

# METAREGRESSION EXAMPLE WITH R

```
## this file replicates the analysis presented in: Harbord, R. M. and J. P. T. Higgins (2008). Meta-
## regression in Stata. Stata Journal 8(4): 493-519.
## But using metafor's R
```

```
> View(chol esterol_data)
> dat <- escalc (measure = "OR", ai=T_Events, bi=T_No_events, ci=C_Events,
di=C_No_events, data=chol esterol_data, append=TRUE)
> View(dat)
> randeff <- rma(yi, vi, data=dat)
> randeff
```

Random-Effects Model (k = 28; tau^2 estimator: REML)

```
tau^2 (estimate of total amount of heterogeneity): 0.0313 (SE = 0.0204)
tau (sqrt of the estimate of total heterogeneity): 0.1770
I^2 (% of total variability due to heterogeneity): 47.24%
H^2 (total variability / sampling variability): 1.90
```

Test for Heterogeneity:

Q(df = 27) = 49.6904, p-val = 0.0049

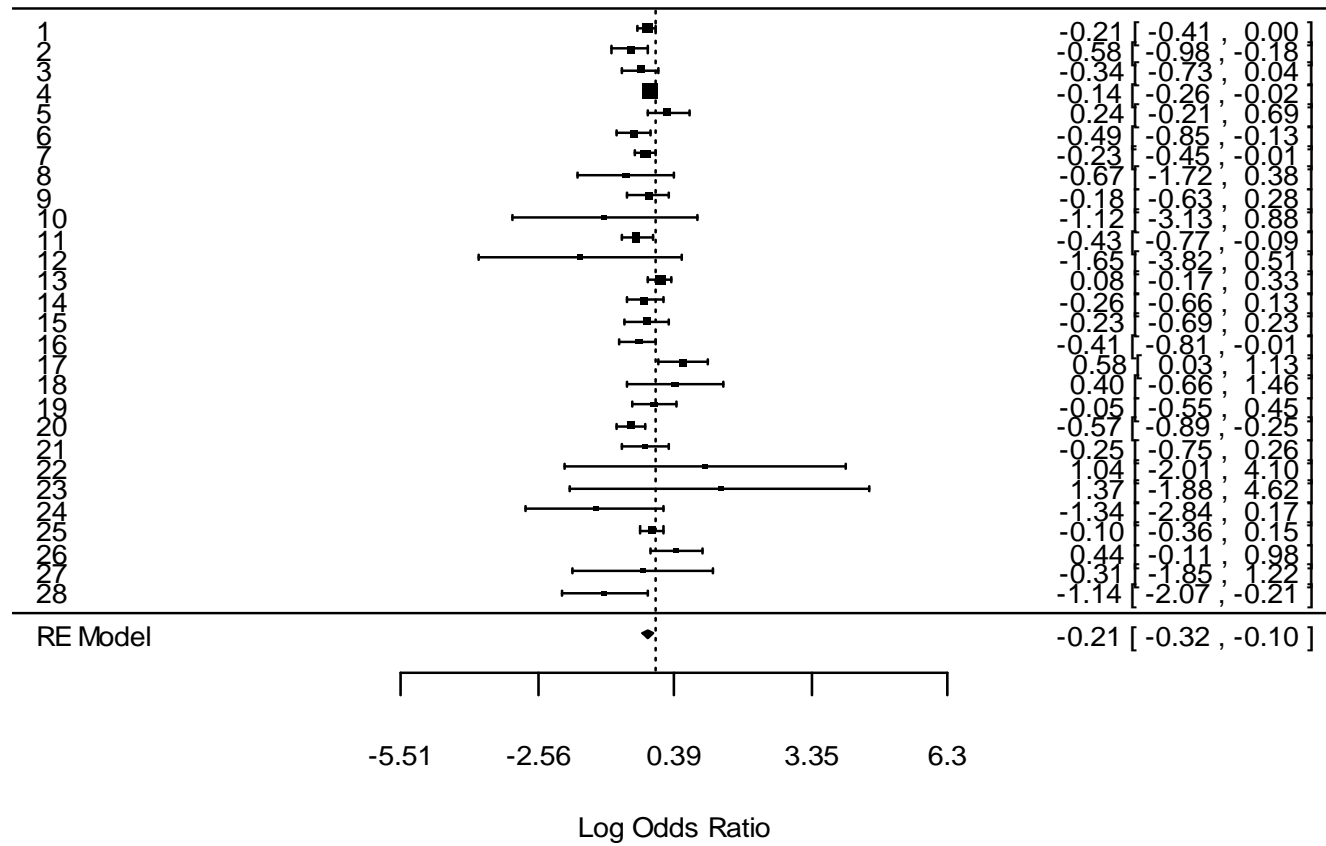
Model Results:

estimate	se	zval	pval	ci.lb	ci.ub	
-0.2128	0.0567	-3.7530	0.0002	-0.3240	-0.1017	***

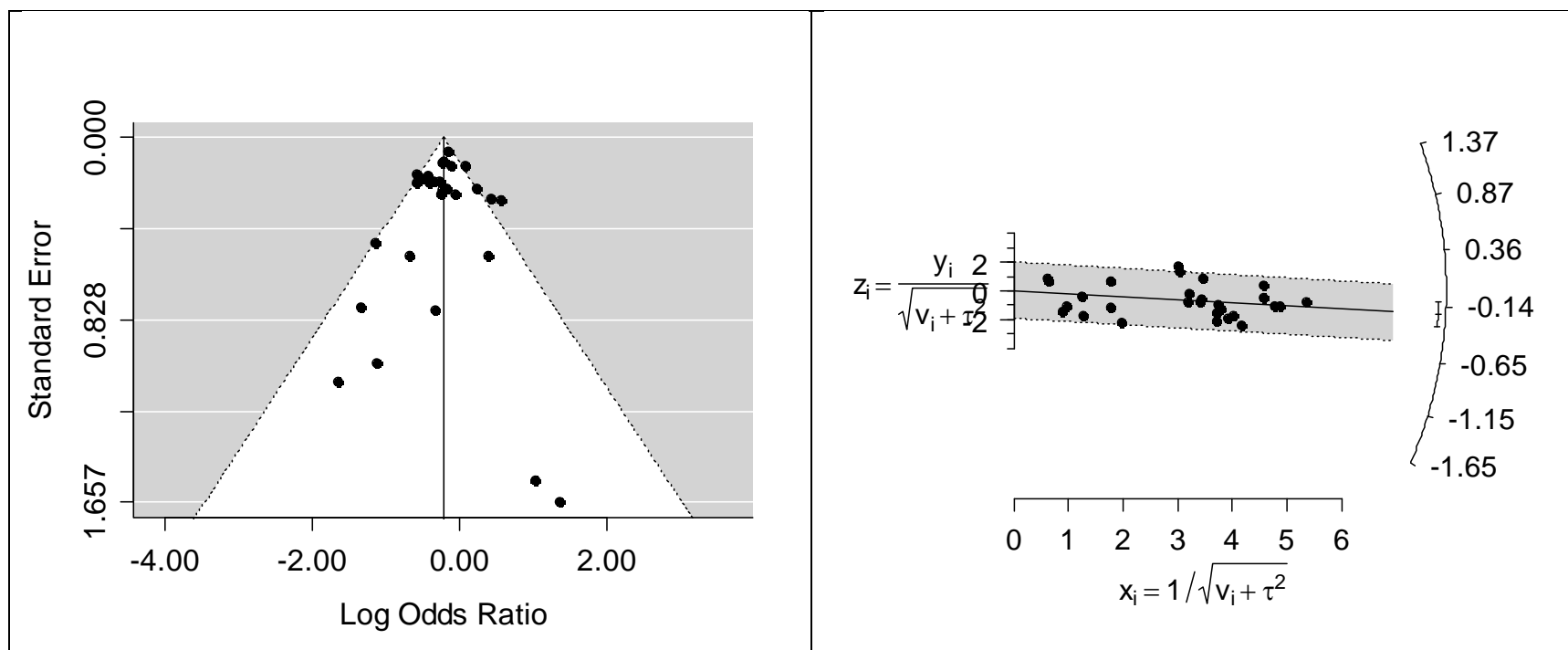
---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> forest(randeff, slab=dat$trial)
```



```
> funnel (randeff)
> radi al (randeff)
```



```
> mregr <- rma(yi, vi, mods = ~choles, data = dat)
```

```
> mregr
```

Mixed-Effects Model (k = 28; tau^2 estimator: REML)

tau^2 (estimate of residual amount of heterogeneity): 0.0097 (SE = 0.0117)

tau (sqrt of the estimate of residual heterogeneity): 0.0985

Test for Residual Heterogeneity:

QE(df = 26) = 37.8663, p-val = 0.0623

Test of Moderators (coefficient(s) 2):

QM(df = 1) = 9.3793, p-val = 0.0022

Model Results:

	estimate	se	zval	pval	ci.lb	ci.ub
intrcpt	0.1467	0.1237	1.1862	0.2356	-0.0957	0.3892
choles	-0.5057	0.1651	-3.0626	0.0022	-0.8293	-0.1821

\*\*

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## the code below changes the default statistical test from QM (heterogeneity accounted by the moderator under the metaregression model) to a test that uses an F test (equivalent to what we do in regression)

> mregr <- rma(yi, vi, mods = ~choles, data=dat, knha=TRUE)

> mregr

Mixed-Effects Model (k = 28; tau^2 estimator: REML)

tau^2 (estimate of residual amount of heterogeneity): 0.0097 (SE = 0.0117)

tau (sqrt of the estimate of residual heterogeneity): 0.0985

Test for Residual Heterogeneity:

QE(df = 26) = 37.8663, p-val = 0.0623

Test of Moderators (coefficient(s) 2):

F(df1 = 1, df2 = 26) = 7.5952, p-val = 0.0106

Model Results:

	estimate	se	tval	pval	ci.lb	ci.ub
intrcpt	0.1467	0.1375	1.0674	0.2956	-0.1358	0.4293
choles	-0.5057	0.1835	-2.7559	0.0106	-0.8829	-0.1285 *

---

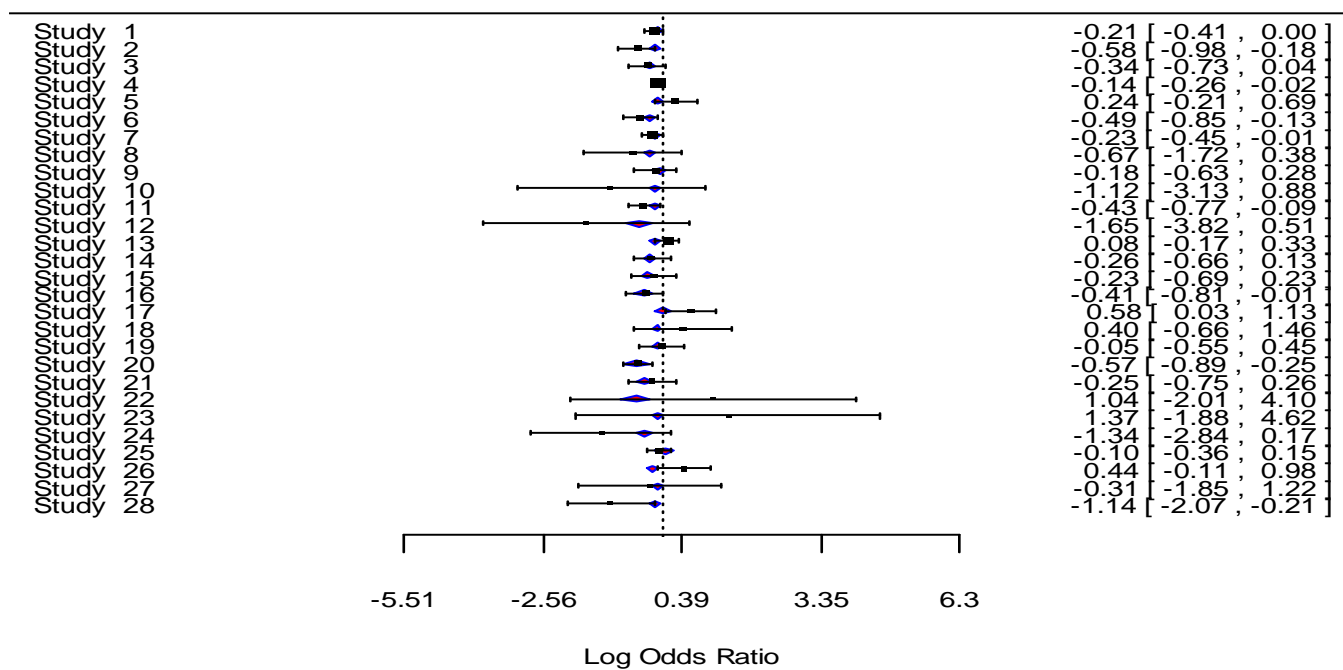
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

> confint(mregr)

	estimate	ci.lb	ci.ub
tau^2	0.0097	0	0.1643
tau	0.0985	0	0.4053

> forest(mregr, col="red", border="blue")

## from the metaphor help file: For models involving moderators, the fitted value for each study is added as a polygon to the plot. With the col and border arguments, one can change the (border) color of these polygons



## one thing the R metaphor program will not calculate is  $I^2$  when running the analysis with moderators  
 ## but we can calculate it based on the equation they provide:  $I^2 = [(QE - (n-k))/QE]$ :  
 ##  $(37.8663 - 27) / 37.8663 = 31.33\%$ .  
 ##  $R^2$  is also not calculated by R, but it can be easily calculated, as long as we run the random-effect  
 ## model with no covariates first. The equation for calculating adjusted  $R^2$  is  
 ##  $[(\tau_{2\_zero} - \tau_2) / \tau_{2\_zero}]$ , where  $\tau_{2\_zero}$  is  $\tau_2$  for the random effect model with no covariate.  
 ## In this case:  $[(.0313 - .0097) / .0313] = 69.00\%$

## calculate predicted values for the regression line between odds-ratio and cholesterol 

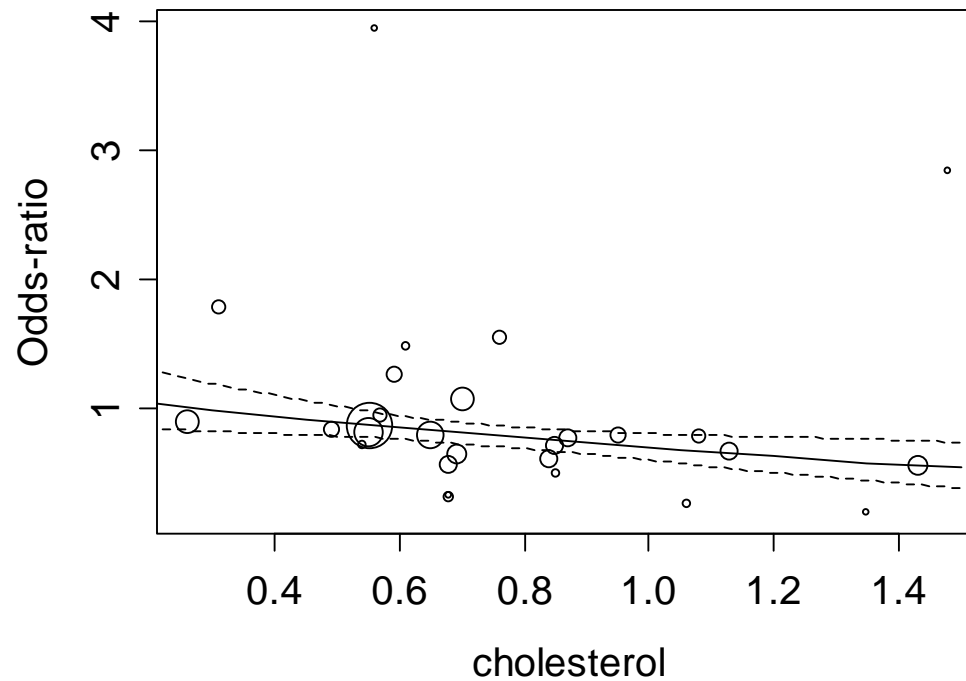
```
> preds <- predict(mreg, newmods = cbind(seq(from = 0, to = 1.5, by = 0.15)), transf=exp, addx=TRUE)
```

```
> preds
      pred      se ci.lb ci.ub cr.lb cr.ub X.intrcpt X.chol es
1  1.1581    NA 0.8730 1.5362 0.8180 1.6395      1      0.00
2  1.0735    NA 0.8524 1.3519 0.7897 1.4591      1      0.15
3  0.9950    NA 0.8299 1.1930 0.7581 1.3060      1      0.30
4  0.9224    NA 0.8034 1.0589 0.7218 1.1786      1      0.45
5  0.8550    NA 0.7676 0.9523 0.6797 1.0754      1      0.60
6  0.7925    NA 0.7151 0.8783 0.6315 0.9946      1      0.75
7  0.7346    NA 0.6476 0.8334 0.5787 0.9326      1      0.90
8  0.6810    NA 0.5766 0.8042 0.5240 0.8850      1      1.05
9  0.6312    NA 0.5096 0.7819 0.4701 0.8475      1      1.20
10 0.5851    NA 0.4488 0.7628 0.4191 0.8169      1      1.35
11 0.5424    NA 0.3945 0.7456 0.3719 0.7909      1      1.50
```

```
## if you have one covariate only, you can create a chart that will help you see how the fit is working
## using a variation of the "bubble chart", using the predicted values calculated above
```

```
> wi <- 1/sqrt(dat$vi)
> size <- 0.5 + 3*(wi -min(wi))/(max(wi)-min(wi))
> plot(dat$chol es, exp(dat$yi), main="Cholesterol covariate", xlab="cholesterol", ylab= "Odds-ratio",
      cex=size)
> lines(c(0, .15, .30, .45, .60, .75, .90, 1.05, 1.20, 1.35, 1.5), preds$pred )
> lines(c(0, .15, .30, .45, .60, .75, .90, 1.05, 1.20, 1.35, 1.5), preds$ci.lb, lty = "dashed" )
> lines(c(0, .15, .30, .45, .60, .75, .90, 1.05, 1.20, 1.35, 1.5), preds$ci.ub, lty = "dashed" )
```

## Cholesterol covariate



```
## this approach shows the importance of the weighting. Though some of the studies are far away from the
## predicted line, their weights are very small, which explains why they are not that important for the
## final result
```