

Correlation between Amyloid burden and Delay Recall on Memory (from ADNI data)

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library("ADNIMERGE")
library(psych)
dxmci=dxsum[dxsum[, "DXMDUE"] == "MCI due to Alzheimer's Disease" &
!is.na(dxsum$DXMDUE) & dxsum[, "DXMDES"] == "MCI - Memory features
(amnestic)" & !is.na(dxsum$DXMDES),]
mcimerged0 <- merge(dxmci, adnimerge, by=c("RID", "VISCODE"))
mcimerged1 <- merge(mcimerged0, neurobat, by=c("RID", "VISCODE"))
mcimerged2 <- merge(mcimerged1, adas, by=c("RID", "VISCODE"))
mciwav <- mcimerged2[!is.na(mcimerged2$AV45) & mcimerged2[, "VISCODE"] ==
"bl" ,]
#mCIF1 <- mciwav[mciwav[, "AVDEL30MIN"] < 4 & !is.na(mciwav$AVDEL30MIN),]
#mCIF1a <- mCIF1[mCIF1[, "Q4SCORE"] > 6 & !is.na(mCIF1$Q4SCORE),]
#mCIF2 <- mCIF1a[mCIF1a[, "AVDELTOT"] < 11 & !is.na(mCIF1a$AVDELTOT),]
#mCIF2 <- mciwav[!is.na(mciwav$Q8SCORE) & !is.na(mciwav$Q4SCORE) &
!is.na(mciwav$AVDELTOT) & !is.na(mciwav$AVDEL30MIN) & !is.na(mciwav$Q4SCORE)&
mciwav[, "VISCODE"] == "bl" & mciwav[, "AGE"] > 65 & mciwav[, "AVDEL30MIN"]
< 4 & mciwav[, "AVDELTOT"] < 11 & mciwav[, "Q4SCORE"] > 6 & mciwav[,
"Q8SCORE"] > 6,]
mCIF2 <- mciwav[!is.na(mciwav$Q4SCORE) & !is.na(mciwav$AVDEL30MIN) & mciwav[,
"VISCODE"] == "bl",]
mCIF2$zAVD = (mCIF2$AVDEL30MIN -
mean(mCIF2$AVDEL30MIN))/sd(mCIF2$AVDEL30MIN)
mCIF2$zDR = (mean(mCIF2$Q4SCORE) - mCIF2$Q4SCORE)/sd(mCIF2$Q4SCORE)
gfam <- data.frame(mCIF2$zAVD, mCIF2$zDR)
famod <- fa(gfam, scores="regression")
mCIF2$cs <- famod$scores
mCIF2$cAGE = mCIF2$AGE + mCIF2$Years
a <- lm(mCIF2$cs ~ mCIF2$AV45.bl + mCIF2$PTGENDER + mCIF2$PTEDUCAT +
mCIF2$AGE)
summary(a)
y.data <- data.frame(mCIF2["cs"], mCIF2["AV45.bl"], mCIF2["PTGENDER"],
mCIF2["PTEDUCAT"], mCIF2["AGE"])
y.data$Gender <- as.integer(factor(y.data$PTGENDER,
levels=c("Male","Female"), labels=c(0,1)))
pcv <- pcor.test(y.data["AV45.bl"], y.data["cs"], y.data[, c("Gender",
"PTEDUCAT", "AGE")])
pcv

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Con PiB

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library("ADNIMERGE")
library(psych)
dxmci=dxsum[dxsum[, "DXMDUE"] == "MCI due to Alzheimer's Disease" &

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!is.na(dxsum$DXMDUE) & dxsum[, "DXMDES"] == "MCI - Memory features
(amnestic)" & !is.na(dxsum$DXMDES),]
mcimerged0 <- merge(dxmci, adnimerge, by=c("RID", "VISCODE"))
mcimerged1 <- merge(mcimerged0, neurobat, by=c("RID", "VISCODE"))
mcimerged2 <- merge(mcimerged1, adas, by=c("RID", "VISCODE"))
mciwav <- mcimerged2[!is.na(mcimerged2$PIB.bl) & mcimerged2[, "VISCODE"] ==
"bl",]
mcif2 <- mciwav[!is.na(mciwav$Q4SCORE) &!is.na(mciwav$AVDEL30MIN),]
mcif2$zAVD = (mcif2$AVDEL30MIN -
mean(mcif2$AVDEL30MIN))/sd(mcif2$AVDEL30MIN)
mcif2$zDR = (mean(mcif2$Q4SCORE) - mcif2$Q4SCORE)/sd(mcif2$Q4SCORE)
gfam <- data.frame(mcif2$zAVD, mcif2$zDR)
famod <- fa(gfam, scores="regression")
mcif2$cs <- famod$scores
a <- lm(mcif2$cs ~ mcif2$PIB.bl + mcif2$PTGENDER + mcif2$PTEDUCAT +
mcif2$AGE)
summary(a)
y.data <- data.frame(mcif2["cs"], mcif2["PIB.bl"], mcif2["PTGENDER"],
mcif2["PTEDUCAT"], mcif2["AGE"])
y.data$Gender <- as.integer(factor(y.data$PTGENDER,
levels=c("Male","Female"), labels=c(0,1)))
pcv <- pcor.test(y.data["PIB.bl"], y.data["cs"], y.data[, c("Gender",
"PTEDUCAT", "AGE")])
pcv

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Doing it right

PIB

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library("ADNIMERGE")
library(psych)
library(ppcor)
zscore <- function(x, inv=FALSE){
  if (!inv) {
    result <- (x - mean(x))/sd(x)
  } else {
    result <- (mean(x) - x)/sd(x)};
  return(result)
}
dxmci=dxsum[dxsum[, "DXMDUE"] == "MCI due to Alzheimer's Disease" &
!is.na(dxsum$DXMDUE) & dxsum[, "DXMDES"] == "MCI - Memory features
(amnestic)" & !is.na(dxsum$DXMDES),]
mcimerged0 <- merge(dxmci, adnimerge, by=c("RID", "VISCODE"))
mcimerged1 <- merge(mcimerged0, neurobat, by=c("RID", "VISCODE"))
mcimerged2 <- merge(mcimerged1, adas, by=c("RID", "VISCODE"))
mciwav <- mcimerged2[!is.na(mcimerged2$PIB),]
mcif1 <- mciwav[!is.na(mciwav$Q4SCORE) &!is.na(mciwav$AVDEL30MIN),]
mcif1[!duplicated(mcif1$RID),] -> mcif2

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mcif2$zAVD = zscore(mcif2$AVDEL30MIN)
mcif2$zDR = zscore(mcif2$Q4SCORE, TRUE)
gfam <- data.frame(mcif2$zAVD, mcif2$zDR)
famod <- fa(gfam, scores="regression")
mcif2$cs <- zscore(famod$scores)
mcif2$cAGE = mcif2$AGE + mcif2$Years
y.data <- data.frame(mcif2["RID"], mcif2["cs"], mcif2["PIB"],
mcif2["PTGENDER"], mcif2["PTEDUCAT"], mcif2["cAGE"], mcif2["VISCODE"])
y.data$Gender <- as.integer(factor(y.data$PTGENDER,
levels=c("Male","Female"), labels=c(0,1)))
y.data$visit <- as.integer(factor(y.data$VISCODE,
levels=c("bl","m12","m24","m36","m48"), labels=c(0,1,2,3,4)))
pcv <- pcor.test(y.data["PIB"], y.data["cs"], y.data[, c("Gender",
"PTEDUCAT", "cAGE")])
pcv

for(i in 1:length(mcif2$RID)){
  tmp <- adnimerge[adnimerge$RID==mcif2$RID[i],]
  if(i == 1){
    mcihist <- tmp
  } else {
    mcihist <- rbind(mcihist, tmp)
  }
}
mcihist[mcihist$DX == "MCI to Dementia" & !is.na(mcihist$DX),] -> mciconv
data.frame(mciconv$RID, mciconv$VISCODE,
mciconv$DX)[!duplicated(mciconv$RID),] -> mciconv2
colnames(mciconv2) <- c("RID", "CVISCODE", "DX")

# tratar de sacar la ultima visita de cada uno
require(data.table)
data.frame(mcihist$RID, mcihist$VISCODE, mcihist$DX) -> mciallvis
colnames(mciallvis) <- c("RID", "VISCODE", "DX")
visits <- read.csv("viscode.csv", header = FALSE)
mciallvis$visit <- as.integer(factor(mciallvis$VISCODE, levels=visits$V2,
labels=visits$V1))
as.data.table(mciallvis) -> mciallvis
mciallvis[mciallvis[, .I[which.max(visit)], by=RID]$V1] -> lastvis

y.data$visit <- as.integer(factor(y.data$VISCODE, levels=visits$V2,
labels=visits$V1))
mciconv2$cvisit <- as.integer(factor(mciconv2$CVISCODE, levels=visits$V2,
labels=visits$V1))

y.data$cvisit <- NA
y.data$lvisit <- NA

for(i in 1:length(mciconv2$RID)){
  y.data$cvisit[y.data$RID==mciconv2$RID[i]] <- mciconv2$cvisit[i]
}
for(i in 1:length(lastvis$RID)){

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y.data$lvisit[y.data$RID==lastvis$RID[i]] <- lastvis$visit[i]
}

y.data$Conversion <- ifelse(!is.na(y.data$cvisit), 1, 0)
y.data$Seguimiento <- ifelse(!is.na(y.data$cvisit), y.data$cvisit-
y.data$visit,y.data$lvisit-y.data$visit)
towrite <- data.frame("RID", "cs", "Conversion", "Seguimiento", "cAGE",
"PTGENDER", "PTEDUCAT" )
colnames(towrite) <- c("RID", "cs", "Conversion", "Seguimiento", "Age",
"Gender", "Education")

write.csv(towrite, file="adni_conversion.csv", row.names=F)

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AV45

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library("ADNIMERGE")
library(psych)
library(ppcor)
dxmci=dxsum[dxsum[, "DXMDUE"] == "MCI due to Alzheimer's Disease" &
!is.na(dxsum$DXMDUE) & dxsum[, "DXMDES"] == "MCI - Memory features
(amnestic)" & !is.na(dxsum$DXMDES),]
mcimerged0 <- merge(dxmci, adnimerge, by=c("RID", "VISCODE"))
mcimerged1 <- merge(mcimerged0, neurobat, by=c("RID", "VISCODE"))
mcimerged2 <- merge(mcimerged1, adas, by=c("RID", "VISCODE"))
mciwav <- mcimerged2[!is.na(mcimerged2$AV45),]
mcif1 <- mciwav[!is.na(mciwav$Q4SCORE) &!is.na(mciwav$AVDEL30MIN),]
mcif1[!duplicated(mcif1$RID),] -> mcif2
mcif2$zAVD = (mcif2$AVDEL30MIN -
mean(mcif2$AVDEL30MIN))/sd(mcif2$AVDEL30MIN)
mcif2$zDR = (mean(mcif2$Q4SCORE) - mcif2$Q4SCORE)/sd(mcif2$Q4SCORE)
gfam <- data.frame(mcif2$zAVD, mcif2$zDR)
famod <- fa(gfam, scores="regression")
mcif2$cs <- famod$scores
mcif2$cAGE = mcif2$AGE + mcif2$Years
y.data <- data.frame(mcif2["RID"], mcif2["cs"], mcif2["AV45"],
mcif2["PTGENDER"], mcif2["PTEDUCAT"], mcif2["AGE"], mcif2["VISCODE"])
y.data$Gender <- as.integer(factor(y.data$PTGENDER,
levels=c("Male","Female"), labels=c(0,1)))
pcv <- pcor.test(y.data["AV45"], y.data["cs"], y.data[, c("Gender",
"PTEDUCAT", "AGE")])
pcv

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