rma.mv för meta-analyses, raw values, (rma.mv då leffa är samma patienter + control vid två olika tidpunkter)

| library(metafor)    originalstudier <- read.csv("studier.csv", sep = ",", header = TRUE)  datoriginal <- escalc(measure = "SMD",  m1i = originalstudier$meanIL6\_adhd,  sd1i = originalstudier$sdIL6\_adhd,  n1i = originalstudier$n\_adhd,  m2i = originalstudier$meanIL6\_control,  sd2i = originalstudier$sdIL6\_control,  n2i = originalstudier$n\_control)    result <- rma.mv(datoriginal$yi, datoriginal$vi, random = ~ 1 | StudyNumber/Group, data = originalstudier)  forest(result, slab = originalstudier$Studies, main = "Expanded meta-analysis")  result |
| --- |

Higgins method 1 för att transformera värden till log-värden då IL-6 inte är normalfördelade  
[Meta-analysis of skewed data: Combining results reported on log-transformed or raw scales (nih.gov)](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2978323/pdf/sim0027-6072.pdf)

| library(metafor) # exponentiell fördelning/log original studies  orginalstudier <- read.csv("studier.csv", sep = ",", header = TRUE)  orginalstudier$logtransformmean\_adhd <- log(orginalstudier$meanIL6\_adhd) - 0.5 \* log((orginalstudier$sdIL6\_adhd^2/orginalstudier$meanIL6\_adhd^2) + 1)  orginalstudier$logtransformSD\_adhd <- sqrt(log(orginalstudier$sdIL6\_adhd^2/orginalstudier$meanIL6\_adhd^2 + 1))  orginalstudier$logtransformmean\_control <- log(orginalstudier$meanIL6\_control) - 0.5 \* log((orginalstudier$sdIL6\_control^2/orginalstudier$meanIL6\_control^2) + 1)  orginalstudier$logtransformSD\_control <- sqrt(log(orginalstudier$sdIL6\_control^2/orginalstudier$meanIL6\_control^2 + 1))    logdat <- escalc(measure = "SMD",  m1i = orginalstudier$logtransformmean\_adhd,  sd1i = orginalstudier$logtransformSD\_adhd,  n1i = orginalstudier$n\_adhd,  m2i = orginalstudier$logtransformmean\_control,  sd2i = orginalstudier$logtransformSD\_control,  n2i = orginalstudier$n\_control)    logresult <- rma.mv(logdat$yi, logdat$vi, random = ~ 1 | StudyNumber/Group, data = orginalstudier)  forest(logresult, slab = orginalstudier$Studies, main = "log transformed original studies") |
| --- |

Kombinationsmetod: Higgins metod 1 och extraherade loggade värden från Leffa som redovisade loggade värden. Datan i filen 'logexpand' kommer från forest plotten i den tidigare koden som använder metod 1 från Higgins. Däremot är datan i Leffa manuellt inskriven i 'logexpand', så alla rader förutom Leffa18 och Leffa22 ska ha samma estimat i forest-plotten.

| library(metafor) # kombinationsmetod med Higgins och extraherade loggade värden  logexpand <- read.csv("logexpand.csv", sep = ",", header = TRUE)  logexpand$se <- (logexpand$upper - logexpand$lower) / (3.92) # CI --> SE  logexpand$V <- logexpand$se^2  resultlogexpand <- rma.mv(V = logexpand$V, yi = logexpand$hedgesg, random = ~ 1 | StudyNumber/Group, data = logexpand)  forest(resultlogexpand, slab = logexpand$AStudies, main = "Extended meta-analysis: Log transformation using Higgins except Leffa") |
| --- |

Poolad subgrupps analys av de studier där ADHD personerna var omedicinerade, kodmässigt en “vanlig meta-analys”

| library(metafor)  originalstudier <- read.csv("unmedicated.csv", sep = ",", header = TRUE) # pooled unmedicated meta-analysis  datoriginal <- escalc(measure = "SMD",  m1i = originalstudier$meanIL6\_adhd,  sd1i = originalstudier$sdIL6\_adhd,  n1i = originalstudier$n\_adhd,  m2i = originalstudier$meanIL6\_control,  sd2i = originalstudier$sdIL6\_control,  n2i = originalstudier$n\_control)  result <- rma(datoriginal$yi, datoriginal$vi, data = originalstudier)  forest(result, slab = originalstudier$Studies, main = "Expanded meta-analysis")  result |
| --- |

Nu kommer lite meta-regressioner, är lite osäker på den här koden

Age meta-regression

| library(metafor) # exponentiell fördelning/log original studies  orginalstudier <- read.csv("studier.csv", sep = ",", header = TRUE)  orginalstudier$logtransformmean\_adhd <- log(orginalstudier$meanIL6\_adhd) - 0.5 \* log((orginalstudier$sdIL6\_adhd^2/orginalstudier$meanIL6\_adhd^2) + 1)  orginalstudier$logtransformSD\_adhd <- sqrt(log(orginalstudier$sdIL6\_adhd^2/orginalstudier$meanIL6\_adhd^2 + 1))  orginalstudier$logtransformmean\_control <- log(orginalstudier$meanIL6\_control) - 0.5 \* log((orginalstudier$sdIL6\_control^2/orginalstudier$meanIL6\_control^2) + 1)  orginalstudier$logtransformSD\_control <- sqrt(log(orginalstudier$sdIL6\_control^2/orginalstudier$meanIL6\_control^2 + 1))  smdil6 <- escalc(measure = "SMD",  m1i = orginalstudier$logtransformmean\_adhd,  sd1i = orginalstudier$logtransformSD\_adhd,  n1i = orginalstudier$n\_adhd,  m2i = orginalstudier$logtransformmean\_control,  sd2i = orginalstudier$logtransformSD\_control,  n2i = orginalstudier$n\_control)  SmdAge <- escalc(measure="SMD", m1i=Age\_ADHD\_mean, m2i=AgeHealthymean,  sd1i=Age\_ADHD\_SD, sd2i=Age\_Healthy\_SD,  n1i=n\_adhd, n2i=n\_control,  data=orginalstudier)    regression <- rma(yi=smdil6$yi, vi=smdil6$vi,  mods = ~ SmdAge$yi, SmdAge$vi,  data=smdil6, method="REML")  summary(regression)  regplot(regression) |
| --- |

sex meta-regression

| library(metafor) # exponentiell fördelning/log original studies  orginalstudier <- read.csv("studier.csv", sep = ",", header = TRUE)  orginalstudier$logtransformmean\_adhd <- log(orginalstudier$meanIL6\_adhd) - 0.5 \* log((orginalstudier$sdIL6\_adhd^2/orginalstudier$meanIL6\_adhd^2) + 1)  orginalstudier$logtransformSD\_adhd <- sqrt(log(orginalstudier$sdIL6\_adhd^2/orginalstudier$meanIL6\_adhd^2 + 1))  orginalstudier$logtransformmean\_control <- log(orginalstudier$meanIL6\_control) - 0.5 \* log((orginalstudier$sdIL6\_control^2/orginalstudier$meanIL6\_control^2) + 1)  orginalstudier$logtransformSD\_control <- sqrt(log(orginalstudier$sdIL6\_control^2/orginalstudier$meanIL6\_control^2 + 1))  smdil6 <- escalc(measure = "SMD",  m1i = orginalstudier$logtransformmean\_adhd,  sd1i = orginalstudier$logtransformSD\_adhd,  n1i = orginalstudier$n\_adhd,  m2i = orginalstudier$logtransformmean\_control,  sd2i = orginalstudier$logtransformSD\_control,  n2i = orginalstudier$n\_control)  orginalstudier procentmen <- orginalstudier$ADHDprocentmales - orginalstudier$Healthyprocentmales regression <- rma(yi=smdil6$yi, vi=smdil6$vi,  mods = ~ procentmen,  data=smdil6, method="REML")    summary(regression) regplot(regression) |
| --- |

Nos-score metaregression

| library(metafor)  score <- read.csv("studier.csv", sep = ",", header = TRUE)  score$logtransformmean\_adhd <- log(score$meanIL6\_adhd) - 0.5 \* log((score$sdIL6\_adhd^2/score$meanIL6\_adhd^2) + 1)  score$logtransformSD\_adhd <- sqrt(log(score$sdIL6\_adhd^2/score$meanIL6\_adhd^2 + 1))  score$logtransformmean\_control <- log(score$meanIL6\_control) - 0.5 \* log((score$sdIL6\_control^2/score$meanIL6\_control^2) + 1)  score$logtransformSD\_control <- sqrt(log(score$sdIL6\_control^2/score$meanIL6\_control^2 + 1))    smdil6 <- escalc(measure = "SMD",  m1i = score$logtransformmean\_adhd,  sd1i = score$logtransformSD\_adhd,  n1i = score$n\_adhd,  m2i = score$logtransformmean\_control,  sd2i = score$logtransformSD\_control,  n2i = score$n\_control)    regression <- rma(yi=smdil6$yi, vi=smdil6$vi,  mods = ~ score$NOS,  data=smdil6, method="REML")    summary(regression)  regplot(regression) |
| --- |