#PAV

library(readxl)

library(meta)

# meta

getwd()

dta1<-read\_excel("PAV.xlsx")

View(dta1)

m2 <- metacont(dta1$N\_T, dta1$PAV\_diff\_T, dta1$PAV\_diff\_sd\_T, dta1$N\_C, dta1$PAV\_diff\_C, dta1$PAV\_diff\_sd\_C,studlab = dta1$study,data = dta1, sm = "SMD",method.tau = "REML")

summary(m2)

forest(m2)

m2\_reg\_1<-metareg(m2,CRP\_per\_diff,intercept = T)

summary(m2\_reg\_1)

m2\_reg\_2<-metareg(m2,LDL\_per\_diff,intercept = T)

summary(m2\_reg\_2)

m2\_reg\_3<-metareg(m2,CRP\_per\_diff+LDL\_per\_diff,intercept = T)

summary(m2\_reg\_3)

m2\_reg\_5<-metareg(m2,duration,intercept = T)

summary(m2\_reg\_5)

m2\_reg\_4<-metareg(m2,CRP\_per\_diff+LDL\_per\_diff+Age\_mean+Male\_mean+duration,intercept = T)

summary(m2\_reg\_4)

#图片优化

# PAV

m2 <- metacont(dta1$N\_T, dta1$PAV\_diff\_T, dta1$PAV\_diff\_sd\_T, dta1$N\_C, dta1$PAV\_diff\_C, dta1$PAV\_diff\_sd\_C,studlab = dta1$study,data = dta1, sm = "SMD",fixed=F,random=T,method.tau = "REML")

summary(m2)

#jpeg("picture.jpeg",height=700,width=700)

forest(m2)

forest(m2,label.e = "Experimental", label.c = "Control",colgap.studlab="0.1cm",just.forest="center",label.left="favour [experimental]",label.right="favour [control]",

digits=2,digits.se=2,digits.tau2=2,digits.pval=2,family="sans",fontsize =10,lwd=2,col.diamond.fixed = "maroon",col.diamond.lines.fixed ="maroon",col.diamond.random = "maroon",

col.diamond.lines.random = "maroon",col.square = "skyblue",col.square.lines = "skyblue",col.study = "lightslategray",plotwidth="6cm",colgap.forest.left="0.2cm",colgap.forest.right="0.2cm",colgap.right="0.2cm",colgap.left ="0.2cm",just.forest="left")

#dev.off()

#######TAV

library(readxl)

library(meta)

# meta

getwd()

dta1<-read\_excel("TAV.xlsx")

View(dta1)

# TAV

m1 <- metacont(dta1$N\_T, dta1$TAV\_diff\_T, dta1$TAV\_diff\_sd\_T, dta1$N\_C, dta1$TAV\_diff\_C, dta1$TAV\_diff\_sd\_C,studlab = dta1$study,data = dta1, sm = "SMD",method.tau = "REML")

summary(m1)

forest(m1)

m1\_reg\_1<-metareg(m1,CRP\_per\_diff,intercept = T)

summary(m1\_reg\_1)

m1\_reg\_2<-metareg(m1,LDL\_per\_diff,intercept = T)

summary(m1\_reg\_2)

m1\_reg\_3<-metareg(m1,CRP\_per\_diff+LDL\_per\_diff,intercept = T)

summary(m1\_reg\_3)

m1\_reg\_5<-metareg(m1,duration,intercept = T)

summary(m1\_reg\_5)

m1\_reg\_4<-metareg(m1,CRP\_per\_diff+LDL\_per\_diff+Age\_mean+Male\_mean+duration,intercept = T)

summary(m1\_reg\_4)

# PAV

getwd()

dta2<-read\_excel("PAV.xlsx")

View(dta2)

m2 <- metacont(dta1$N\_T, dta1$PAV\_diff\_T, dta1$PAV\_diff\_sd\_T, dta1$N\_C, dta1$PAV\_diff\_C, dta1$PAV\_diff\_sd\_C,studlab = dta1$study,data = dta2, sm = "SMD",method.tau = "REML")

summary(m2)

forest(m2)

m2\_reg\_1<-metareg(m2,CRP\_per\_diff,intercept = T)

summary(m2\_reg\_1)

m2\_reg\_2<-metareg(m2,LDL\_per\_diff,intercept = T)

summary(m2\_reg\_2)

m2\_reg\_3<-metareg(m2,CRP\_per\_diff+LDL\_per\_diff,intercept = T)

summary(m2\_reg\_3)

m2\_reg\_5<-metareg(m2,duration,intercept = T)

summary(m2\_reg\_5)

m2\_reg\_4<-metareg(m2,CRP\_per\_diff+LDL\_per\_diff+Age\_mean+Male\_mean+duration,intercept = T)

summary(m2\_reg\_4)

metainf(m1,pooled = "random")

forest(metainf(m1,pooled = "random"))

funnel(m1)

funnel(m2)

metabias(m1, method.bias = "rank")

metabias(m1, method.bias = "linreg")

metabias(m2, method.bias = "rank")

metabias(m2, method.bias = "linreg")

# TAV

m1 <- metacont(dta1$N\_T, dta1$TAV\_diff\_T, dta1$TAV\_diff\_sd\_T, dta1$N\_C, dta1$TAV\_diff\_C, dta1$TAV\_diff\_sd\_C,studlab = dta1$study,data = dta1, sm = "SMD",fixed=F,random=T,method.tau = "REML")

summary(m1)

#jpeg("picture.jpeg",height=700,width=700)

forest(m1)

forest(m1,label.e = "Experimental", label.c = "Control",colgap.studlab="0.1cm",just.forest="center",label.left="favour [experimental]",label.right="favour [control]",

digits=2,digits.se=2,digits.tau2=2,digits.pval=2,family="sans",fontsize =10,lwd=2,col.diamond.fixed = "maroon",col.diamond.lines.fixed ="maroon",col.diamond.random = "maroon",

col.diamond.lines.random = "maroon",col.square = "skyblue",col.square.lines = "skyblue",col.study = "lightslategray",plotwidth="6cm",colgap.forest.left="0.2cm",colgap.forest.right="0.2cm",colgap.right="0.2cm",colgap.left ="0.2cm",just.forest="left")

dev.off()