1. **Cardiac cell therapy datasets**

##########################

########## Dataset Cardiac cell therapy CSCs

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# Load Files

setwd("XXXXX")

# Load Packages and Data

library(metafor)

library(lattice)

library(xlsx)

read.xlsx("Cardiac stem cells and MI\_PPnew.xlsx",sheetIndex=1)->PPdat

#Re-adjust some factor issues

PPdat$Animal<-factor(PPdat$Animal,levels=c("Mouse","Rat","Dog","Pig"))

PPdat[with(PPdat, order(Animal)), ]-> PPdat

#Simple Model

EFma<-rma(yi=-ln\_ROM,sei=ROM\_se,data=PPdat)

#Exhaustive Forest Plot

pdf("LVEF\_forest.pdf",height=12,width=8)

forest(EFma,atransf=exp,xlim=c(-3, 3),slab=PPdat$AuthorYear,ilab=as.character(PPdat $Animal),ilab.xpos=(c(-1.6)),cex=0.6,main="",at=c(log(0.5),0,log(2),log(4)))

text(-3,111,"Author and Year",font=4,cex=0.8,pos=4)

text(-1.6,111,"Animal",font=4,cex=0.8)

text(-0,111,"LVEF Improvement",font=4,cex=0.8)

text(3,111,"ROM & 95% CI",font=4,cex=0.8,pos=2)

text(0,-5,"<-Deterioration Improvement->",cex=0.6)

dev.off()

##################### Species model

EFma2<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Animal-1),data=PPdat)

EFma2.1<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Animal),data=PPdat)

#Stuff for tables

as.data.frame(table(PPdat $Animal))->Speciestable

signif(EFma2 $pval,digits=2)-> EFpvals

# Species plot

pdf("LVEFspecies.pdf",width=9,height=4)

forest(EFma2 $b,sei= EFma2 $se,atransf=exp,slab=paste(Speciestable $Var1),ilab=cbind(Speciestable$Freq, EFpvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Species")

text(-6,6,"Species",pos=4,font=4)

text(-5,6,"# Studycohorts",pos=4,font=4)

text(-3.5,6,"P-value",pos=4,font=4)

text(-3.5,5.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,6,"LVEF Improvement",pos=4,font=4)

text(3,6,"ROM + 95% CI",font=4,pos=2)

text(1,2.2,paste(c("P = ",round(EFma2.1 $QMp,7))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=4,length=0.05,angle=90,code=3)

dev.off()

##################### Cell type Model

EFmaCell<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Drug2-1),data=PPdat)

EFmaCell2<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Drug2),data=PPdat)

EFmaCell

EFmaCell2

#Stuff for tables

as.data.frame(table(PPdat $Drug2))->Celltable

signif(EFmaCell2 $pval,digits=2)-> EFCellpvals

# plot

pdf("LVEFCell.pdf",width=9,height=4)

forest(EFmaCell2 $b,sei= EFmaCell2 $se,atransf=exp,slab=paste(Celltable $Var1),ilab=cbind(Celltable$Freq, EFCellpvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-Type")

text(-6,6,"Cell-Type",pos=4,font=4)

text(-5,6,"# Studycohorts",pos=4,font=4)

text(-3.5,6,"P-value",pos=4,font=4)

text(-3.5,5.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,6,"LVEF Improvement",pos=4,font=4)

text(3,6,"ROM + 95% CI",font=4,pos=2)

text(1,2.2,paste(c("P = ",round(EFmaCell2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=4,length=0.05,angle=90,code=3)

dev.off()

##################### Cell Source Model

EFmaXeno<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Stem.cell.origin-1),data=PPdat)

EFmaXeno2<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Stem.cell.origin),data=PPdat)

EFmaXeno

EFmaXeno2

#Stuff for tables

as.data.frame(table(PPdat $Stem.cell.origin))->Xenotable

signif(EFmaXeno2 $pval,digits=2)-> EFXenopvals

# plot

pdf("LVEFSource.pdf",width=9,height=4)

forest(EFmaXeno2 $b,sei= EFmaXeno2 $se,atransf=exp,slab=paste(Xenotable $Var1),ilab=cbind(Xenotable$Freq, EFXenopvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-Source")

text(-6,7,"Cell-Source",pos=4,font=4)

text(-5,7,"# Studycohorts",pos=4,font=4)

text(-3.5,7,"P-value",pos=4,font=4)

text(-3.5,6.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,7,"LVEF Improvement",pos=4,font=4)

text(3,7,"ROM + 95% CI",font=4,pos=2)

text(1,3,paste(c("P = ",round(EFmaXeno2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.9,y1=5.1,length=0.05,angle=90,code=3)

dev.off()

##################### Immunosupression

PPdat$Immuno<-factor(PPdat$Immuno,levels=c("No Immunosupression","Immunosupression"))

PPdat$Immuno2

EFmaImmuno<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Immuno-1),data=PPdat)

EFmaImmuno2<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Immuno),data=PPdat)

EFmaImmuno

EFmaImmuno2

#Stuff for tables

as.data.frame(table(PPdat $Immuno))->Immunotable

signif(EFmaImmuno2 $pval,digits=2)-> EFImmunopvals

# plot

pdf("LVEFImmuno.pdf",width=9,height=4)

forest(EFmaImmuno2 $b,sei= EFmaImmuno2 $se,atransf=exp,slab=paste(Immunotable $Var1),ilab=cbind(Immunotable$Freq, EFImmunopvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Immunosupression")

text(-6,4,"Imm.",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,4,"LVEF Improvement",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1,paste(c("P = ",round(EFmaXeno2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.9,y1=2.1,length=0.05,angle=90,code=3)

dev.off()

##################### Immunosupression with genetic knockouts

PPdat$Immuno2<-factor(PPdat$Immuno2,levels=c("Immunocompetent","Drug-induced","Genetic suppression"))

EFmaImmuno<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Immuno2-1),data=PPdat)

EFmaImmuno2<-rma(yi=-ln\_ROM,sei=ROM\_se,mods=~(Immuno2),data=PPdat)

EFmaImmuno

EFmaImmuno2

#Stuff for tables

as.data.frame(table(PPdat $Immuno2))->Immunotable

signif(EFmaImmuno2 $pval,digits=2)-> EFImmunopvals

# plot

pdf("LVEFImmuno.pdf",width=9,height=4)

forest(EFmaImmuno $b,sei= EFmaImmuno $se,atransf=exp,slab=paste(Immunotable $Var1),ilab=cbind(Immunotable$Freq, EFImmunopvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Immunosupression")

text(-6,5,"Imm.",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3.5,5,"P-value",pos=4,font=4)

text(-3.5,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"LVEF Improvement",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.9,paste(c("p = ",round(EFmaImmuno2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.9,y1=3.1,length=0.05,angle=90,code=3)

dev.off()

##########################

########## Dataset Cardiac cell therapy large animals

###########################

read.xlsx("Stem Cells in large animal MI\_Sanne2.xlsx",sheetIndex=1)->SanneEF

EFmaSanne<-rma(yi=-lnROM,sei= ROM\_se,data=SanneEF)

PPdat[with(PPdat, order(Animal)), ]-> PPdat

forest(EFmaSanne,atransf=exp,xlim=c(-3, 3),slab=SanneEF$Author.ID,ilab=as.character(SanneEF $Animal),ilab.xpos=(c(-1.6)),cex=0.6,main="",at=c(log(0.5),0,log(2),log(4)))

pdf("LVEF\_forest.pdf",height=12,width=8)

forest(EFma,atransf=exp,xlim=c(-3, 3),slab=PPdat$AuthorYear,ilab=as.character(PPdat $Animal),ilab.xpos=(c(-1.6)),cex=0.6,main="",at=c(log(0.5),0,log(2),log(4)))

text(-3,111,"Author and Year",font=4,cex=0.8,pos=4)

text(-1.6,111,"Animal",font=4,cex=0.8)

text(-0,111,"LVEF Improvement",font=4,cex=0.8)

text(3,111,"ROM & 95% CI",font=4,cex=0.8,pos=2)

text(0,-5,"<-Deterioration Improvement->",cex=0.6)

dev.off()

#Re-adjust some factor thingies

PPdat[with(PPdat, order(Animal)), ]-> PPdat

#Simple Model

#Exhaustive Forest Plot

##################### Species model

factor(SanneEF$Animal,levels=c("Dog","Sheep","Pig"))->SanneEF$Animal

EFma2Sanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Animal-1),data=SanneEF)

EFma2.1Sanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Animal),data=SanneEF)

EFma2Sanne

EFma2.1Sanne

#Stuff for tables

as.data.frame(table(SanneEF $Animal))->SpeciestableSanne

signif(EFma2Sanne $pval,digits=2)-> EFpvalsSanne

# Species plot

pdf("LVEFlargespecies.pdf",width=9,height=4)

forest(EFma2Sanne $b,sei= EFma2Sanne $se,atransf=exp,slab=paste(SpeciestableSanne $Var1),ilab=cbind(SpeciestableSanne$Freq, EFpvalsSanne),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Species")

text(-6,5,"Species",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3.5,5,"P-value",pos=4,font=4)

text(-3.5,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"LVEF Improvement",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.9,paste(c("p = ",round(EFma2.1Sanne $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=3,length=0.05,angle=90,code=3)

dev.off()

######################### Immunosuppression

EFmaImmSanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Immuno-1),data=SanneEF)

EFmaImm1Sanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Immuno),data=SanneEF)

EFmaImmSanne

EFmaImm1Sanne

as.data.frame(table(SanneEF $Immuno))->ImmunotableSanne

signif(EFmaImmSanne $pval,digits=2)-> EFpvalsSanneimm

pdf("LVEFlargeimmuno.pdf",width=9,height=4)

forest(EFmaImmSanne $b,sei= EFmaImmSanne $se,atransf=exp,slab=paste(ImmunotableSanne $Var1),ilab=cbind(ImmunotableSanne$Freq, EFpvalsSanneimm),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Immunosuppression")

text(-6,4,"Imm. supp.",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3,4,"P-value",pos=4,font=4)

text(-3,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,4,"LVEF Improvement",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.2,paste(c("p = ",round(EFmaImm1Sanne $QMp,2))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=2,length=0.05,angle=90,code=3)

dev.off()

######################### Cell Type

EFmacellSanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Cell.source-1),data=SanneEF)

EFmacell1Sanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Cell.source),data=SanneEF)

EFmacellSanne

EFmacell1Sanne

as.data.frame(table(SanneEF $Cell.source))->CelltableSanne

signif(EFmacellSanne $pval,digits=2)-> EFpvalsSannecell

pdf("LVEFlargecell.pdf",width=9,height=4)

forest(EFmacellSanne $b,sei= EFmacellSanne $se,atransf=exp,slab=paste(CelltableSanne $Var1),ilab=cbind(CelltableSanne$Freq, EFpvalsSannecell),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2),log(4))),xlim=c(-6, 3),main="Effects of Cell type")

text(-6,10,"Cell",pos=4,font=4)

text(-5,10,"# Studycohorts",pos=4,font=4)

text(-3,10,"P-value",pos=4,font=4)

text(-3,9.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,10,"LVEF Improvement",pos=4,font=4)

text(3,10,"ROM + 95% CI",font=4,pos=2)

text(1,4.7,paste(c("p = ",round(EFmacell1Sanne $QMp,2))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.8,y1=8.7,length=0.05,angle=90,code=3)

dev.off()

###################### Cells source

EFmaxenoSanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Stem.cell.origin-1),data=SanneEF)

EFmaxeno1Sanne<-rma(yi=-lnROM,sei=ROM\_se,mods=~(Stem.cell.origin),data=SanneEF)

EFmaxenoSanne

EFmaxeno1Sanne

as.data.frame(table(SanneEF $Stem.cell.origin))->xenotableSanne

signif(EFmaxenoSanne $pval,digits=2)-> EFpvalsSannexeno

pdf("LVEFlargexeno.pdf",width=9,height=4)

forest(EFmaxenoSanne $b,sei= EFmaxenoSanne $se,atransf=exp,slab=paste(xenotableSanne $Var1),ilab=cbind(xenotableSanne$Freq, EFpvalsSannexeno),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2),log(4))),xlim=c(-6, 3),main="Effects of Cell Source")

text(-6,5,"Cell Source",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3,5,"P-value",pos=4,font=4)

text(-3,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"LVEF Improvement",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.7,paste(c("p = ",round(EFmaxeno1Sanne $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.8,y1=3.2,length=0.05,angle=90,code=3)

dev.off()

1. **Kidney cell therapy datasets**

# Load Files

setwd “XXXXX"

# Load Packages and Data

library(metafor)

library(lattice)

library(xlsx)

read.xlsx("Kidney Stuff with ROM.xlsx",sheetIndex=1)->metadat

# Systolic Blood Pressure

read.xlsx("Kidney Stuff with ROM.xlsx",sheetIndex=3)->BPdata

BPdata $Species<-factor(BPdata $Species,levels=c("rat","pig"))

BPdata[with(BPdata, order(Species)), ]-> BPdata

BPma<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,data=BPdata)

BPma<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,data=BPdata)

pdf("BloodPressure.pdf",height=10,width=8)

forest(BPma,atransf=exp,xlim=c(-10, 6),slab=paste(BPdata $Auteur, " (", BPdata $Year, ")", sep=""),ilab=cbind(as.character(BPdata $Species),as.character(BPdata $Cell\_paraplu)),ilab.xpos=(c(-6,-3)),cex=0.6,main="",at=c(log(0.5),0,log(2), log(4)))

text(-10,34,"Author and Year",font=4,cex=0.8,pos=4)

text(-6,34,"Animal",font=4,cex=0.8)

text(-3,34,"Cell Type",font=4,cex=0.8)

text(-0,34,"Clearance Increase",font=4,cex=0.8)

text(6,34,"ROM & 95% CI",font=4,cex=0.8,pos=2)

text(0,-2,"<-Deterioration Improvement->",cex=0.6)

dev.off()

# Species

BPma2<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~Species-1,data=BPdata)

BPma2

BPma2.2<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~Species,data=BPdata)

BPma2.2

as.data.frame(table(BPdata $Species))-> BPdata\_tab

signif(BPma2 $pval,digits=2)-> BPma2\_pvals

pdf("BP\_Species.pdf",width=9,height=4)

#par(oma=c(0,3,0,0))

forest(BPma2 $b,sei= BPma2 $se,atransf=exp,slab=paste(BPdata\_tab $Var1),ilab=cbind(BPdata\_tab $Freq, BPma2\_pvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Species on Bloodpressure Improvement")

text(-6,4,"Species",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-0.5,4,"Relative BP",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.3,paste(c("P = ",round(BPma2.2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.75,y1=2.25,length=0.05,angle=90,code=3)

dev.off()

# Cell Type

BPmaCelltype<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~ Cell\_paraplu-1,data=BPdata)

BPmaCelltype

BPmaCelltype2<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~ Cell\_paraplu,data=BPdata)

BPmaCelltype2

as.data.frame(table(BPdata $Cell\_paraplu))-> BPdata\_tabCell

signif(BPmaCelltype $pval,digits=2)-> BPmaCell\_pvals

pdf("BP\_Celltype.pdf",width=9,height=4)

#par(oma=c(0,3,0,0))

forest(BPmaCelltype $b,sei= BPmaCelltype $se,atransf=exp,slab=paste(BPdata\_tabCell $Var1),ilab=cbind(BPdata\_tabCell $Freq, BPmaCell\_pvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell Type on Bloodpressure Improvement")

text(-6,7,"Cell Type",pos=4,font=4)

text(-5,7,"# Studycohorts",pos=4,font=4)

text(-3.5,7,"P-value",pos=4,font=4)

text(-3.5,6.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-0.5,7,"Relative BP",pos=4,font=4)

text(3,7,"ROM + 95% CI",font=4,pos=2)

text(1,3,paste(c("P = ",round(BPmaCelltype2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.8,y1=5.2,length=0.05,angle=90,code=3)

dev.off()

# Cell Source

BPmaXeno<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~ Xenotransplantation-1,data=BPdata)

BPmaXeno

BPmaXeno2<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~ Xenotransplantation,data=BPdata)

BPmaXeno2

as.data.frame(table(BPdata $Xenotransplantation))-> BPdata\_tabXeno

signif(BPmaXeno $pval,digits=2)-> BPXeno\_pvals

pdf("BP\_Xeno.pdf",width=9,height=4)

#par(oma=c(0,3,0,0))

forest(BPmaXeno $b,sei= BPmaXeno $se,atransf=exp,slab=paste(BPdata\_tabXeno $Var1),ilab=cbind(BPdata\_tabXeno $Freq, BPXeno\_pvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell Source on Bloodpressure Improvement")

text(-6,4,"Source",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-0.5,4,"Relative BP",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.3,paste(c("P = ",round(BPmaXeno2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=2,length=0.05,angle=90,code=3)

dev.off()

# Immunosupression

BPmaIm<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~ Immunosupression-1,data=BPdata)

BPmaIm

BPmaIm2<-rma(yi= BP\_lnROM,sei= BP\_ROMSE,mods=~ Immunosupression,data=BPdata)

BPmaIm2

as.data.frame(table(BPdata $Immunosupression))-> BPdata\_tabXeno

signif(BPmaXeno $pval,digits=2)-> BPXeno\_pvals

pdf("BP\_Xeno.pdf",width=9,height=4)

#par(oma=c(0,3,0,0))

forest(BPmaXeno $b,sei= BPmaXeno $se,atransf=exp,slab=paste(BPdata\_tabXeno $Var1),ilab=cbind(BPdata\_tabXeno $Freq, BPXeno\_pvals),ilab.xpos=c(-4,-3),at=(c(log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell Source on Bloodpressure Improvement")

text(-6,4,"Source",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-0.5,4,"Relative BP",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.3,paste(c("P = ",round(BPmaXeno2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=2,length=0.05,angle=90,code=3)

dev.off()

# ------------------

######### ###########

#--------------- Urinary potein POOL----------######

######### ###########

read.xlsx("Kidney Stuff with ROM.xlsx",sheetIndex=4)->uriprot

uriprot $Species<-factor(uriprot $Species,levels=c("mouse","rat","pig"))

uriprot[with(uriprot, order(Species)), ]-> uriprot

uriprot$Follow<-factor(uriprot$Follow,labels=c("a","b",""))

uriprotMA<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,data=uriprot)

pdf("Urinary Protein.pdf",height=10,width=8)

forest(uriprotMA,atransf=exp,xlim=c(-10, 6),slab=paste(uriprot $Auteur, " (", uriprot $Year, ")", sep=""),ilab=cbind(as.character(uriprot $Species),as.character(uriprot $Cell\_paraplu)),ilab.xpos=(c(-6,-4)),cex=0.6,main="",at=c(log(0.5),0,log(2), log(4)))

text(-10,109,"Author and Year",font=4,cex=0.8,pos=4)

text(-6,109,"Animal",font=4,cex=0.8)

text(-4,109,"Cell Type",font=4,cex=0.8)

text(-0,109,"Urinary Protein Decrease",font=4,cex=0.8)

text(6,109,"ROM & 95% CI",font=4,cex=0.8,pos=2)

text(0,-3,"<-Improvement Deterioration->",cex=0.6)

dev.off()

# Species

uriprotMA2<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Species-1),data=uriprot)

uriprotMA2.2<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Species),data=uriprot)

as.data.frame(table(uriprot $Species))-> uriprotdata\_tab

signif(uriprotMA2 $pval,digits=2)-> uriprot\_pvals

pdf("Uriprot\_Species.pdf",width=9,height=4)

forest(uriprotMA2 $b,sei= uriprotMA2 $se,atransf=exp,slab=paste(uriprotdata\_tab $Var1),ilab=cbind(uriprotdata\_tab $Freq, uriprot\_pvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Species on Urinary Protein")

text(-6,5,"Species",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3.5,5,"P-value",pos=4,font=4)

text(-3.5,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"Urinary Protein",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.8,paste(c("P = ",round(uriprotMA2.2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=3,length=0.05,angle=90,code=3)

dev.off()

# Immunosuppression

uriprotMA2im<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Immunosupression-1),data=uriprot)

uriprotMA2.2im<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Immunosupression),data=uriprot)

as.data.frame(table(uriprot $Immunosupression))-> uriprotdata\_tabim

signif(uriprotMA2im $pval,digits=2)-> uriprot\_pvalsim

pdf("Uriprot\_immuno.pdf",width=9,height=4)

forest(uriprotMA2im $b,sei= uriprotMA2im $se,atransf=exp,slab=paste(uriprotdata\_tabim $Var1),ilab=cbind(uriprotdata\_tabim $Freq, uriprot\_pvalsim),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Immunosupression on Urinary Protein")

text(-6,5,"Imm. Supp",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3.5,5,"P-value",pos=4,font=4)

text(-3.5,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"Urinary Protein",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.25,paste(c("P = ",round(uriprotMA2.2im $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=2,length=0.05,angle=90,code=3)

dev.off()

# Celltype

uriprotMA2cell<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Cell\_paraplu-1),data=uriprot)

uriprotMA2cell2<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Cell\_paraplu),data=uriprot)

as.data.frame(table(uriprot $Cell\_paraplu))-> uriprotdata\_tabcell

signif(uriprotMA2cell$pval,digits=2)-> uriprot\_pvalscell

pdf("Uriprot\_Cell.pdf",width=9,height=4)

forest(uriprotMA2cell $b,sei= uriprotMA2cell $se,atransf=exp,slab=paste(uriprotdata\_tabcell $Var1),ilab=cbind(uriprotdata\_tabcell $Freq, uriprot\_pvalscell),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-type on Urinary Protein")

text(-6,7,"Cell-type",pos=4,font=4)

text(-5,7,"# Studycohorts",pos=4,font=4)

text(-3.5,7,"P-value",pos=4,font=4)

text(-3.5,6.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,7,"Urinary Protein",pos=4,font=4)

text(3,7,"ROM + 95% CI",font=4,pos=2)

text(1,2.95,paste(c("p = ",round(uriprotMA2cell2 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.75,y1=5.3,length=0.05,angle=90,code=3)

dev.off()

# Cell source

uriprotMA2xeno<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Xenotransplantation-1),data=uriprot)

uriprotMA2xeno22<-rma(yi=ProtUlnROM,sei= ProtU\_ROM\_SE,mods=~(Xenotransplantation),data=uriprot)

as.data.frame(table(uriprot $Xenotransplantation))-> uriprotdata\_tabxeno

signif(uriprotMA2xeno$pval,digits=2)-> uriprot\_pvalsxeno

pdf("Uriprot\_xeno.pdf",width=9,height=4)

forest(uriprotMA2xeno $b,sei= uriprotMA2xeno $se,atransf=exp,slab=paste(uriprotdata\_tabxeno$Var1),ilab=cbind(uriprotdata\_tabxeno$Freq, uriprot\_pvalsxeno),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-Source on Urinary Protein")

text(-6,4,"Origin",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,4,"Urinary Protein",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.4,paste(c("p = ",round(uriprotMA2xeno22 $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.75,y1=2.3,length=0.05,angle=90,code=3)

dev.off()

1. **Neurological cell therapy datasets**

# Load Files

setwd("XXXXX")

# Load Packages and Data

library(metafor)

library(lattice)

library(xlsx)

read.xlsx("Combined stem cells STROKE and SCI.AA 071216 CORRECT.xlsx",sheetIndex=1)->Neurodata

table(Neurodata$Cell.Type)

factor(gsub(" ","",Neurodata$Cell.Type))->Neurodata$Cell.Type

###################

## Infarct Size ##

###################

subset(Neurodata,Neurodata$Type.of.Disease=="Stroke IV")->strokeIV

droplevels(strokeIV$Animal)-> strokeIV$Animal

strokeIV $Animal<-factor(strokeIV $Animal,levels=c("Mouse","Gerbil","Rat","Rabbit"))

#simple Model

StrokeIVMA<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV)

pdf("totalstrokeiv.pdf",height=50,width=10)

forest(StrokeIVMA,atransf=exp,slab=strokeIV$Author.Year,data=strokeIV)

dev.off()

############################Species Model

StrokeIVMAspec<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~Animal-1)

StrokeMAspec2<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~Animal)

#Table Stuff

as.data.frame(table(strokeIV$Animal))->speciestableIV

signif(StrokeIVMAspec $pval,digits=2)-> strokeAnimalpvals

# Speciesplot

pdf("strokespecies.pdf",width=9,height=4)

forest(StrokeIVMAspec $b,sei= StrokeIVMAspec $se,atransf=exp,slab=paste(speciestableIV $Var1),ilab=cbind(speciestableIV $Freq, strokeAnimalpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Species on Stroke Infarct Volume")

text(-6,6,"Species",pos=4,font=4)

text(-5,6,"# Studycohorts",pos=4,font=4)

text(-3.5,6,"P-value",pos=4,font=4)

text(-3.5,5.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,6,"Infarct Size",pos=4,font=4)

text(-1,5.5,"Reduction",pos=4,font=4)

text(3,6,"ROM + 95% CI",font=4,pos=2)

text(1,2.2,paste(c("P = ",round(StrokeMAspec2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=4,length=0.05,angle=90,code=3)

dev.off()

##################################

droplevels(strokeIV$Immunisupp)->strokeIV$Immunisupp

factor(strokeIV$Immunisupp,levels=c("none","cyclosporin A"))->strokeIV$Immunisupp

factor(strokeIV$Immunisupp,labels=c("None","Cyclosporin A"))->strokeIV$Immunisupp

StrokeMA2im<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Immunisupp-1)

StrokeMA2.1im<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Immunisupp)

StrokeMA2.1im

#Table Stuff

as.data.frame(table(strokeIV$Immunisupp))->immtable

signif(StrokeMA2im $pval,digits=2)-> immpvals

pdf("strokeimmunisupp.pdf",width=9,height=4)

forest(StrokeMA2im $b,sei= StrokeMA2im $se,atransf=exp,slab=paste(immtable $Var1),ilab=cbind(immtable$Freq, immpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Immunosupression on Stroke Infarct Volume")

text(-6,4,"Imm.supp",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,4,"Infarct Size",pos=4,font=4)

text(-1,3.5,"Reduction",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.25,paste(c("p = ",round(StrokeMA2.1im $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=2,length=0.05,angle=90,code=3)

dev.off()

##################################

############### Cell type ---

StrokeMACell<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Type-1)

StrokeMACell2<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Type)

StrokeMACell

StrokeMACell2

#Table Stuff

as.data.frame(table(strokeIV$Cell.Type))->Cellstable

signif(StrokeMACell $pval,digits=2)-> strokecellpvals

# Speciesplot

pdf("strokecelltype.pdf",width=9,height=4)

forest(StrokeMACell $b,sei= StrokeMACell $se,atransf=exp,slab=paste(Cellstable $Var1),ilab=cbind(Cellstable$Freq, strokecellpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-type on Stroke Infarct Volume")

text(-6,8,"Cell-type",pos=4,font=4)

text(-5,8,"# Studycohorts",pos=4,font=4)

text(-3.5,8,"P-value",pos=4,font=4)

text(-3.5,7.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,8,"Infarct Size",pos=4,font=4)

text(-1,7.5,"Reduction",pos=4,font=4)

text(3,8,"ROM + 95% CI",font=4,pos=2)

text(1,3.2,paste(c("P = ",round(StrokeMACell2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=6,length=0.05,angle=90,code=3)

dev.off()

####### Source

factor(strokeIV$Cell.Source,levels=c("Autologous","Allogeneic","Xenogeneic"))->strokeIV$Cell.Source

StrokeMASource<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Source-1)

StrokeMASource2<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Source)

StrokeMASource

StrokeMASource2

#Table Stuff

as.data.frame(table(strokeIV$Cell.Source))->Sourcestable

signif(StrokeMASource $pval,digits=2)-> strokeSourcepvals

# Speciesplot

pdf("strokecellsource.pdf",width=9,height=4)

forest(StrokeMASource $b,sei= StrokeMASource $se,atransf=exp,slab=paste(Sourcestable $Var1),ilab=cbind(Sourcestable$Freq, strokeSourcepvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-Source on Stroke Infarct Volume")

text(-6,5,"Cell-Source",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3.5,5,"P-value",pos=4,font=4)

text(-3.5,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"Infarct Size",pos=4,font=4)

text(-1,4.5,"Reduction",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.9,paste(c("P = ",round(StrokeMASource2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.8,y1=3.2,length=0.05,angle=90,code=3)

dev.off()

###########################################

####### Spinal Cord Injury ################

###########################################

subset(Neurodata,Neurodata$Type.of.Disease=="SCI")->SCI

droplevels(SCI $Animal)-> SCI $Animal

SCI $Animal<-factor(SCI $Animal,levels=c("Mouse","Rat","Rabbit","Marmoset"))

#simple Model

SCIMA<-rma(yi=lnROM,sei=ROM\_se,data= SCI,method="DL")

pdf("total SCI iv.pdf",height=50,width=10)

forest(SCIMA,atransf=exp,slab=SCI$Author.Year,data= SCI)

dev.off()

############################Species Model

SCIspec<-rma(yi=lnROM,sei=ROM\_se,data=SCI,mods=~Animal-1)

SCIspec2<-rma(yi=lnROM,sei=ROM\_se,data=SCI,mods=~Animal)

#Table Stuff

as.data.frame(table(SCI$Animal))->speciestableSCI

signif(SCIspec $pval,digits=2)-> SCIAnimalpvals

# Speciesplot

pdf("SCIspecies.pdf",width=9,height=4)

forest(SCIspec $b,sei= SCIspec $se,atransf=exp,slab=paste(speciestableSCI $Var1),ilab=cbind(speciestableSCI $Freq, SCIAnimalpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Species on Spinal Cord Injury")

text(-6,6,"Species",pos=4,font=4)

text(-5,6,"# Studycohorts",pos=4,font=4)

text(-3.5,6,"P-value",pos=4,font=4)

text(-3.5,5.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,6,"Infarct Size",pos=4,font=4)

text(-1,5.5,"Reduction",pos=4,font=4)

text(3,6,"ROM + 95% CI",font=4,pos=2)

text(1,2.2,paste(c("P = ",round(StrokeMAspec2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=4,length=0.05,angle=90,code=3)

dev.off()

##################################

droplevels(SCI$Immunisupp)->SCI$Immunisupp

table(SCI$Immunisupp)

droplevel

factor(SCI$Immunisupp,levels=c("None","Cyclosporin A","Cyclosporin A/Methylprenisone","Prograf"))->SCI$Immunisupp

SCIma<-rma(yi=lnROM,sei=ROM\_se,data=SCI,mods=~ Immunisupp-1)

SCIma2<-rma(yi=lnROM,sei=ROM\_se,data=SCI,mods=~ Immunisupp)

SCIma2

#Table Stuff

as.data.frame(table(strokeIV$Immunisupp))->immtable

signif(StrokeMA2im $pval,digits=2)-> immpvals

pdf("strokeimmunisupp.pdf",width=9,height=4)

forest(StrokeMA2im $b,sei= StrokeMA2im $se,atransf=exp,slab=paste(immtable $Var1),ilab=cbind(immtable$Freq, immpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Immunosupression on Stroke Infarct Volume")

text(-6,4,"Imm.supp",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,4,"Infarct Size",pos=4,font=4)

text(-1,3.5,"Reduction",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.25,paste(c("p = ",round(StrokeMA2.1im $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=2,length=0.05,angle=90,code=3)

dev.off()

##################################

############### Cell type ---

StrokeMACell<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Type-1)

StrokeMACell2<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Type)

StrokeMACell

StrokeMACell2

#Table Stuff

as.data.frame(table(strokeIV$Cell.Type))->Cellstable

signif(StrokeMACell $pval,digits=2)-> strokecellpvals

# Speciesplot

pdf("strokecelltype.pdf",width=9,height=4)

forest(StrokeMACell $b,sei= StrokeMACell $se,atransf=exp,slab=paste(Cellstable $Var1),ilab=cbind(Cellstable$Freq, strokecellpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-type on Stroke Infarct Volume")

text(-6,8,"Cell-type",pos=4,font=4)

text(-5,8,"# Studycohorts",pos=4,font=4)

text(-3.5,8,"P-value",pos=4,font=4)

text(-3.5,7.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,8,"Infarct Size",pos=4,font=4)

text(-1,7.5,"Reduction",pos=4,font=4)

text(3,8,"ROM + 95% CI",font=4,pos=2)

text(1,3.2,paste(c("P = ",round(StrokeMACell2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=6,length=0.05,angle=90,code=3)

dev.off()

####### Source

factor(strokeIV$Cell.Source,levels=c("Autologous","Allogeneic","Xenogeneic"))->strokeIV$Cell.Source

StrokeMASource<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Source-1)

StrokeMASource2<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Source)

StrokeMASource

StrokeMASource2

#Table Stuff

as.data.frame(table(strokeIV$Cell.Source))->Sourcestable

signif(StrokeMASource $pval,digits=2)-> strokeSourcepvals

# Speciesplot

pdf("strokecellsource.pdf",width=9,height=4)

forest(StrokeMASource $b,sei= StrokeMASource $se,atransf=exp,slab=paste(Sourcestable $Var1),ilab=cbind(Sourcestable$Freq, strokeSourcepvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-Source on Stroke Infarct Volume")

text(-6,5,"Cell-Source",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3.5,5,"P-value",pos=4,font=4)

text(-3.5,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"Infarct Size",pos=4,font=4)

text(-1,4.5,"Reduction",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.9,paste(c("P = ",round(StrokeMASource2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.8,y1=3.2,length=0.05,angle=90,code=3)

dev.off()

##############################

### Stroke Neurobehaviour ####

##############################

subset(Neurodata,Neurodata$Type.of.Disease=="Stroke NB")->strokeNB

droplevels(strokeNB$Animal)->strokeNB$Animal

strokeNB$Animal<-factor(strokeNB$Animal,levels=c("Mouse","Gerbil","Rat","Rabbit"))

StrokeNBMAspec<-rma(yi=lnROM,sei=ROM\_se,data= strokeNB)->test

forest(test)

############################Species Model

StrokeNBMAspec<-rma(yi=lnROM,sei=ROM\_se,data= strokeNB,mods=~Animal-1)

StrokeNBMAspec2<-rma(yi=lnROM,sei=ROM\_se,data= strokeNB,mods=~Animal)

#Table Stuff

as.data.frame(table(strokeIV$Animal))->speciestableIV

signif(StrokeIVMAspec $pval,digits=2)-> strokeAnimalpvals

# Speciesplot

pdf("strokespecies.pdf",width=9,height=4)

forest(StrokeIVMAspec $b,sei= StrokeIVMAspec $se,atransf=exp,slab=paste(speciestableIV $Var1),ilab=cbind(speciestableIV $Freq, strokeAnimalpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Species on Stroke Infarct Volume")

text(-6,6,"Species",pos=4,font=4)

text(-5,6,"# Studycohorts",pos=4,font=4)

text(-3.5,6,"P-value",pos=4,font=4)

text(-3.5,5.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,6,"Infarct Size",pos=4,font=4)

text(-1,5.5,"Reduction",pos=4,font=4)

text(3,6,"ROM + 95% CI",font=4,pos=2)

text(1,2.2,paste(c("P = ",round(StrokeMAspec2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=4,length=0.05,angle=90,code=3)

dev.off()

##################################

droplevels(strokeIV$Immunisupp)->strokeIV$Immunisupp

factor(strokeIV$Immunisupp,levels=c("none","cyclosporin A"))->strokeIV$Immunisupp

factor(strokeIV$Immunisupp,labels=c("None","Cyclosporin A"))->strokeIV$Immunisupp

StrokeMA2im<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Immunisupp-1)

StrokeMA2.1im<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Immunisupp)

StrokeMA2.1im

#Table Stuff

as.data.frame(table(strokeIV$Immunisupp))->immtable

signif(StrokeMA2im $pval,digits=2)-> immpvals

pdf("strokeimmunisupp.pdf",width=9,height=4)

forest(StrokeMA2im $b,sei= StrokeMA2im $se,atransf=exp,slab=paste(immtable $Var1),ilab=cbind(immtable$Freq, immpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Immunosupression on Stroke Infarct Volume")

text(-6,4,"Imm.supp",pos=4,font=4)

text(-5,4,"# Studycohorts",pos=4,font=4)

text(-3.5,4,"P-value",pos=4,font=4)

text(-3.5,3.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,4,"Infarct Size",pos=4,font=4)

text(-1,3.5,"Reduction",pos=4,font=4)

text(3,4,"ROM + 95% CI",font=4,pos=2)

text(1,1.25,paste(c("p = ",round(StrokeMA2.1im $QMp,3))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=2,length=0.05,angle=90,code=3)

dev.off()

############### Cell type ---

StrokeMACell<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Type-1)

StrokeMACell2<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Type)

StrokeMACell

StrokeMACell2

#Table Stuff

as.data.frame(table(strokeIV$Cell.Type))->Cellstable

signif(StrokeMACell $pval,digits=2)-> strokecellpvals

# Speciesplot

pdf("strokecelltype.pdf",width=9,height=4)

forest(StrokeMACell $b,sei= StrokeMACell $se,atransf=exp,slab=paste(Cellstable $Var1),ilab=cbind(Cellstable$Freq, strokecellpvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-type on Stroke Infarct Volume")

text(-6,8,"Cell-type",pos=4,font=4)

text(-5,8,"# Studycohorts",pos=4,font=4)

text(-3.5,8,"P-value",pos=4,font=4)

text(-3.5,7.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,8,"Infarct Size",pos=4,font=4)

text(-1,7.5,"Reduction",pos=4,font=4)

text(3,8,"ROM + 95% CI",font=4,pos=2)

text(1,3.2,paste(c("P = ",round(StrokeMACell2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=1,y1=6,length=0.05,angle=90,code=3)

dev.off()

####### Source

factor(strokeIV$Cell.Source,levels=c("Autologous","Allogeneic","Xenogeneic"))->strokeIV$Cell.Source

StrokeMASource<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Source-1)

StrokeMASource2<-rma(yi=lnROM,sei=ROM\_se,data=strokeIV,mods=~ Cell.Source)

StrokeMASource

StrokeMASource2

#Table Stuff

as.data.frame(table(strokeIV$Cell.Source))->Sourcestable

signif(StrokeMASource $pval,digits=2)-> strokeSourcepvals

# Speciesplot

pdf("strokecellsource.pdf",width=9,height=4)

forest(StrokeMASource $b,sei= StrokeMASource $se,atransf=exp,slab=paste(Sourcestable $Var1),ilab=cbind(Sourcestable$Freq, strokeSourcepvals),ilab.xpos=c(-4,-3),at=(c(log(0.25),log(0.5), 0, log(1),log(2))),xlim=c(-6, 3),main="Effects of Cell-Source on Stroke Infarct Volume")

text(-6,5,"Cell-Source",pos=4,font=4)

text(-5,5,"# Studycohorts",pos=4,font=4)

text(-3.5,5,"P-value",pos=4,font=4)

text(-3.5,4.5,"(vs no-effect)",pos=4,font=1,cex=0.8)

text(-1,5,"Infarct Size",pos=4,font=4)

text(-1,4.5,"Reduction",pos=4,font=4)

text(3,5,"ROM + 95% CI",font=4,pos=2)

text(1,1.9,paste(c("P = ",round(StrokeMASource2 $QMp,4))),srt=-90,cex=0.8)

arrows(x0=0.8,x1=0.8,y0=0.8,y1=3.2,length=0.05,angle=90,code=3)

dev.off()

1. **Multivariable model (all datasets) (performed in STATA, code below)**

import excel "XXXXX", sheet("Sheet1\_wodoubles") firstrow clear

encode TypeofDisease, generate (data)

tabulate data, gen(data)

encode Animal2, generate (animal)

tabulate animal, gen(animal)

encode CellType2, generate (cell)

tabulate cell, gen(cell)

encode CellSource2, generate (origin)

tabulate origin, gen(origin)

encode Immunisupp2, generate (immuno)

tabulate immuno, gen(immuno)

encode Delivery, generate (deliver)

tabulate deliver, gen(deliver)

encode Delivery, generate (deliver)

tabulate deliver, gen(deliver)

gen logallo = log(allonetric+1)

encode TimeofAdmin, generate (timing)

tabulate timing, gen(timing)

#multivariable model with all data!#

metareg (lnROM) data1 data2 data3 data4 data5 animal1 animal2 animal3 animal4 animal5 origin1 origin2 immuno1 immuno2 immuno3 immuno4 immuno5 cell10 cell1 cell2 cell3 cell4 cell5 cell6 cell7 cell9 logallo deliver1 deliver2 deliver3 deliver4 timing1 timing2 timing3, wsse (ROM\_se)

metareg(lnROM) deliver1 deliver2, wsse(ROM\_se)

metareg(lnROM) Dose, wsse(ROM\_se)

metareg (lnROM) animal1 animal2 animal3 animal4 animal5 animal6 animal8, wsse (ROM\_se)

metareg (lnROM) data1 data2 data3 data4 data5 animal1 animal2 animal3 animal4 animal5 origin1 origin2 immuno1 immuno2 immuno3 immuno4 cell10 cell1 cell2 cell3 cell4 cell5 cell6 cell7 cell9, wsse (ROM\_se)

SINGLE DATASETS Multivariable

import excel "/Users/peterpaulzw/Dropbox/CAMARADES joint stem cell in animal research project/Datafiles/201702ALL DATASETS.PP.xlsx", sheet("Kidney\_U") firstrow clear

import excel "/Users/peterpaulzw/Dropbox/CAMARADES joint stem cell in animal research project/Datafiles/201702ALL DATASETS.PP.xlsx", sheet("Kidney\_BP") firstrow clear

import excel "/Users/peterpaulzw/Dropbox/CAMARADES joint stem cell in animal research project/Datafiles/201702ALL DATASETS.PP.xlsx", sheet("Stroke") firstrow clear

import excel "/Users/peterpaulzw/Dropbox/CAMARADES joint stem cell in animal research project/Datafiles/201702ALL DATASETS.PP.xlsx", sheet("SCI") firstrow clear

import excel "/Users/peterpaulzw/Dropbox/CAMARADES joint stem cell in animal research project/Datafiles/201702ALL DATASETS.PP.xlsx", sheet("MI\_large") firstrow clear

import excel "/Users/peterpaulzw/Dropbox/CAMARADES joint stem cell in animal research project/Datafiles/201702ALL DATASETS.PP.xlsx", sheet("MI\_CSC") firstrow clear

metareg(lnROM) Dose deliver1 deliver2 deliver3 animal1 animal2 cell1 cell2 cell3 cell4 cell5 cell6 timing1 timing2, wsse(ROM\_se)