, 2020, 9:54 AM

Next Time: Formally testing for moderators and funnel plots

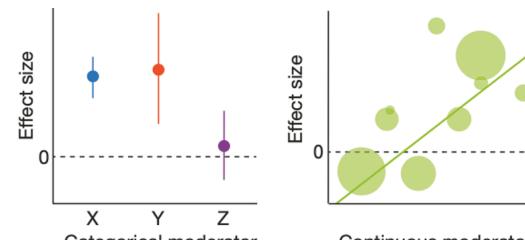
1. PRISMA flow diagram



2. Forest plot



3. Moderator plots



4. Funnel plot

