

# Supplementary Material

**Estimates of Intracellular Dopamine in Parkinson's Disease: A Systematic Review and Meta-Analysis**

**Supplementary File 1.** R-code for analysis

**Supplementary File 2.** Excel file with data used for the meta-analyses.

## Supplementary File 1.

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## PD Cell View v.2.1
## 04.08.2021 for Journal of Parkinson's Disease
## by Jonathan Sackner-Bernstein
setwd("~/Sync/Neurosciences/Manuscript/JournPD Submission/Analysis")
#
library(readxl)
library(metafor)
# read in data:
dopamine <- read_excel("Dopaminergic Biochem 2021.APR.05.xlsx",
  sheet = "Dopamine")
cells <- read_excel("Dopaminergic Biochem 2021.APR.05.xlsx", sheet = "Cells")
vmat2 <- read_excel("Dopaminergic Biochem 2021.APR.05.xlsx", sheet = "VMAT2")
### Impute missing sd as max SD/mean ratio for that parameter in other studies
# Some of the included studies do not include SD or variance.
sink("PD Dopamine Analysis 2021.APR.08.txt", append=TRUE, split=TRUE)
####
### 1. create variable of "sd/value" for each meta-analysis dataset
dopamine$nm1.caudate.dopamine.sd_value <- dopamine$nm1.caudate.dopamine.sd /
  dopamine$nm1.caudate.dopamine.value
dopamine$nm1.putamen.dopamine.sd_value <- dopamine$nm1.putamen.dopamine.sd /
  dopamine$nm1.putamen.dopamine.value
dopamine$pd.caudate.dopamine.sd_value <- dopamine$pd.caudate.dopamine.sd /
  dopamine$pd.caudate.dopamine.value
dopamine$pd.putamen.dopamine.sd_value <- dopamine$pd.putamen.dopamine.sd /
  dopamine$pd.putamen.dopamine.value
#
cells$nm1.sn.cells.sd_value <- cells$nm1.sn.cells.sd / cells$nm1.sn.cells.value
cells$pd.sn.cells.sd_value <- cells$pd.sn.cells.sd / cells$pd.sn.cells.value
#
vmat2$nm1.caudate.vmat2.sd_value <- vmat2$nm1.caudate.vmat2.sd /
  vmat2$nm1.caudate.vmat2.value
vmat2$nm1.putamen.vmat2.sd_value <- vmat2$nm1.putamen.vmat2.sd /
  vmat2$nm1.putamen.vmat2.value
vmat2$pd.caudate.vmat2.sd_value <- vmat2$pd.caudate.vmat2.sd /
  vmat2$pd.caudate.vmat2.value
vmat2$pd.putamen.vmat2.sd_value <- vmat2$pd.putamen.vmat2.sd /
  vmat2$pd.putamen.vmat2.value
### 2. find maximum of "sd/value" ratio
max.nm1.caudate.dopa.ratio <- max(dopamine$nm1.caudate.dopamine.sd_value,
  na.rm = TRUE)
max.nm1.putamen.dopa.ratio <- max(dopamine$nm1.putamen.dopamine.sd_value,
  na.rm = TRUE)
max.pd.caudate.dopa.ratio <- max(dopamine$pd.caudate.dopamine.sd_value,
  na.rm = TRUE)
max.pd.putamen.dopa.ratio <- max(dopamine$pd.putamen.dopamine.sd_value,
  na.rm = TRUE)
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# Find the maximum ratio, which will be used to impute missing sd
max.nml.sn.cell.ratio <- max(cells$nml.sn.cells.sd_value, na.rm = TRUE)
max.pd.sn.cell.ratio <- max(cells$pd.sn.cells.sd_value, na.rm = TRUE)
#
max.nml.caudate.vmat2.ratio <- max(vmat2$nml.caudate.vmat2.sd_value,
  na.rm = TRUE)
max.nml.putamen.vmat2.ratio <- max(vmat2$nml.putamen.vmat2.sd_value,
  na.rm = TRUE)
max.pd.caudate.vmat2.ratio <- max(vmat2$pd.caudate.vmat2.sd_value,
  na.rm = TRUE)
max.pd.putamen.vmat2.ratio <- max(vmat2$pd.putamen.vmat2.sd_value,
  na.rm = TRUE)
### 3. where sd=NA, multiply "sd/value" * max.ratio
# impute dopamine SDs for caudate
for(i in 1:nrow(dopamine)){
  if(is.na(dopamine$nml.caudate.dopamine.sd[i])){
    dopamine$nml.caudate.dopamine.sd[i] <-
      dopamine$nml.caudate.dopamine.value[i] * max.nml.caudate.dopa.ratio}
  if(is.na(dopamine$pd.caudate.dopamine.sd[i])){
    dopamine$pd.caudate.dopamine.sd[i] <-
      dopamine$pd.caudate.dopamine.value[i] * max.pd.caudate.dopa.ratio}
  # impute dopamine SDs for putamen
  if(is.na(dopamine$nml.putamen.dopamine.sd[i])){
    dopamine$nml.putamen.dopamine.sd[i] <-
      dopamine$nml.putamen.dopamine.value[i] * max.nml.putamen.dopa.ratio}
  if(is.na(dopamine$pd.putamen.dopamine.sd[i])){
    dopamine$pd.putamen.dopamine.sd[i] <-
      dopamine$pd.putamen.dopamine.value[i] * max.pd.putamen.dopa.ratio}
}
# impute cell numbers for substantia nigra
for(i in 1:nrow(cells)){
  if(is.na(cells$nml.sn.cells.sd[i])){
    cells$nml.sn.cells.sd[i] <- cells$nml.sn.cells.value[i] *
      max.nml.sn.cell.ratio}
  if(is.na(cells$pd.sn.cells.sd[i])){
    cells$pd.sn.cells.sd[i] <- cells$pd.sn.cells.value[i] *
      max.pd.sn.cell.ratio}
}
# impute vmat2 for caudate
for(i in 1:nrow(vmat2)){
  if(is.na(vmat2$nml.caudate.vmat2.sd[i])){
    vmat2$nml.caudate.vmat2.sd[i] <-
      vmat2$nml.caudate.vmat2.value[i] * max.nml.caudate.vmat2.ratio}
  if(is.na(vmat2$pd.caudate.vmat2.sd[i])){
    vmat2$pd.caudate.vmat2.sd[i] <-
      vmat2$pd.caudate.vmat2.value[i] * max.pd.caudate.vmat2.ratio}
  # impute vmat2 SDs for putamen
  if(is.na(vmat2$nml.putamen.vmat2.sd[i])){
    vmat2$nml.putamen.vmat2.sd[i] <-

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      vmat2$nl.putamen.vmat2.value[i] * max.nlm.putamen.vmat2.ratio)
if(is.na(vmat2$pd.putamen.vmat2.sd[i])){
  vmat2$pd.putamen.vmat2.sd[i] <-
    vmat2$pd.putamen.vmat2.value[i] * max.pd.putamen.vmat2.ratio}
}
#####
# Cells Meta-Analysis #
# Log Transformed ROM #
#####
cat("01.Difference in Log Transformed Cell Counts within SN\n")
cell_data_1 <- escalc(nli=nl.sn.cells.n, n2i = pd.sn.cells.n,
  m1i = nl.sn.cells.value, m2i = pd.sn.cells.value,
  sd1i = nl.sn.cells.sd, sd2i = pd.sn.cells.sd,
  data = cells, measure = "ROM", append = TRUE)
cell_model_1 <- rma(yi, vi, data = cell_data_1)
####
png(file = (paste("2021.APR.08 - ", "01.SN.Cells.ROM.png", sep="")),
  width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(cell_model_1, slab=paste(cells$study, sep=", "),
  cex=1.5, xlim=c(-3.5, 5), at=c(-1,0,1,2,3), alim=c(-1, 3))
par("usr")
title(main="01.Log Transformed Cell Count Difference in Substantia Nigra",
  font.main=2,cex.main=2.2)
text(-1.5, -1, paste("p=", round(cell_model_1$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-3, cell_model_1$k+2, "Study", pos=4, font=1, cex=1.75)
text(4, cell_model_1$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-1, -1.7, "Parkinson's Higher", cex=1.25)
text(3, -1.7, "Normals Higher", cex=1.25)
dev.off()
cat("02.Difference in Cell Counts within SN\n")
png(file = (paste("2021.APR.08 - ", "02.SN.Cells.Linear.png", sep="")),
  width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(cell_model_1, slab=paste(cells$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-7.5, 15), at=c(-2.5,0,2.5,5,7.5,10), alim=c(-2.5, 10))
par("usr")
title(main="02.Cell Count Difference with PD in Substantia Nigra",
  font.main=2,cex.main=2.2)
text(-3, -1, paste("p=", round(cell_model_1$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, cell_model_1$k+2, "Study", pos=4, font=1, cex=1.75)
text(14, cell_model_1$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(10, -1.7, "Normals Higher", cex=1.25)
dev.off()
### Calculate Ratio of PD/Nml SN Cell Counts
cells$ratio.sn.cells.value <- cells$pd.sn.cells.value /
  cells$nl.sn.cells.value
cells$ratio.sn.cells.sd <- sqrt( (cells$pd.sn.cells.value^2 /

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cells$nm1.sn.cells.value^2) *
((cells$pd.sn.cells.sd^2 / cells$pd.sn.cells.value^2) +
(cells$nm1.sn.cells.sd^2 / cells$nm1.sn.cells.value^2 )) )
cat("03.Log Transformed Ratio of PD/Nml SN Cell Counts\n")
cell_data_a <- escalc(ni=nm1.sn.cells.n, mi = ratio.sn.cells.value,
sdi = ratio.sn.cells.sd, data = cells, measure = "MNLN", append = TRUE)
cell_model_a <- rma(yi, vi, data = cell_data_a)
#
png(file = (paste("2021.APR.08 - ", "03.SN.Cells.Ratio.MNLN.png", sep="")),
width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(cell_model_a, slab=paste(cells$study, sep=", "),
cex=1.5, xlim=c(-5.5, 3), at=c(-3,-2,-1,0,1), alim=c(-3, 1))
par("usr")
title(main="03.Ratio of Cell Counts PD/Nml in Substantia Nigra",
font.main=2,cex.main=2.2)
text(-3.5, -1, paste("p=", round(cell_model_a$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-4.5, cell_model_a$k+2, "Study", pos=4, font=1, cex=1.75)
text(2.5, cell_model_a$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(1, -1.7, "Log PD/Normal", cex=1.25)
dev.off()
###
cat("04.Linear Ratio of PD/Nml SN Cell Counts\n")
png(file=(paste("2021.APR.08 - ", "04.SN.Cells.Ratio.Linear.png", sep="")),
width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(cell_model_a, slab=paste(cells$study, sep=", "), transf=transf.exp.int,
cex=1.5, xlim=c(-2, 2.5), at=c(-0.5,0,0.5,1), alim=c(-0.5, 1))
par("usr")
title(main="04.Linear Ratio of Cell Counts PD/Nml in Substantia Nigra",
font.main=2,cex.main=2.2)
text(-1, -1, paste("p=", round(cell_model_a$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-1.75, cell_model_a$k+2, "Study", pos=4, font=1, cex=1.75)
text(2.25, cell_model_a$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-0.5, -1.7, "Parkinson's Higher", cex=1.25)
text(1, -1.7, "Normals Higher", cex=1.25)
dev.off()
#####
# VMAT2 Meta-Analysis #
# Log Transformed ROM #
#####
cat("05.Mean Difference in Log Transformed Putamen VMAT2 Levels\n")
vm_data_1 <- escalc(nli=nm1.putamen.vmat2.n, n2i = pd.putamen.vmat2.n,
mli = nm1.putamen.vmat2.value, m2i = pd.putamen.vmat2.value,
sdli = nm1.putamen.vmat2.sd, sd2i = pd.putamen.vmat2.sd,
data = vmat2, measure = "ROM", append = TRUE)
vm_model_1 <- rma(yi, vi, data = vm_data_1)
####
png(file = (paste("2021.APR.08 - ", "05.VMAT2.Putamen.ROM.png", sep="")),

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width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(vm_model_1, slab=paste(vmat2$study, sep=", "),
       cex=1.5, xlim=c(-5, 7.5), at=c(-2.5,0,2.5,5), alim=c(-2.5,5))
par("usr")
title(main="05.Mean Log Transformed VMAT2 Difference with PD in Putamen",
      font.main=2,cex.main=2.2)
text(-2.5, -1, paste("p=", round(vm_model_1$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-4.5, vm_model_1$k+2, "Study", pos=4, font=1, cex=1.75)
text(7, vm_model_1$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(5, -1.7, "Log PD/Normal", cex=1.25)
dev.off()
#####
cat("06.Linear Mean Difference in Putamen VMAT2 Levels\n")
png(file=(paste("2021.APR.08 - ", "06.VMAT2.Putamen.Linear.png", sep="")),
    width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(vm_model_1, slab=paste(vmat2$study, sep=", "), transf=transf.exp.int,
       cex=1.5, xlim=c(-5, 10), at=c(-2.5,0,2.5,5,7.5), alim=c(-2.5,7.5))
par("usr")
title(main="06.Linear Mean VMAT2 Difference with PD in Putamen",
      font.main=2,cex.main=2.2)
text(-2.5, -1, paste("p=", round(vm_model_1$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-4, vm_model_1$k+2, "Study", pos=4, font=1, cex=1.75)
text(9.5, vm_model_1$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(5, -1.7, "Normals Higher", cex=1.25)
dev.off()
#####
cat("07.Mean Difference in Log Transformed Caudate VMAT2 Levels\n")
vm_data_2 <- escalc(nli=nml.caudate.vmat2.n, n2i = pd.caudate.vmat2.n,
  m1i = nml.caudate.vmat2.value, m2i = pd.caudate.vmat2.value,
  sd1i = nml.caudate.vmat2.sd, sd2i = pd.caudate.vmat2.sd,
  data = vmat2, measure = "ROM", append = TRUE)
vm_model_2 <- rma(yi, vi, data = vm_data_2)
####
png(file = (paste("2021.APR.08 - ", "07.VMAT2.Caudate.ROM.png", sep="")),
    width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(vm_model_2, slab=paste(vmat2$study, sep=", "),
       cex=1.5, xlim=c(-5, 7.5), at=c(-2.5,0,2.5,5), alim=c(-2.5,5))
par("usr")
title(main="07.Mean Log Transformed VMAT2 Difference with PD in Caudate",
      font.main=2,cex.main=2.2)
text(-2.5, -1, paste("p=", round(vm_model_2$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-4, vm_model_2$k+2, "Study", pos=4, font=1, cex=1.75)
text(7.5, vm_model_2$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(5, -1.7, "Normals Higher", cex=1.25)

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dev.off()
#####
cat("08.Mean Difference in Caudate VMAT2 Levels\n")
png(file = (paste("2021.APR.08 - ", "08.VMAT2.Caudate.Linear.png", sep="")),
     width = 1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(vm_model_2, slab=paste(vmat2$study, sep=", "), transf=transf.exp.int,
       cex=1.5, xlim=c(-3.5, 7.5), at=c(-1,0,1,2,3,4,5), alim=c(-1,5))
par("usr")
title(main="08.Linear Mean VMAT2 Difference with PD in Caudate",
      font.main=2,cex.main=2.2)
text(-1.5, -1, paste("p=", round(vm_model_2$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-2.5, vm_model_2$k+2, "Study", pos=4, font=1, cex=1.75)
text(7, vm_model_2$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-1, -1.7, "Parkinson's Higher", cex=1.25)
text(5, -1.7, "Normals Higher", cex=1.25)
dev.off()
#####
### Calculate Ratio of PD/Nml Putamen VMAT2 Protein Levels
vmat2$ratio.putamen.vmat2.value <- vmat2$pd.putamen.vmat2.value /
  vmat2$nml.putamen.vmat2.value
vmat2$ratio.putamen.vmat2.sd <- sqrt( (vmat2$pd.putamen.vmat2.value^2 /
  vmat2$nml.putamen.vmat2.value^2) *
  ((vmat2$pd.putamen.vmat2.sd^2 / vmat2$pd.putamen.vmat2.value^2) +
  (vmat2$nml.putamen.vmat2.sd^2 / vmat2$nml.putamen.vmat2.value^2) ) )
cat("09.Log Transformed Ratio of PD/Nml Putamen VMAT2 Protein Levels\n")
vm_data_a <- escalc(ni=nml.putamen.vmat2.n, mi = ratio.putamen.vmat2.value,
  sdi = ratio.putamen.vmat2.sd, data = vmat2, measure = "MNLN", append = TRUE)
vm_model_a <- rma(yi, vi, data = vm_data_a)
#
png(file = (paste("2021.APR.08 - ", "09.Putamen.VMAT2.Ratio.MNLN.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(vm_model_a, slab=paste(vmat2$study, sep=", "),
       cex=1.5, xlim=c(-8.5, 4.5), at=c(-6,-4,-2,0,2), alim=c(-6, 2))
par("usr")
title(main="09.Log Transformed Ratio of PD/Nml Putamen VMAT2 Protein Levels",
      font.main=2,cex.main=2.2)
text(-6, -1, paste("p=", round(vm_model_a$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-7.5, vm_model_a$k+2, "Study", pos=4, font=1, cex=1.75)
text(4, vm_model_a$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(2, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#
cat("10.Linear Ratio of PD/Nml Putamen VMAT2 Protein Levels\n")
png(file = (paste("2021.APR.08 - ", "10.Putamen.VMAT2.Ratio.Linear.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")

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forest(vm_model_a, slab=paste(vmat2$study, sep=", "), transf=transf.exp.int,
      cex=1.5, xlim=c(-1.25, 2), at=c(-0.25,0,0.25,0.5,0.75,1), alim=c(-0.25, 1))
par("usr")
title(main="10.Linear Ratio of PD/Nml Putamen VMAT2 Protein Levels",
      font.main=2,cex.main=2.2)
text(-0.5, -1, paste("p=", round(vm_model_a$pval, digits =3), sep=""),
      pos=2, font=1, cex=1.5)
text(-1, vm_model_a$k+2, "Study", pos=4, font=1, cex=1.75)
text(1.75, vm_model_a$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(1, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
### Calculate Ratio of PD/Nml Caudate VMAT2 Protein Levels
vmat2$ratio.caudate.vmat2.value <- vmat2$pd.caudate.vmat2.value /
  vmat2$nml.caudate.vmat2.value
vmat2$ratio.caudate.vmat2.sd <- sqrt((vmat2$pd.caudate.vmat2.value^2 /
  vmat2$nml.caudate.vmat2.value^2) *
  ((vmat2$pd.caudate.vmat2.sd^2 / vmat2$pd.caudate.vmat2.value^2) +
  (vmat2$nml.caudate.vmat2.sd^2 / vmat2$nml.caudate.vmat2.value^2 )) )
cat("11.Mean Ratio of PD/Nml Caudate VMAT2 Protein Levels\n")
vm_data_b <- escalc(ni=nml.caudate.vmat2.n, mi = ratio.caudate.vmat2.value,
  sdi = ratio.caudate.vmat2.sd, data = vmat2, measure = "MNLN", append = TRUE)
vm_model_b <- rma(yi, vi, data = vm_data_b)
#
png(file = (paste("2021.APR.08 - ", "11.Caudate.VMAT2.Ratio.MNLN.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(vm_model_b, slab=paste(vmat2$study, sep=", "),
      cex=1.5, xlim=c(-5, 5), at=c(-3,-2,-1,0,1,2,3), alim=c(-3, 3))
par("usr")
title(main="11.Log Transformed Ratio of PD/Nml Caudate VMAT2 Protein Levels",
      font.main=2,cex.main=2.2)
text(-3, -1, paste("p=", round(vm_model_b$pval, digits =3), sep=""),
      pos=2, font=1, cex=1.5)
text(-4.5, vm_model_b$k+2, "Study", pos=4, font=1, cex=1.75)
text(4.5, vm_model_b$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.5, "Parkinson's / Normal", cex=1.25)
dev.off()
#
cat("12.Ratio of PD/Nml Caudate VMAT2 Protein Levels\n")
png(file = (paste("2021.APR.08 - ", "12.Caudate.VMAT2.Ratio.Linear.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(vm_model_b, slab=paste(vmat2$study, sep=", "), transf=transf.exp.int,
      ref=1, cex=1.5, xlim=c(-2.5, 7.5), at=c(-1,0,1,2,3,4,5), alim=c(0, 5))
par("usr")
title(main="12.Linear Ratio of PD/Nml Caudate VMAT2 Protein Levels",
      font.main=2,cex.main=2.2)
text(-1, -1, paste("p=", round(vm_model_b$pval, digits =3), sep=""),
      pos=2, font=1, cex=1.5)

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text(-2, vm_model_b$k+2, "Study", pos=4, font=1, cex=1.75)
text(6.5, vm_model_b$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(5, -1.5, "Parkinson's / Normal", cex=1.25)
dev.off()
#####
# Calculate Ratios and Scale Dopamine #
#####
# After running meta-analyses for cell # and VMAT2, differences and ratios
# 1. Extract the point estimate/SE (to calculate SD) of cell number ratio
# 2. Assign values for value/SD of ratio of axon number
# 3. Extract point estimates/SE (to calculate SD) of VMAT2 ratio for PUTA/CAUD
# 4. Create new variables for DA scaled (cell # & axon)
# 5. Create new variables for DA scaled also for VMAT2
# 6. Run part 2 of meta-analyses: dopamine for Putamen/Caudate, then adjust
#     for cell/axon ratio and each also with VMAT2 ratio
# 1. Data for Cell Number ratio
cell_ratio <- as.vector(exp(cell_model_a$b))
cell_sd <- cell_model_a$se * sqrt(cell_model_a$k)
axon_ratio <- 0.28 # Kordower reports 28% of normal for total
axon_sd <- 0.15 # with group sd at 15% assumed same for both C & P
# 3. Data for VMAT2 ratio
vm_putamen_ratio <- as.vector(exp(vm_model_a$b))
vm_putamen_sd <- vm_model_a$se * sqrt(vm_model_a$k)
vm_caudate_ratio <- as.vector(exp(vm_model_b$b))
vm_caudate_sd <- vm_model_b$se * sqrt(vm_model_b$k)
# 4. Scale PD dopamine data to cell ratio & axon ratio
dopamine$pd.putamen.dopamine.adj.cell.value <-
  dopamine$pd.putamen.dopamine.value / c(cell_ratio)
dopamine$pd.putamen.dopamine.adj.cell.sd <-
  sqrt((dopamine$pd.putamen.dopamine.value^2 / cell_ratio^2) *
    ((dopamine$pd.putamen.dopamine.sd^2 /
    dopamine$pd.putamen.dopamine.value^2) +
    (cell_sd^2 / cell_ratio^2)))
dopamine$pd.caudate.dopamine.adj.cell.value <-
  dopamine$pd.caudate.dopamine.value / cell_ratio
dopamine$pd.caudate.dopamine.adj.cell.sd <-
  sqrt((dopamine$pd.caudate.dopamine.value^2 / cell_ratio^2) *
    ((dopamine$pd.caudate.dopamine.sd^2 /
    dopamine$pd.caudate.dopamine.value^2) +
    (cell_sd^2 / cell_ratio^2)))
dopamine$pd.putamen.dopamine.adj.axon.value <-
  dopamine$pd.putamen.dopamine.value / axon_ratio
dopamine$pd.putamen.dopamine.adj.axon.sd <-
  sqrt((dopamine$pd.putamen.dopamine.value^2 / axon_ratio^2) *
    ((dopamine$pd.putamen.dopamine.sd^2 /
    dopamine$pd.putamen.dopamine.value^2) +
    (axon_sd^2 / axon_ratio^2)))
dopamine$pd.caudate.dopamine.adj.axon.value <-
  dopamine$pd.caudate.dopamine.value / axon_ratio

```

```

dopamine$pd.caudate.dopamine.adj.axon.sd <-
  sqrt((dopamine$pd.caudate.dopamine.value^2 / axon_ratio^2) *
    ((dopamine$pd.caudate.dopamine.sd^2 /
      dopamine$pd.caudate.dopamine.value^2) +
      (axon_sd^2 / axon_ratio^2)))
# 5. Scale the scaled PD dopamine data to VMAT2 ratio
dopamine$pd.putamen.dopamine.adj.cell.vm.value <-
  dopamine$pd.putamen.dopamine.adj.cell.value / vm_putamen_ratio
dopamine$pd.putamen.dopamine.adj.cell.vm.sd <-
  sqrt((dopamine$pd.putamen.dopamine.adj.cell.value^2 /
    vm_putamen_ratio^2) *
    ((dopamine$pd.putamen.dopamine.adj.cell.sd^2 /
      dopamine$pd.putamen.dopamine.adj.cell.value^2 ) +
      (vm_putamen_sd^2 / vm_putamen_ratio^2) ) )
dopamine$pd.caudate.dopamine.adj.cell.vm.value <-
  dopamine$pd.caudate.dopamine.adj.cell.value / vm_caudate_ratio
dopamine$pd.caudate.dopamine.adj.cell.vm.sd <-
  sqrt( (dopamine$pd.caudate.dopamine.adj.cell.value^2 /
    vm_putamen_ratio^2) *
    ((dopamine$pd.caudate.dopamine.adj.cell.sd^2 /
      dopamine$pd.caudate.dopamine.adj.cell.value^2 ) +
      (vm_caudate_sd^2 / vm_caudate_ratio^2) ) )
dopamine$pd.putamen.dopamine.adj.axon.vm.value <-
  dopamine$pd.putamen.dopamine.adj.axon.value / vm_putamen_ratio
dopamine$pd.putamen.dopamine.adj.axon.vm.sd <-
  sqrt((dopamine$pd.putamen.dopamine.adj.axon.value^2 /
    vm_putamen_ratio^2) *
    ((dopamine$pd.putamen.dopamine.adj.axon.sd^2 /
      dopamine$pd.putamen.dopamine.adj.axon.value^2 ) +
      (vm_putamen_sd^2 / vm_putamen_ratio^2) ) )
dopamine$pd.caudate.dopamine.adj.axon.vm.value <-
  dopamine$pd.caudate.dopamine.adj.axon.value / vm_caudate_ratio
dopamine$pd.caudate.dopamine.adj.axon.vm.sd <-
  sqrt( (dopamine$pd.caudate.dopamine.adj.axon.value^2 /
    vm_putamen_ratio^2) *
    ((dopamine$pd.caudate.dopamine.adj.axon.sd^2 /
      dopamine$pd.caudate.dopamine.adj.axon.value^2 ) +
      (vm_caudate_sd^2 / vm_caudate_ratio^2) ) )
# 6. Run part 2 of meta-analyses
# - dopamine for Putamen and caudate
# - dopamine adjusted for cell/axon ratio
# - dopamine adjusted for cell/axon ratio and VMAT2 ratio
#####
#      Unscaled Dopamine Meta-Analysis      #
#      Log Transformed ROM Differences      #
#####
cat("13.Mean Difference in Log Transformed Putamen Dopamine Levels]\n")
da_data_1 <- escalc(nli=nml.putamen.dopamine.n, n2i = pd.putamen.dopamine.n,
  mli = nml.putamen.dopamine.value, m2i = pd.putamen.dopamine.value,

```

```

sdli = nml.putamen.dopamine.sd, sd2i = pd.putamen.dopamine.sd,
data = dopamine, measure = "ROM", append = TRUE)
da_model_1 <- rma(yi, vi, data = da_data_1)
####
png(file = (paste("2021.APR.08 - ", "13.DA.Putamen.ROM.png", sep="")),
width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_1, slab=paste(dopamine$study, sep=", "),
cex=1.5, xlim=c(-10,12.5), at=c(-2.5,-0,2.5,5,7.5), alim=c(-2.5,7.5))
par("usr")
title(main="13.Log Transformed DA Difference with PD in Putamen", font.main=2,
cex.main=2.2)
text(-5, -1, paste("p=", round(da_model_1$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-8, da_model_1$k+2, "Study", pos=4, font=1, cex=1.75)
text(11.5, da_model_1$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.75, "Parkinson's Higher", cex=1.25)
text(7.5, -1.75, "Normals Higher", cex=1.25)
dev.off()
###
cat("14.Linear Mean Difference in Putamen Dopamine Levels]\n")
png(file = (paste("2021.APR.08 - ", "14.DA.Putamen.Linear.png", sep="")),
width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_1, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
cex=1.5, xlim=c(-25,75), at=c(0,10,20,30,40,50), alim=c(0,50))
par("usr")
title(main="DA Difference with PD in Putamen", font.main=2,
cex.main=2.2)
text(-10, -1, paste("p=", round(da_model_1$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-15, da_model_1$k+2, "Study", pos=4, font=1, cex=1.75)
text(70, da_model_1$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.75, "Parkinson's Higher", cex=1.25)
text(55, -1.75, "Normals Higher", cex=1.25)
dev.off()
#####
cat("15.Mean Difference in Log Transformed Caudate Dopamine Levels\n")
da_data_2 <- escalc(nli=nml.caudate.dopamine.n, n2i = pd.caudate.dopamine.n,
mli = nml.caudate.dopamine.value, m2i = pd.caudate.dopamine.value,
sdli = nml.caudate.dopamine.sd, sd2i = pd.caudate.dopamine.sd,
data = dopamine, measure = "ROM", append = TRUE)
da_model_2 <- rma(yi, vi, data = da_data_2)
summary(da_model_2)
####
png(file = (paste("2021.APR.08 - ", "15.DA.Caudate.ROM.png", sep="")),
width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_2, slab=paste(dopamine$study, sep=", "),
cex=1.5, xlim=c(-7.5,12.5), at=c(-2.5,-0,2.5,5,7.5), alim=c(-2.5,7.5))
par("usr")
title(main="15.Log Transformed DA Difference with PD in Caudate",

```

```

font.main=2,cex.main=2.2)
text(-4, -1, paste("p=", round(da_model_2$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, da_model_2$k+2, "Study", pos=4, font=1, cex=1.75)
text(11.5, da_model_2$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(7.5, -1.7, "Normals Higher", cex=1.25)
dev.off()
###
cat("16.Linear Mean Difference in Caudate Dopamine Levels]\n")
png(file = (paste("2021.APR.08 - ", "16.DA.Caudate.Linear.png", sep="")),
  width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_2, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-10,25), at=c(0,5,10,15,20), alim=c(0,20))
par("usr")
title(main="16.DA Difference with PD in Caudate",
  font.main=2,cex.main=2.2)
text(-3.5, -1, paste("p=", round(da_model_2$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-8, da_model_2$k+2, "Study", pos=4, font=1, cex=1.75)
text(24, da_model_2$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
#text(0, -1.7, "Parkinson's Higher", cex=1.25)
text(20, -1.7, "Normals Higher", cex=1.25)
dev.off()
#####
###                                     ###
### Calculate Ratio of PD/Nml Putamen Dopamine Levels ###
###                                     ###
#####
dopamine$ratio.putamen.dopamine.value <- dopamine$pd.putamen.dopamine.value /
  dopamine$nml.putamen.dopamine.value
dopamine$ratio.putamen.dopamine.sd <-
  sqrt((dopamine$pd.putamen.dopamine.value^2 /
    dopamine$nml.putamen.dopamine.value^2) *
    ((dopamine$pd.putamen.dopamine.sd^2 / dopamine$pd.putamen.dopamine.value^2) +
    (dopamine$nml.putamen.dopamine.sd^2 / dopamine$nml.putamen.dopamine.value^2)))
cat("17.Mean Ratio of PD/Nml Putamen Dopamine Levels\n")
da_data_a <- escalc(ni=nml.putamen.dopamine.n, mi =ratio.putamen.dopamine.value,
  sdi = ratio.putamen.dopamine.sd, data = dopamine, measure = "MNLN",
  append = TRUE)
da_model_a <- rma(yi, vi, data = da_data_a)
#
png(file = (paste("2021.APR.08 - ", "17.Putamen.DA.Ratio.MNLN.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_a, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-10, 5), at=c(-6,-4,-2,0,2), alim=c(-6,2))
par("usr")
title(main="17.Log Transformed Ratio of PD/Nml Putamen Dopamine Levels",

```

```

font.main=2,cex.main=2.2)
text(-7, -1, paste("p=", round(da_model_a$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-9.5, da_model_a$k+2, "Study", pos=4, font=1, cex=1.75)
text(4.5, da_model_a$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(2, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#
cat("18.Ratio of PD/Nml Putamen Dopamine Levels\n")
png(file = (paste("2021.APR.08 - ", "18.Putamen.DA.Ratio.Linear.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_a, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-0.75, 1.5), at=c(-0.5,-0.25,0,0.25,0.5,0.75), alim=c(-0.25, 0.75))
par("usr")
title(main="18.Ratio of PD/Nml Putamen Dopamine Levels",
  font.main=2,cex.main=2.2)
text(-0.3, -1, paste("p=", round(da_model_a$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-0.5, da_model_a$k+2, "Study", pos=4, font=1, cex=1.75)
text(0.6, da_model_a$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(0.75, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#
### Calculate Ratio of PD/Nml Caudate Dopamine Levels
dopamine$ratio.caudate.dopamine.value <- dopamine$pd.caudate.dopamine.value /
  dopamine$nml.caudate.dopamine.value
dopamine$ratio.caudate.dopamine.sd <-
  sqrt((dopamine$pd.caudate.dopamine.value^2 /
  dopamine$nml.caudate.dopamine.value^2) *
  ((dopamine$pd.caudate.dopamine.sd^2 / dopamine$pd.caudate.dopamine.value^2) +
  (dopamine$nml.caudate.dopamine.sd^2 / dopamine$nml.caudate.dopamine.value^2)))
cat("19.Log Transformed Mean Ratio of PD/Nml Caudate Dopamine Levels\n")
da_data_b <- escalc(ni=nml.caudate.dopamine.n, mi =ratio.caudate.dopamine.value,
  sdi = ratio.caudate.dopamine.sd, data = dopamine, measure = "MNLN",
  append = TRUE)
da_model_b <- rma(yi, vi, data = da_data_b)
#
png(file = (paste("2021.APR.08 - ", "19.Caudate.DA.Ratio.MNLN.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_b, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-7.5, 3.5), at=c(-5,-4,-3,-2,-1,0,1), alim=c(-5, 1))
par("usr")
title(main="19.Log Transformed Ratio of PD/Nml Caudate Dopamine Levels",
  font.main=2,cex.main=2.2)
text(-5.5, -1, paste("p=", round(da_model_b$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-7, da_model_b$k+2, "Study", pos=4, font=1, cex=1.75)

```

```

text(3, da_model_b$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(1, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#
cat("20.Linear Mean Ratio in Caudate Dopamine Levels]\n")
png(file = (paste("2021.APR.08 - ", "20.Caudate.DA.Ratio.Linear.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_b, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-1, 2), at=c(0,0.25,0.5,0.75,1), alim=c(0,1))
par("usr")
title(main="20.Linear Ratio of PD/Nml Caudate Dopamine Levels",
  font.main=2,cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_b$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-0.75, da_model_b$k+2, "Study", pos=4, font=1, cex=1.75)
text(1.85, da_model_b$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(1, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#####
# Scale Dopamine Ratios for Meta-Analysis #
#####
### Calculate Ratio of PD/Nml Putamen Dopamine Levels Scaled to Cell Number
dopamine$ratio.putamen.dopamine.adj.cell.value <-
  dopamine$pd.putamen.dopamine.adj.cell.value /
  dopamine$nml.putamen.dopamine.value
dopamine$ratio.putamen.dopamine.adj.cell.sd <-
  sqrt((dopamine$pd.putamen.dopamine.adj.cell.value^2 /
  dopamine$nml.putamen.dopamine.value^2)*
  ((dopamine$pd.putamen.dopamine.adj.cell.sd^2 /
  dopamine$pd.putamen.dopamine.adj.cell.value^2) +
  (dopamine$nml.putamen.dopamine.sd^2 / dopamine$nml.putamen.dopamine.value^2)))
### Calculate Ratio of PD/Nml Caudate Dopamine Levels Scaled to Cell Number
dopamine$ratio.caudate.dopamine.adj.cell.value <-
  dopamine$pd.caudate.dopamine.adj.cell.value /
  dopamine$nml.caudate.dopamine.value
dopamine$ratio.caudate.dopamine.adj.cell.sd <-
  sqrt((dopamine$pd.caudate.dopamine.adj.cell.value^2 /
  dopamine$nml.caudate.dopamine.value^2)*
  ((dopamine$pd.caudate.dopamine.adj.cell.sd^2 /
  dopamine$pd.caudate.dopamine.adj.cell.value^2) +
  (dopamine$nml.caudate.dopamine.sd^2 / dopamine$nml.caudate.dopamine.value^2)))
### Calculate Ratio of PD/Nml Putamen Dopamine Levels Scaled to Axon Number
dopamine$ratio.putamen.dopamine.adj.axon.value <-
  dopamine$pd.putamen.dopamine.adj.axon.value /
  dopamine$nml.putamen.dopamine.value
dopamine$ratio.putamen.dopamine.adj.axon.sd <-
  sqrt( (dopamine$pd.putamen.dopamine.adj.axon.value^2 /
  dopamine$nml.putamen.dopamine.value^2)*

```

```

    ((dopamine$pd.putamen.dopamine.adj.axon.sd^2 /
    dopamine$pd.putamen.dopamine.adj.axon.value^2) +
    (dopamine$nml.putamen.dopamine.sd^2 / dopamine$nml.putamen.dopamine.value^2)))
### Calculate Ratio of PD/Nml Caudate Dopamine Levels Scaled to Axon Number
dopamine$ratio.caudate.dopamine.adj.axon.value <-
    dopamine$pd.caudate.dopamine.adj.axon.value /
    dopamine$nml.caudate.dopamine.value
dopamine$ratio.caudate.dopamine.adj.axon.sd <-
    sqrt((dopamine$pd.caudate.dopamine.adj.axon.value^2 /
    dopamine$nml.caudate.dopamine.value^2) *
    ((dopamine$pd.caudate.dopamine.adj.axon.sd^2 /
    dopamine$pd.caudate.dopamine.adj.axon.value^2) +
    (dopamine$nml.caudate.dopamine.sd^2 / dopamine$nml.caudate.dopamine.value^2)))
### Calculate Ratio of PD/Nml Putamen Dopamine Levels Scaled to Cell & VMAT2
dopamine$ratio.putamen.dopamine.adj.cell.vm.value <-
    dopamine$pd.putamen.dopamine.adj.cell.vm.value /
    dopamine$nml.putamen.dopamine.value
dopamine$ratio.putamen.dopamine.adj.cell.vm.sd <-
    sqrt((dopamine$pd.putamen.dopamine.adj.cell.vm.value^2 /
    dopamine$nml.putamen.dopamine.value^2) *
    ((dopamine$pd.putamen.dopamine.adj.cell.vm.sd^2 /
    dopamine$pd.putamen.dopamine.adj.cell.vm.value^2) +
    (dopamine$nml.putamen.dopamine.sd^2 / dopamine$nml.putamen.dopamine.value^2)))
### Calculate Ratio of PD/Nml Caudate Dopamine Levels Scaled to Cell & VMAT2
dopamine$ratio.caudate.dopamine.adj.cell.vm.value <-
    dopamine$pd.caudate.dopamine.adj.cell.vm.value /
    dopamine$nml.caudate.dopamine.value
dopamine$ratio.caudate.dopamine.adj.cell.vm.sd <-
    sqrt((dopamine$pd.caudate.dopamine.adj.cell.vm.value^2 /
    dopamine$nml.caudate.dopamine.value^2) *
    ((dopamine$pd.caudate.dopamine.adj.cell.vm.sd^2 /
    dopamine$pd.caudate.dopamine.adj.cell.vm.value^2) +
    (dopamine$nml.caudate.dopamine.sd^2 / dopamine$nml.caudate.dopamine.value^2)))
### Calculate Ratio of PD/Nml Putamen Dopamine Levels Scaled to Axon& VMAT2
dopamine$ratio.putamen.dopamine.adj.axon.vm.value <-
    dopamine$pd.putamen.dopamine.adj.axon.vm.value /
    dopamine$nml.putamen.dopamine.value
dopamine$ratio.putamen.dopamine.adj.axon.vm.sd <-
    sqrt((dopamine$pd.putamen.dopamine.adj.axon.vm.value^2 /
    dopamine$nml.putamen.dopamine.value^2) *
    ((dopamine$pd.putamen.dopamine.adj.axon.vm.sd^2 /
    dopamine$pd.putamen.dopamine.adj.axon.vm.value^2) +
    (dopamine$nml.putamen.dopamine.sd^2 / dopamine$nml.putamen.dopamine.value^2)))
### Calculate Ratio of PD/Nml Caudate Dopamine Levels Scaled to Axon & VMAT2
dopamine$ratio.caudate.dopamine.adj.axon.vm.value <-
    dopamine$pd.caudate.dopamine.adj.axon.vm.value /
    dopamine$nml.caudate.dopamine.value
dopamine$ratio.caudate.dopamine.adj.axon.vm.sd <-
    sqrt((dopamine$pd.caudate.dopamine.adj.axon.vm.value^2 /

```

```

dopamine$nml.caudate.dopamine.value^2)*
((dopamine$pd.caudate.dopamine.adj.axon.vm.sd^2 /
dopamine$pd.caudate.dopamine.adj.axon.vm.value^2) +
(dopamine$nml.caudate.dopamine.sd^2 / dopamine$nml.caudate.dopamine.value^2))
#####
# Dopamine Ratios Scaled "MNLN" #
#####
### Calculate Scaled Ratios of Dopamine Levels
cat("23.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Cell Number\n")
da_data_c <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.cell.value,
  sdi = ratio.putamen.dopamine.adj.cell.sd, data = dopamine, measure = "MNLN",
  append = TRUE)
da_model_c <- rma(yi, vi, data = da_data_c)
####
png(file = (paste("2021.APR.08 - ", "23.DA.Putamen.Cell.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_c, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-8.5, 3.5), at=c(-6,-5,-4,-3,-2,-1,0,1), alim=c(-6,1))
par("usr")
title(main="23.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Cell Number\n",
  font.main=2, cex.main=2.2)
text(-6.5, -1, paste("p=", round(da_model_c$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-8, da_model_c$k+2, "Study", pos=4, font=1, cex=1.75)
text(3, da_model_c$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(1, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("24.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Cell Number\n")
da_data_d <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.caudate.dopamine.adj.cell.value,
  sdi = ratio.caudate.dopamine.adj.cell.sd, data = dopamine, measure = "MNLN",
  append = TRUE)
da_model_d <- rma(yi, vi, data = da_data_d)
####
png(file = (paste("2021.APR.08 - ", "24.DA.caudate.Cell.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_d, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-7.5, 4.5), at=c(-5,-4,-3,-2,-1,0,1,2), alim=c(-5,2))
par("usr")
title(main="24.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Cells\n",
  font.main=2, cex.main=2.2)
text(-5.5, -1, paste("p=", round(da_model_d$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, da_model_d$k+2, "Study", pos=4, font=1, cex=1.75)
text(4, da_model_d$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-1, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()

```

```

###
cat("25.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Axon Number\n")
da_data_e <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.axon.value,
  sdi = ratio.putamen.dopamine.adj.axon.sd, data = dopamine, measure = "MNLN",
  append = TRUE)
da_model_e <- rma(yi, vi, data = da_data_e)
####
png(file = (paste("2021.APR.08 - ", "25.DA.Putamen.Axon.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_e, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-7.5, 4.5), at=c(-5,-4,-3,-2,-1,0,1,2), alim=c(-5,2))
par("usr")
title(main="25.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Axons\n",
  font.main=2, cex.main=2.2)
text(-5.5, -1, paste("p=", round(da_model_e$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, da_model_e$k+2, "Study", pos=4, font=1, cex=1.75)
text(4, da_model_e$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(2, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
###
cat("26.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Axon Number\n")
da_data_f <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.axon.value,
  sdi = ratio.caudate.dopamine.adj.axon.sd, data = dopamine, measure = "MNLN",
  append = TRUE)
da_model_f <- rma(yi, vi, data = da_data_f)
####
png(file = (paste("2021.APR.08 - ", "26.DA.caudate.Axon.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_f, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-5.5, 4.5), at=c(-3,-2,-1,0,1,2), alim=c(-3,2))
par("usr")
title(main="26.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Axons\n",
  font.main=2, cex.main=2.2)
text(-3.5, -1, paste("p=", round(da_model_f$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-5, da_model_f$k+2, "Study", pos=4, font=1, cex=1.75)
text(4, da_model_f$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(2, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("27.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Cell & VMAT2\n")
da_data_g <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.cell.vm.value,
  sdi = ratio.putamen.dopamine.adj.cell.vm.sd, data = dopamine, measure="MNLN",
  append = TRUE)
da_model_g <- rma(yi, vi, data = da_data_g)

```

```

####,
png(file=(paste("2021.APR.08 - ","27.DA.Putamen.Cell.VMAT.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_g, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-7.5,5.5), at=c(-5,-4,-3,-2,-1,0,1,2,3), alim=c(-5,3))
par("usr")
title(main="27.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Cell & VMAT2\n",
  font.main=2, cex.main=2.2)
text(-5.25, -1, paste("p=", round(da_model_g$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-7, da_model_g$k+2, "Study", pos=4, font=1, cex=1.75)
text(5, da_model_g$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("28.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Cell & VMAT2\n")
da_data_h <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.cell.vm.value,
  sdi = ratio.caudate.dopamine.adj.cell.vm.sd, data = dopamine, measure="MNLN",
  append = TRUE)
da_model_h <- rma(yi, vi, data = da_data_h)
summary(da_model_h)
####,
png(file = (paste("2021.APR.08 - ","28.DA.caudate.Cell.VMAT.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_h, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-12.5,10), at=c(-7.5,-5,-2.5,0,2.5,5), alim=c(-7.5,5))
par("usr")
title(main="28.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Cell & VMAT2\n",
  font.main=2, cex.main=2.2)
text(-8.5, -1, paste("p=", round(da_model_h$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-11.5, da_model_h$k+2, "Study", pos=4, font=1, cex=1.75)
text(8.5, da_model_h$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(5, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("29.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Axon & VMAT2\n")
da_data_i <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.axon.vm.value,
  sdi = ratio.putamen.dopamine.adj.axon.vm.sd, data = dopamine, measure="MNLN",
  append = TRUE)
da_model_i <- rma(yi, vi, data = da_data_i)
####,
png(file = (paste("2021.APR.08 - ","29.DA.Putamen.Axon.VMAT.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_i, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-7, 6), at=c(-4,-3,-2,-1,0,1,2,3), alim=c(-4,3))
par("usr")

```

```

title(main="29.Log Ratio (PD/Nml) of Putamen Dopamine Scaled to Axon & VMAT2\n",
      font.main=2, cex.main=2.2)
text(-4.5, -1, paste("p=", round(da_model_i$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-6.5, da_model_i$k+2, "Study", pos=4, font=1, cex=1.75)
text(5.5, da_model_i$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("30.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Axon & VMAT2\n")
da_data_j <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.axon.vm.value,
  sdi = ratio.caudate.dopamine.adj.axon.vm.sd, data = dopamine, measure="MNLN",
  append = TRUE)
da_model_j <- rma(yi, vi, data = da_data_j)
####,
png(file=(paste("2021.APR.08 - ", "30.DA.caudate.Axon.VMAT.MNLN.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_j, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-8,6), at=c(-5,-4,-3,-2,-1,0,1,2,3), alim=c(-5,3))
par("usr")
title(main="30.Log Ratio (PD/Nml) of Caudate Dopamine Scaled to Axon & VMAT2\n",
      font.main=2, cex.main=2.2)
text(-5.5, -1, paste("p=", round(da_model_j$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-7.5, da_model_j$k+2, "Study", pos=4, font=1, cex=1.75)
text(5.5, da_model_j$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#####
#       Scaled Dopamine Meta-Analysis       #
#       Log Transformed ROM Differences       #
#####
cat("31.Log Transformed Difference in Putamen Dopamine Scaled to Cells\n")
da_data_5 <- escalc(nli=nml.putamen.dopamine.n, n2i = pd.putamen.dopamine.n,
  mli = nml.putamen.dopamine.value, m2i = pd.putamen.dopamine.adj.cell.value,
  sdli = nml.putamen.dopamine.sd, sd2i = pd.putamen.dopamine.adj.cell.sd,
  data = dopamine, measure = "ROM", append = TRUE)
da_model_5 <- rma(yi, vi, data = da_data_5)
####
png(file = (paste("2021.APR.08 - ", "31.DA.Putamen.Cell.ROM.png", sep="")),
  width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_5, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-15, 20), at=c(-5,0,5,10), alim=c(-5,10))
par("usr")
title(main="31.Log Transformed DA Difference in Putamen Scaled to Cells\n",
      font.main=2, cex.main=2.2)
text(-8, -1, paste("p=", round(da_model_5$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)

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text(-12.5, da_model_5$k+2, "Study", pos=4, font=1, cex=1.75)
text(17.5, da_model_5$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-5, -1.7, "Parkinson's Higher", cex=1.25)
text(10, -1.7, "Normals Higher", cex=1.25)
dev.off()
## funnel plot
png(filename = (paste("2021.APR.08 - ", "31.Funnel.DA.Putamen.Cell.ROM.png",
  sep="")), res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))
### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_5, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
  refline=0)
dev.off()
####
cat("32.Log Transformed Difference in Caudate Dopamine Scaled to Cells\n")
da_data_6 <- escalc(nli=nml.caudate.dopamine.n, n2i = pd.caudate.dopamine.n,
  mli = nml.caudate.dopamine.value, m2i = pd.caudate.dopamine.adj.cell.value,
  sdli = nml.caudate.dopamine.sd, sd2i = pd.caudate.dopamine.adj.cell.sd,
  data = dopamine, measure = "ROM", append = TRUE)
da_model_6 <- rma(yi, vi, data = da_data_6)
####
png(file = (paste("2021.APR.08 - ", "32.DA.Caudate.Cell.ROM.png", sep="")),
  width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_6, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-10,10), at=c(-5,-2.5,0,2.5,5), alim=c(-5,5))
par("usr")
title(main="32.Log Transformed DA Difference in Caudate Scaled to Cells\n",
  font.main=2,cex.main=2.2)
text(-6.5, -1, paste("p=", round(da_model_6$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-9, da_model_6$k+2, "Study", pos=4, font=1, cex=1.75)
text(9, da_model_6$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-5, -1.7, "Parkinson's Higher", cex=1.25)
text(5, -1.7, "Normals Higher", cex=1.25)
dev.off()
## funnel plot
png(filename=(paste("2021.APR.08 - ", "32.Funnel.DA.Caudate.Cell.ROM.png", sep="")),
  res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))
### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_6, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
  refline=0)
dev.off()
####
cat("33.Log Transformed Difference in Putamen Dopamine Scaled to Axons\n")
da_data_7 <- escalc(nli=nml.putamen.dopamine.n, n2i = pd.putamen.dopamine.n,
  mli = nml.putamen.dopamine.value, m2i = pd.putamen.dopamine.adj.axon.value,

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sdli = nml.putamen.dopamine.sd, sd2i = pd.putamen.dopamine.adj.axon.sd,
data = dopamine, measure = "ROM", append = TRUE)
da_model_7 <- rma(yi, vi, data = da_data_7)
####
png(file = (paste("2021.APR.08 - ", "33.DA.Putamen.Axon.ROM.png", sep="")),
width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_7, slab=paste(dopamine$study, sep=", "),
cex=1.5, xlim=c(-10,10), at=c(-5,-2.5,0,2.5,5), alim=c(-5,5))
par("usr")
title(main="33.Log Transformed DA Difference in Putamen Scaled to Axons\n",
font.main=2, cex.main=2.2)
text(-6.5, -1, paste("p=", round(da_model_7$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-9, da_model_7$k+2, "Study", pos=4, font=1, cex=1.75)
text(9, da_model_7$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-5, -1.7, "Parkinson's Higher", cex=1.25)
text(5, -1.7, "Normals Higher", cex=1.25)
dev.off()
## funnel plot
png(filename = (paste("2021.APR.08 - ", "33.Funnel.DA.Putamen.Axon.ROM.png",
sep="")),res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))
### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_7, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
refline=0)
dev.off()
####
cat("34.Log Transformed Difference in Caudate Dopamine Scaled to Axons\n")
da_data_8 <- escalc(nli=nml.caudate.dopamine.n, n2i = pd.caudate.dopamine.n,
m1i = nml.caudate.dopamine.value, m2i = pd.caudate.dopamine.adj.axon.value,
sdli = nml.caudate.dopamine.sd, sd2i = pd.caudate.dopamine.adj.axon.sd,
data = dopamine, measure = "ROM", append = TRUE)
da_model_8 <- rma(yi, vi, data = da_data_8)
####
png(file = (paste("2021.APR.08 - ", "34.DA.Caudate.Axon.ROM.png", sep="")),
width=1048, height = 1048, units = "px", pointsize = 14, bg = "white")
forest(da_model_8, slab=paste(dopamine$study, sep=", "),
cex=1.5, xlim=c(-6,6), at=c(-3,-2,-1,0,1,2,3), alim=c(-3,3))
par("usr")
title(main="34.Log Transformed DA Difference in Caudate Scaled to Axons",
font.main=2,cex.main=2.2)
text(-3.5, -1, paste("p=", round(da_model_8$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-5.5, da_model_8$k+2, "Study", pos=4, font=1, cex=1.75)
text(5.5, da_model_8$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-3, -1.7, "Parkinson's Higher", cex=1.25)
text(3, -1.7, "Normals Higher", cex=1.25)
dev.off()

```

```

## funnel plot
png(filename = (paste("2021.APR.08 - ", "34.Funnel.DA.Caudate.Axon.ROM.png",
  sep="")), res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))
### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_8, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
  refline=0)
dev.off()
####
cat("35.Log Transformed Difference in Putamen Dopamine Scaled to Cells VMAT2\n")
da_data_9 <- escalc(nli=nml.putamen.dopamine.n, n2i = pd.putamen.dopamine.n,
  mli = nml.putamen.dopamine.value, m2i = pd.putamen.dopamine.adj.cell.vm.value,
  sdli = nml.putamen.dopamine.sd, sd2i = pd.putamen.dopamine.adj.cell.vm.sd,
  data = dopamine, measure = "ROM", append = TRUE)
da_model_9 <- rma(yi, vi, data = da_data_9)
####
png(file = (paste("2021.APR.08 - ", "35.DA.Putamen.Cell.VMAT.ROM.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_9, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-10,10), at=c(-5,-2.5,0,2.5,5), alim=c(-5,5))
par("usr")
title(main="35.Log Transformed DA Difference in Putamen Scaled to Cells&VMAT\n",
  font.main=2, cex.main=2.2)
text(-6.5, -1, paste("p=", round(da_model_9$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-9.5, da_model_9$k+2, "Study", pos=4, font=1, cex=1.75)
text(9.5, da_model_9$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-5, -1.7, "Parkinson's Higher", cex=1.25)
text(5, -1.7, "Normals Higher", cex=1.25)
dev.off()
## funnel plot
png(filename = (paste("2021.APR.08 - ", "35.Funnel.DA.Putamen.Cell.VMAT.ROM.png",
  sep="")), res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))
### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_9, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
  refline=0)
dev.off()
####
cat("36.Log Transformed Difference in Caudate Dopamine Scaled to Cells&VMAT2\n")
da_data_10 <- escalc(nli=nml.caudate.dopamine.n, n2i = pd.caudate.dopamine.n,
  mli = nml.caudate.dopamine.value, m2i = pd.caudate.dopamine.adj.cell.vm.value,
  sdli = nml.caudate.dopamine.sd, sd2i = pd.caudate.dopamine.adj.cell.vm.sd,
  data = dopamine, measure = "ROM", append = TRUE)
da_model_10 <- rma(yi, vi, data = da_data_10)
####
png(file=(paste("2021.APR.08 - ", "36.DA.Caudate.Cell.VMAT.ROM.png",

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    sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_10, slab=paste(dopamine$study, sep=", "),
    cex=1.5, xlim=c(-15, 10), at=c(-7.5,-5,-2.5,0,2.5,5), alim=c(-7.5,5))
par("usr")
title(main="36.Log Transformed DA Difference in Caudate Scaled to Cells&VMAT\n",
    font.main=2,cex.main=2.2)
text(-10, -1, paste("p=", round(da_model_10$pval, digits =3), sep=""),
    pos=2, font=1, cex=1.5)
text(-12.5, 6.5, "Study", pos=4, font=1, cex=1.75)
text(9, 6.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-7.5, -1.75, "Parkinson's Higher", cex=1.25)
text(5, -1.75, "Normals Higher", cex=1.25)
dev.off()
## funnel plot
png(filename = (paste("2021.APR.08 - ", "36.Funnel.DA.Caudate.Cell.VMAT.ROM.png",
    sep="")), res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))
### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_10, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
    refline=0)
dev.off()
####
cat("37.Log Transformed Difference in Putamen Dopamine Scaled to Axons&VMAT2\n")
da_data_11 <- escalc(nli=nml.putamen.dopamine.n, n2i = pd.putamen.dopamine.n,
    mli = nml.putamen.dopamine.value, m2i = pd.putamen.dopamine.adj.axon.vm.value,
    sdli = nml.putamen.dopamine.sd, sd2i = pd.putamen.dopamine.adj.axon.vm.sd,
    data = dopamine, measure = "ROM", append = TRUE)
da_model_11 <- rma(yi, vi, data = da_data_11)
####
png(file = (paste("2021.APR.08 - ", "37.DA.Putamen.Axon.VMAT.ROM.png",
    sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_11, slab=paste(dopamine$study, sep=", "),
    cex=1.5, xlim=c(-10, 7.5), at=c(-6,-4,-2,0,2,4), alim=c(-6,4))
par("usr")
title(main="37.Log Transformed DA Difference in Putamen Scaled to Axon&VMAT\n",
    font.main=2, cex.main=2.2)
text(-7, -1, paste("p=", round(da_model_11$pval, digits =3), sep=""),
    pos=2, font=1, cex=1.5)
text(-9, da_model_11$k+2, "Study", pos=4, font=1, cex=1.75)
text(6.5, da_model_11$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-6, -1.75, "Parkinson's Higher", cex=1.25)
text(4, -1.75, "Normals Higher", cex=1.25)
dev.off()
## funnel plot
png(filename = (paste("2021.APR.08 - ", "37.Funnel.DA.Putamen.Axon.VMAT.ROM.png",
    sep="")), res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))

```

```

### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_11, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
  refline=0)
dev.off()
####
cat("38.Log Transformed Difference in Caudate Dopamine Scaled to Axons&VMAT2\n")
da_data_12 <- escalc(nli=nml.caudate.dopamine.n, n2i = pd.caudate.dopamine.n,
  mli = nml.caudate.dopamine.value,m2i = pd.caudate.dopamine.adj.axon.vm.value,
  sdli = nml.caudate.dopamine.sd, sd2i = pd.caudate.dopamine.adj.axon.vm.sd,
  data = dopamine, measure = "ROM", append = TRUE)
da_model_12 <- rma(yi, vi, data = da_data_12)
####
png(file=(paste("2021.APR.08 - ", "38.DA.Caudate.Axon.VMAT.ROM.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_12, slab=paste(dopamine$study, sep=", "),
  cex=1.5, xlim=c(-10, 7.5), at=c(-6,-4,-2,0,2,4), alim=c(-6,4))
par("usr")
title(main="38.Log Transformed DA Difference in Caudate Scale to Axons&VMAT2\n",
  font.main=2,cex.main=2.2)
text(-7, -1, paste("p=", round(da_model_12$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-9, da_model_12$k+2, "Study", pos=4, font=1, cex=1.75)
text(6.5, da_model_12$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-6, -1.7, "Parkinson's Higher", cex=1.25)
text(4, -1.7, "Normals Higher", cex=1.25)
dev.off()
## funnel plot
png(filename = (paste("2021.APR.08 - ", "38.Funnel.DA.Caudate.Axon.VMAT.ROM.png",
  sep="")), res=92, width=680, height=600, type="cairo")
### decrease margins so the full space is used
par(mar=c(5,4,1,2))
### create contour enhanced funnel plot (with funnel centered at 0)
funnel(da_model_12, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),
  refline=0)
dev.off()
#####
# Linearized Versions of Differences Models #
#####
cat("39.Linear Difference in Putamen Dopamine Scaled to Cells\n")
png(file = (paste("2021.APR.08 - ", "39.DA.Putamen.Cell.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_5, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-50, 125), at=c(0,25,50,75), alim=c(0,75))
par("usr")
title(main="39.Linear DA Difference in Putamen Scaled to Cells\n",
  font.main=2, cex.main=2.2)
text(-15, -1, paste("p=", round(da_model_5$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)

```

```

text(-40, da_model_5$k+2, "Study", pos=4, font=1, cex=1.75)
text(120, da_model_5$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(0, -1.7, "Parkinson's Higher", cex=1.25)
text(75, -1.7, "Normals Higher", cex=1.25)
dev.off()
###
cat("40.Linear Difference in Caudate Dopamine Scaled to Cells\n")
png(file = (paste("2021.APR.08 - ", "40.DA.Caudate.Cell.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_6, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-10, 20), at=c(-2.5,0,2.5,5,7.5,10,12.5), alim=c(-2.5,12.5))
par("usr")
title(main="40.Linear DA Difference in Caudate Scaled to Cells\n",
  font.main=2,cex.main=2.2)
text(-3, -1, paste("p=", round(da_model_6$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-8.5, da_model_6$k+2, "Study", pos=4, font=1, cex=1.75)
text(19.5, da_model_6$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(12.5, -1.7, "Normals Higher", cex=1.25)
dev.off()
###
cat("41.Linear Difference in Putamen Dopamine Scaled to Axons\n")
png(file = (paste("2021.APR.08 - ", "41.DA.Putamen.Axon.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_7, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-7.5, 15), at=c(-2.5,0,2.5,5,7.5,10), alim=c(-2.5,10))
par("usr")
title(main="41.Linear DA Difference in Putamen Scaled to Axons\n",
  font.main=2, cex.main=2.2)
text(-4, -1, paste("p=", round(da_model_7$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, da_model_7$k+2, "Study", pos=4, font=1, cex=1.75)
text(14, da_model_7$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(10, -1.7, "Normals Higher", cex=1.25)
dev.off()
###
cat("42.Linear Difference in Caudate Dopamine Scaled to Axons\n")
png(file = (paste("2021.APR.08 - ", "42.DA.Caudate.Axon.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_8, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-7.5, 15), at=c(-2.5,0,2.5,5,7.5,10), alim=c(-2.5,10))
par("usr")
title(main="42.Linear DA Difference in Caudate Scaled to Axons",
  font.main=2,cex.main=2.2)
text(-4, -1, paste("p=", round(da_model_8$pval, digits =3), sep=""),

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    pos=2, font=1, cex=1.5)
text(-6.5, da_model_8$k+2, "Study", pos=4, font=1, cex=1.75)
text(14, da_model_8$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(10, -1.7, "Normals Higher", cex=1.25)
dev.off()
###
cat("43.Linear Difference in Putamen Dopamine Scaled to Cells & VMAT2\n")
png(file=(paste("2021.APR.08 - ", "43.DA.Putamen.Cell.VMAT.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_9, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-7.5, 15), at=c(-2.5,0,2.5,5,7.5,10), alim=c(-2.5,10))
par("usr")
title(main="43.Linear DA Difference in Putamen Scaled to Cells&VMAT\n",
  font.main=2, cex.main=2.2)
text(-3.5, -1, paste("p=", round(da_model_9$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, da_model_9$k+2, "Study", pos=4, font=1, cex=1.75)
text(14, da_model_9$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(10, -1.7, "Normals Higher", cex=1.25)
dev.off()
###
cat("44.Linear Difference in Caudate Dopamine Scaled to Cells & VMAT2\n")
png(file=(paste("2021.APR.08 - ", "44.DA.Caudate.Cell.VMAT.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_10, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-7.5, 15), at=c(-2.5,0,2.5,5,7.5,10), alim=c(-2.5,10))
par("usr")
title(main="44.Linear DA Difference in Caudate Scaled to Cells&VMAT\n",
  font.main=2,cex.main=2.2)
text(-3.5, -1, paste("p=", round(da_model_10$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, 6.5, "Study", pos=4, font=1, cex=1.75)
text(14, 6.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.75, "Parkinson's Higher", cex=1.25)
text(10, -1.75, "Normals Higher", cex=1.25)
dev.off()
###
cat("45.Linear Difference in Putamen Dopamine Scaled to Axons & VMAT2\n")
png(file=(paste("2021.APR.08 - ", "45.DA.Putamen.Axon.VMAT.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_11, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-7.5, 15), at=c(-2.5,0,2.5,5,7.5,10), alim=c(-2.5,10))
par("usr")
title(main="45.Linear DA Difference in Putamen Scaled to Axon&VMAT\n",
  font.main=2, cex.main=2.2)
text(-3.5, -1, paste("p=", round(da_model_11$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)

```

```

text(-6.5, da_model_11$k+2, "Study", pos=4, font=1, cex=1.75)
text(14, da_model_11$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.75, "Parkinson's Higher", cex=1.25)
text(10, -1.75, "Normals Higher", cex=1.25)
dev.off()
###
cat("46.Linear Difference in Caudate Dopamine Scaled to Axons & VMAT2\n")
png(file=(paste("2021.APR.08 - ", "46.DA.Caudate.Axon.VMAT.ROM.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize=12, bg="white")
forest(da_model_12, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  cex=1.5, xlim=c(-7.5, 15), at=c(-2.5,0,2.5,5,7.5,10), alim=c(-2.5,10))
par("usr")
title(main="46.Linear DA Difference in Caudate Scaled to Axons & VMAT2\n",
  font.main=2,cex.main=2.2)
text(-3.5, -1, paste("p=", round(da_model_12$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-6.5, da_model_12$k+2, "Study", pos=4, font=1, cex=1.75)
text(14, da_model_12$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(-2.5, -1.7, "Parkinson's Higher", cex=1.25)
text(10, -1.7, "Normals Higher", cex=1.25)
dev.off()
#####
#   Linearized Versions of Ratio Models   #
#####
cat("47.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Cell")
png(file = (paste("2021.APR.08 - ", "47.DA.Putamen.Cell.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_c, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-2.5, 5), at=c(0,1, 2, 3), alim=c(0,3))
par("usr")
title(main="\n47.Ratio of Putamen Dopamine\nScaled to Cell",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_c$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-2, da_model_c$k+2, "Study", pos=4, font=1, cex=1.75)
text(4.5, da_model_c$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("48.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Cell")
png(file = (paste("2021.APR.08 - ", "48.DA.Caudate.Cell.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_d, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-2.5, 6.5), at=c(0,1,2,3,4), alim=c(0,4))
par("usr")
title(main="\n48.Ratio of Caudate Dopamine\nScaled to Cell",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_d$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)

```

```

text(-2, da_model_d$k+2, "Study", pos=4, font=1, cex=1.75)
text(6, da_model_d$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(4, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("49.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Axon")
png(file = (paste("2021.APR.08 - ", "49.DA.Putamen.Axon.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_e, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-2.5, 4), at=c(0,0.5,1,1.5,2), alim=c(0,2))
par("usr")
title(main="\n\n49.Ratio of Putamen Dopamine\nScaled to Axon",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_e$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-2, da_model_e$k+2, "Study", pos=4, font=1, cex=1.75)
text(3.5, da_model_e$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(2, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("50.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Axon")
png(file = (paste("2021.APR.08 - ", "50.DA.Caudate.Axon.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_f, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-4, 5.5), at=c(0,0.5,1,1.5, 2,2.5), alim=c(0,3))
par("usr")
title(main="\n\n50.Ratio of Caudate Dopamine\nScaled to Axon",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_f$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-3.5, da_model_f$k+2, "Study", pos=4, font=1, cex=1.75)
text(5.25, da_model_f$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("51.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Cells & VM")
png(file = (paste("2021.APR.08 - ", "51.DA.Putamen.Cell.VM.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_g, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-5, 10), at=c(0,1,2,3,4,5,6,7), alim=c(0,7))
par("usr")
title(main="\n\n51.Ratio of Putamen Dopamine\nScaled to Cells & VM",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_g$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-3.5, da_model_g$k+2, "Study", pos=4, font=1, cex=1.75)
text(9.5, da_model_g$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(7.5, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()

```

```

####
cat("52.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Cells & VM")
png(file = (paste("2021.APR.08 - ", "52.DA.Caudate.Cell.VM.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_h, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-20, 50), at=c(0,5,10,15,20,25,30), alim=c(0,30))
par("usr")
title(main="\n\n52.Ratio of Caudate Dopamine\nScaled to Cells & VM",
  font.main=2, cex.main=2.2)
text(-2.5, -1, paste("p=", round(da_model_h$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-17.5, da_model_h$k+2, "Study", pos=4, font=1, cex=1.75)
text(47.5, da_model_h$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(30, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("53.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Axons & VM")
png(file = (paste("2021.APR.08 - ", "53.DA.Putamen.Axon.VM.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_i, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-5,10), at=c(0,1,2,3,4,5), alim=c(0,5))
par("usr")
title(main="\n\n53.Linear Ratio of Putamen Dopamine\nScaled to Axons & VM",
  font.main=2, cex.main=2.2)
text(-2, -1, paste("p=", round(da_model_i$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-4, da_model_i$k+2, "Study", pos=4, font=1, cex=1.75)
text(8.5, da_model_i$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(5, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("54.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Axons & VM")
png(file = (paste("2021.APR.08 - ", "54.DA.Caudate.Axon.VM.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_j, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-10,25), at=c(0,5,10,15), alim=c(0,15))
par("usr")
title(main="\n\n54.Ratio of Caudate Dopamine\nScaled to Axons & VM",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_j$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-8.5, da_model_j$k+2, "Study", pos=4, font=1, cex=1.75)
text(22, da_model_j$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(15, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#
#####
# Analyses (repeat graphs 51-54): axon ratios set separately for each of C & P
# 3. Extract point estimates/SE (to calculate SD) of VMAT2 ratio for PUTA/CAUD

```

```

# 4. Create new variables for DA scaled (cell # & axon)
# 5. Create new variables for DA scaled also for VMAT2
# 6. Run part 2 of meta-analyses: dopamine for Putamen/Caudate, then adjust
#     for cell/axon ratio and each also with VMAT2 ratio
#
# 2. Axon number (average from Kordower apportioned by relative DA content)
##### the calculation described here: #####
# Total axon density is 0.28. The ratio of CAUDATE/PUTAMEN in dopamine, based
# on point estimates in this analysis, is 0.18/0.4, with the caudate having
# 4.5x as much innervation if axonal innervation is proportional to DA content.
# That means that axon ratio PD to normal for caudate is 0.82*0.28 = 0.23
# and axon ratio PD to normal for putamen is 0.18*0.28 = 0.05
axon_p_ratio <- 0.05 # for putamen
axon_c_ratio <- 0.23 # for caudate
axon_sd <- 0.15 # assume same sd for each region's portion
# 4. Scale PD dopamine data to cell ratio & axon ratio
dopamine$pd.putamen.dopamine.adj.axon_p.value <-
  dopamine$pd.putamen.dopamine.value / axon_p_ratio
dopamine$pd.putamen.dopamine.adj.axon.sd <-
  sqrt((dopamine$pd.putamen.dopamine.value^2 / axon_p_ratio^2) *
    ((dopamine$pd.putamen.dopamine.sd^2 /
    dopamine$pd.putamen.dopamine.value^2) +
    (axon_sd^2 / axon_p_ratio^2)))
dopamine$pd.caudate.dopamine.adj.axon_c.value <-
  dopamine$pd.caudate.dopamine.value / axon_c_ratio
dopamine$pd.caudate.dopamine.adj.axon.sd <-
  sqrt((dopamine$pd.caudate.dopamine.value^2 / axon_c_ratio^2) *
    ((dopamine$pd.caudate.dopamine.sd^2 /
    dopamine$pd.caudate.dopamine.value^2) +
    (axon_sd^2 / axon_c_ratio^2)))
# 5. Scale the scaled PD dopamine data to VMAT2 ratio
dopamine$pd.putamen.dopamine.adj.axon_p.vm.value <-
  dopamine$pd.putamen.dopamine.adj.axon_p.value / vm_putamen_ratio
dopamine$pd.putamen.dopamine.adj.axon.vm.sd <-
  sqrt((dopamine$pd.putamen.dopamine.adj.axon_p.value^2 /
  vm_putamen_ratio^2) *
    ((dopamine$pd.putamen.dopamine.adj.axon.sd^2 /
    dopamine$pd.putamen.dopamine.adj.axon_p.value^2 ) +
    (vm_putamen_sd^2 / vm_putamen_ratio^2) ) )
dopamine$pd.caudate.dopamine.adj.axon_c.vm.value <-
  dopamine$pd.caudate.dopamine.adj.axon_c.value / vm_caudate_ratio
dopamine$pd.caudate.dopamine.adj.axon.vm.sd <-
  sqrt( (dopamine$pd.caudate.dopamine.adj.axon_c.value^2 /
  vm_putamen_ratio^2) *
    ((dopamine$pd.caudate.dopamine.adj.axon.sd^2 /
    dopamine$pd.caudate.dopamine.adj.axon_c.value^2 ) +
    (vm_caudate_sd^2 / vm_caudate_ratio^2) ) )
# 6. Run part 2 of meta-analyses
# - dopamine for Putamen and caudate

```

```

# - dopamine adjusted for cell/axon ratio
# - dopamine adjusted for cell/axon ratio and VMAT2 ratio
#####
# Scale Dopamine Ratios for Meta-Analysis #
#####
### Calculate Ratio of PD/Nml Putamen Dopamine Levels Scaled to Axon Number
dopamine$ratio.putamen.dopamine.adj.axon_p.value <-
  dopamine$pd.putamen.dopamine.adj.axon_p.value /
  dopamine$nml.putamen.dopamine.value
dopamine$ratio.putamen.dopamine.adj.axon.sd <-
  sqrt( (dopamine$pd.putamen.dopamine.adj.axon_p.value^2 /
  dopamine$nml.putamen.dopamine.value^2) *
  ((dopamine$pd.putamen.dopamine.adj.axon.sd^2 /
  dopamine$pd.putamen.dopamine.adj.axon_p.value^2) +
  (dopamine$nml.putamen.dopamine.sd^2 / dopamine$nml.putamen.dopamine.value^2)))
### Calculate Ratio of PD/Nml Caudate Dopamine Levels Scaled to Axon Number
dopamine$ratio.caudate.dopamine.adj.axon_c.value <-
  dopamine$pd.caudate.dopamine.adj.axon_c.value /
  dopamine$nml.caudate.dopamine.value
dopamine$ratio.caudate.dopamine.adj.axon.sd <-
  sqrt((dopamine$pd.caudate.dopamine.adj.axon_c.value^2 /
  dopamine$nml.caudate.dopamine.value^2) *
  ((dopamine$pd.caudate.dopamine.adj.axon.sd^2 /
  dopamine$pd.caudate.dopamine.adj.axon_c.value^2) +
  (dopamine$nml.caudate.dopamine.sd^2 / dopamine$nml.caudate.dopamine.value^2)))
### Calculate Ratio of PD/Nml Putamen Dopamine Levels Scaled to Axon & VMAT2
dopamine$ratio.putamen.dopamine.adj.axon.vm_p.value <-
  dopamine$pd.putamen.dopamine.adj.axon_p.vm.value /
  dopamine$nml.putamen.dopamine.value
dopamine$ratio.putamen.dopamine.adj.axon.vm.sd <-
  sqrt((dopamine$pd.putamen.dopamine.adj.axon_p.vm.value^2 /
  dopamine$nml.putamen.dopamine.value^2) *
  ((dopamine$pd.putamen.dopamine.adj.axon.vm.sd^2 /
  dopamine$pd.putamen.dopamine.adj.axon_p.vm.value^2) +
  (dopamine$nml.putamen.dopamine.sd^2 / dopamine$nml.putamen.dopamine.value^2)))
### Calculate Ratio of PD/Nml Caudate Dopamine Levels Scaled to Axon & VMAT2
dopamine$ratio.caudate.dopamine.adj.axon.vm_c.value <-
  dopamine$pd.caudate.dopamine.adj.axon_c.vm.value /
  dopamine$nml.caudate.dopamine.value
dopamine$ratio.caudate.dopamine.adj.axon.vm.sd <-
  sqrt((dopamine$pd.caudate.dopamine.adj.axon_c.vm.value^2 /
  dopamine$nml.caudate.dopamine.value^2) *
  ((dopamine$pd.caudate.dopamine.adj.axon.vm.sd^2 /
  dopamine$pd.caudate.dopamine.adj.axon_c.vm.value^2) +
  (dopamine$nml.caudate.dopamine.sd^2 / dopamine$nml.caudate.dopamine.value^2)))
####
cat("55.Linearized Putamen-Specific Dopamine Ratio (PD/Nml) of Scaled to Axon")
da_data_e_p <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.axon_p.value,

```

```

sdi = ratio.putamen.dopamine.adj.axon.sd, data = dopamine, measure = "MNLN",
append = TRUE)
da_model_e_p <- rma(yi, vi, data = da_data_e_p)
####
png(file = (paste("2021.APR.08 - ", "55.DA.Putamen.Specific.Axon.MNLN.Linear.png",
sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_e_p, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
ref=1, cex=1.5, xlim=c(-10, 30), at=c(0,5,10,15,20), alim=c(0,20))
par("usr")
title(main="\n\n55.Ratio of Putamen-Specific Dopamine Ratio\nScaled to Axon",
font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_e_p$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-8, da_model_e_p$k+2, "Study", pos=4, font=1, cex=1.75)
text(28.5, da_model_e_p$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(20, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("56.Linearized Caudate-Specific Dopamine Ratio (PD/Nml) of Scaled to Axon")
###
da_data_f_c <- escalc(ni=nml.caudate.dopamine.n,
mi = ratio.caudate.dopamine.adj.axon_c.value,
sdi = ratio.caudate.dopamine.adj.axon.sd, data = dopamine, measure = "MNLN",
append = TRUE)
da_model_f_c <- rma(yi, vi, data = da_data_f_c)
####
png(file = (paste("2021.APR.08 - ", "56.DA.Caudate.Specific.Axon.MNLN.Linear.png",
sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_f_c, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
ref=1, cex=1.5, xlim=c(-2, 5), at=c(0,0.5,1,1.5,2,2.5), alim=c(0,3))
par("usr")
title(main="\n\n56.Ratio of Caudate-Specific Dopamine\nRatio Scaled to Axon",
font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_f_c$pval, digits =3), sep=""),
pos=2, font=1, cex=1.5)
text(-1.5, da_model_f_c$k+2, "Study", pos=4, font=1, cex=1.75)
text(4.75, da_model_f_c$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(2.5, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("57.Linearized Putamen-Specific Dopamine Ratio (PD/Nml) Scaled to Axons & VM")
###
da_data_i_p <- escalc(ni=nml.putamen.dopamine.n,
mi = ratio.putamen.dopamine.adj.axon.vm_p.value,
sdi = ratio.putamen.dopamine.adj.axon.vm.sd, data = dopamine, measure="MNLN",
append = TRUE)
da_model_i_p <- rma(yi, vi, data = da_data_i_p)
###
png(file = (paste("2021.APR.08 - ", "57.DA.Putamen.Specific.Axon.VM.MNLN.Linear.png",

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```

    sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_i_p, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
      ref=1, cex=1.5, xlim=c(-25,75), at=c(0,10,20,30,40,50), alim=c(0,50))
par("usr")
title(main="\n\n57.Ratio of Putamen-Specific Dopamine Ratio\nScaled to Axons & VM",
      font.main=2, cex.main=2.2)
text(-5, -1, paste("p=", round(da_model_i_p$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-17.5, da_model_i_p$k+2, "Study", pos=4, font=1, cex=1.75)
text(65, da_model_i_p$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(50, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("58.Linearized Caudate-Specific Dopamine Ratio (PD/Nml) Scaled to Axons & VM")
###
da_data_i_c <- escalc(ni=dopamine$nml.caudate.dopamine.n,
  mi = dopamine$ratio.caudate.dopamine.adj.axon.vm_c.value,
  sdi = dopamine$ratio.caudate.dopamine.adj.axon.vm.sd, data = dopamine,
measure="MNLN",
  append = TRUE)
da_model_i_c <- rma(yi, vi, data = da_data_i_c)
###
png(file=(paste("2021.APR.08 - ", "58.DA.Caudate.Specific.Axon.VM.MNLN.Linear.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_i_c, slab=paste(dopamine$study, sep=", "), transf=transf.exp.int,
      ref=1, cex=1.5, xlim=c(-10,30), at=c(0,4,8,12,16,20), alim=c(0,20))
par("usr")
title(main="\n\n58.Caudate-Specific Ratio of Dopamine Ratio\nScaled to Axons & VM",
      font.main=2, cex.main=2.2)
text(-2.5, -1, paste("p=", round(da_model_i_c$pval, digits =3), sep=""),
     pos=2, font=1, cex=1.5)
text(-8, da_model_i_c$k+2, "Study", pos=4, font=1, cex=1.75)
text(28, da_model_i_c$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(20, -1.75, "Parkinson's / Normal", cex=1.25)
dev.off()
#
#####
#####
subset_da <- dopamine[1:3,] #####
#####
#####
cat("59.Linear Ratio of PD/Nml Putamen Dopamine Levels (subset)\n")
da_data_as <- escalc(ni=nml.putamen.dopamine.n,
  mi =ratio.putamen.dopamine.value, sdi = ratio.putamen.dopamine.sd,
  data = subset_da, measure = "MNLN", append = TRUE)
da_model_as <- rma(yi, vi, data = da_data_as)
#
png(file = (paste("2021.APR.08 - ", "59.Putamen.DA.Ratio.Linear.subset.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,

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    bg = "white")
forest(da_model_as, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
      ref=1, cex=1.75, xlim=c(-1, 1.75), at=c(0,0.25,0.5,0.75,1,1.25),
      alim=c(-0.25, 1.25))
par("usr")
title(main="\n\n59.Ratio of PD/Nml Putamen Dopamine Levels\n(subset)",
      font.main=2,cex.main=2.2)
text(-0.3, -1, paste("p=", round(da_model_as$pval, digits =3), sep=""),
      pos=2, font=1, cex=1.25)
text(-0.85, da_model_as$k+2, "Study", pos=4, font=1, cex=1.75)
text(1.65, da_model_as$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(0.75, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
#
cat("60.Linear Mean Ratio in Caudate Dopamine Levels (subset1)\n")
da_data_bs <- escalc(ni=nml.caudate.dopamine.n,
  mi =ratio.caudate.dopamine.value, sdi = ratio.caudate.dopamine.sd,
  data = subset_da, measure = "MNLN", append = TRUE)
da_model_bs <- rma(yi, vi, data = da_data_bs)
#
png(file = (paste("2021.APR.08 - ", "60.Caudate.DA.Ratio.Linear.subset.png",
  sep="")), width = 1048, height = 1048, units = "px", pointsize = 14,
  bg = "white")
forest(da_model_bs, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
      ref=1, cex=1.75, xlim=c(-1, 1.75), at=c(0,0.25,0.5,0.75,1,1.25),
      alim=c(-0.25, 1.25))
par("usr")
title(main="\n\n60.Ratio of PD/Nml Caudate Dopamine Levels\n(subset)",
      font.main=2,cex.main=2.2)
text(-0.3, -1, paste("p=", round(da_model_bs$pval, digits =3), sep=""),
      pos=2, font=1, cex=1.5)
text(-0.85, da_model_bs$k+2, "Study", pos=4, font=1, cex=1.75)
text(1.65, da_model_bs$k+2, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(1.25, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
#
cat("61.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Cell (subset)")
da_data_cs <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.cell.value,
  sdi = ratio.putamen.dopamine.adj.cell.sd, data = subset_da, measure = "MNLN",
  append = TRUE)
da_model_cs <- rma(yi, vi, data = da_data_cs)
####
png(file = (paste("2021.APR.08 - ", "61.DA.Putamen.Cell.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_cs, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
      ref=1, cex=1.5, xlim=c(-2.5, 5), at=c(0,1, 2, 3), alim=c(0,3))
par("usr")
title(main="\n\n61.Ratio of Putamen Dopamine Scaled to Cell\n(subset)",

```

```

font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_cs$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-2.2, 4.5, "Study", pos=4, font=1, cex=1.75)
text(4.65, 4.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("62.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Cell (subset)")
da_data_ds <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.cell.value,
  sdi = ratio.caudate.dopamine.adj.cell.sd, data = subset_da, measure = "MNLN",
  append = TRUE)
da_model_ds <- rma(yi, vi, data = da_data_ds)
#
png(file = (paste("2021.APR.08 - ", "62.DA.Caudate.Cell.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_ds, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-2.5, 6.5), at=c(0,1,2,3), alim=c(0,3.5))
par("usr")
title(main="\n\n62.Ratio of Caudate Dopamine Scaled to Cell\n(subset)",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_ds$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-2, 4.5, "Study", pos=4, font=1, cex=1.75)
text(6, 4.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("63.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Axon (subset)")
da_data_es <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.axon.value,
  sdi = ratio.putamen.dopamine.adj.axon.sd, data = subset_da, measure = "MNLN",
  append = TRUE)
da_model_es <- rma(yi, vi, data = da_data_es)
#
png(file = (paste("2021.APR.08 - ", "63.DA.Putamen.Axon.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_es, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-1250, 2500), at=c(0,500,1000,1500), alim=c(0,1500))
par("usr")
title(main="\n\n63.Ratio of Putamen Dopamine Scaled to Axon\n(subset)",
  font.main=2, cex.main=2.2)
text(-350, -1, paste("p=", round(da_model_es$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-1000, 4.5, "Study", pos=4, font=1, cex=1.75)
text(2250, 4.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(1500, -1.65, "Parkinson's / Normal", cex=1.25)

```

```

dev.off()
####
cat("64.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Axon (subset)")
da_data_fs <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.axon.value,
  sdi = ratio.caudate.dopamine.adj.axon.sd, data = subset_da, measure = "MNLN",
  append = TRUE)
da_model_fs <- rma(yi, vi, data = da_data_fs)
#
png(file = (paste("2021.APR.08 - ", "64.DA.Caudate.Axon.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_fs, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-2.5, 5), at=c(0,1, 2, 3), alim=c(0,3))
par("usr")
title(main="\n\n64.Ratio of Caudate Dopamine Scaled to Axon\n(subset)",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_fs$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-2.15, 4.5, "Study", pos=4, font=1, cex=1.75)
text(4.65, 4.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("65.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Cells & VM (subset)")
da_data_gs <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.cell.vm.value,
  sdi = ratio.putamen.dopamine.adj.cell.vm.sd, data = subset_da, measure="MNLN",
  append = TRUE)
da_model_gs <- rma(yi, vi, data = da_data_gs)
#
png(file = (paste("2021.APR.08 - ", "65.DA.Putamen.Cell.VM.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_gs, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-5, 12.5), at=c(0,2.5,5,7.5), alim=c(0,7.5))
par("usr")
title(main="\n\n65.Ratio of Putamen Dopamine Scaled to Cells & VM\n(subset)",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_gs$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-4, da_model_gs$k+1.5, "Study", pos=4, font=1, cex=1.75)
text(11.5, da_model_gs$k+1.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(7.5, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("66.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Cells & VM (subset)")
da_data_hs <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.cell.vm.value,
  sdi = ratio.caudate.dopamine.adj.cell.vm.sd, data = subset_da, measure="MNLN",
  append = TRUE)

```

```

da_model_hs <- rma(yi, vi, data = da_data_hs)
#
png(file = (paste("2021.APR.08 - ", "66.DA.Caudate.Cell.VM.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_hs, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-20, 50), at=c(0,5,10,15,20,25,30), alim=c(0,30))
par("usr")
title(main="\n\n66.Ratio of Caudate Dopamine Scaled to Cells & VM\n(subset)",
  font.main=2, cex.main=2.2)
text(-2.5, -1, paste("p=", round(da_model_hs$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-17, da_model_hs$k+1.5, "Study", pos=4, font=1, cex=1.75)
text(47.5, da_model_hs$k+1.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(30, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
####
str(da_model_is)
exp(da_model_is$b)
exp(da_model_is$ci.lb)
exp(da_model_is$ci.ub)
####
####
cat("67.Linearized Ratio (PD/Nml) of Putamen Dopamine Scaled to Axons & VM (subset)")
da_data_is <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.axon.vm.value,
  sdi = ratio.putamen.dopamine.adj.axon.vm.sd, data = subset_da, measure="MNLN",
  append = TRUE)
da_model_is <- rma(yi, vi, data = da_data_is)
#
png(file = (paste("2021.APR.08 - ", "67.DA.Putamen.Axon.VM.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_is, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-7500,17500), at=c(0,25000,50000,75000,10000),
  alim=c(0,10000))
par("usr")
title(main="\n\n67.Linear Ratio of Putamen Dopamine Scaled to Axons & VM\n(subset)",
  font.main=2, cex.main=2.2)
text(-1750, -1, paste("p=", round(da_model_is$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-5000, da_model_is$k+1.5, "Study", pos=4, font=1, cex=1.75)
text(15500, da_model_is$k+1.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(10000, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
####
cat("68.Linearized Ratio (PD/Nml) of Caudate Dopamine Scaled to Axons & VM (subset)")
da_data_js <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.axon.vm.value,
  sdi = ratio.caudate.dopamine.adj.axon.vm.sd, data = subset_da, measure="MNLN",

```

```

append = TRUE)
da_model_js <- rma(yi, vi, data = da_data_js)
#
png(file = (paste("2021.APR.08 - ", "68.DA.Caudate.Axon.VM.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_js, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-10,30), at=c(0,5,10,15,20), alim=c(0,20))
par("usr")
title(main="\n\n68.Ratio of Caudate Dopamine Scaled to Axons & VM\n(subset)",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_js$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-8, da_model_js$k+1.5, "Study", pos=4, font=1, cex=1.75)
text(28, da_model_js$k+1.5, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(20, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("69.Linearized Putamen-Specific Dopamine Ratio (PD/Nml) of Scaled to Axon
(subset)")
da_data_e_ps <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.axon_p.value,
  sdi = ratio.putamen.dopamine.adj.axon.sd, data = subset_da, measure = "MNLN",
  append = TRUE)
da_model_e_ps <- rma(yi, vi, data = da_data_e_ps)
####
png(file = (paste("2021.APR.08 -
", "69.DA.Putamen.Specific.Axon.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_e_ps, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-10,30), at=c(0,5,10,15,20), alim=c(0,20))
par("usr")
title(main="\n\n69.Ratio of Putamen-Specific Dopamine Ratio Scaled to Axon\n(subset)",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_e_ps$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-8, da_model_e_ps$k+1.25, "Study", pos=4, font=1, cex=1.75)
text(28, da_model_e_ps$k+1.25, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(20, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("70.Linearized Caudate-Specific Dopamine Ratio (PD/Nml) of Scaled to Axon
(subset)")
###
da_data_f_cs <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.axon_c.value,
  sdi = ratio.caudate.dopamine.adj.axon.sd, data = subset_da, measure = "MNLN",
  append = TRUE)
da_model_f_cs <- rma(yi, vi, data = da_data_f_cs)
####

```

```

png(file = (paste("2021.APR.08 -
", "70.DA.Caudate.Specific.Axon.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_f_cs, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-3, 5), at=c(0,1, 2, 3), alim=c(0,3))
par("usr")
title(main="\n\n70.Ratio of Caudate-Specific Dopamine Ratio Scaled to Axon\n(subset)",
  font.main=2, cex.main=2.2)
text(-0.5, -1, paste("p=", round(da_model_f_cs$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-2.5, da_model_f_cs$k+1.25, "Study", pos=4, font=1, cex=1.75)
text(4.5, da_model_f_cs$k+1.25, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(3, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("71.Linearized Putamen-Specific Dopamine Ratio (PD/Nml) Scaled to Axons & VM
(subset)")
###
da_data_i_ps <- escalc(ni=nml.putamen.dopamine.n,
  mi = ratio.putamen.dopamine.adj.axon.vm.p.value,
  sdi = ratio.putamen.dopamine.adj.axon.vm.sd, data = subset_da, measure="MNLN",
  append = TRUE)
da_model_i_ps <- rma(yi, vi, data = da_data_i_ps)
###
png(file = (paste("2021.APR.08 -
", "71.DA.Putamen.Specific.Axon.VM.MNLN.Linear.subset.png",
  sep="")), width=1048, height = 1048, units = "px", pointsize = 14, bg="white")
forest(da_model_i_ps, slab=paste(subset_da$study, sep=", "), transf=transf.exp.int,
  ref=1, cex=1.5, xlim=c(-75,150), at=c(0,25,50,75,100), alim=c(0,100))
par("usr")
title(main="\n\n71.Ratio of Putamen-Specific Dopamine Ratio\nScaled to Axons &
VM\n(subset)",
  font.main=2, cex.main=2.2)
text(-10, -1, paste("p=", round(da_model_i_ps$pval, digits =3), sep=""),
  pos=2, font=1, cex=1.5)
text(-65, da_model_i_ps$k+1.25, "Study", pos=4, font=1, cex=1.75)
text(140, da_model_i_ps$k+1.25, "MD [95% CI]", pos=2, font=1, cex=1.75)
text(100, -1.65, "Parkinson's / Normal", cex=1.25)
dev.off()
####
cat("72.Linearized Caudate-Specific Dopamine Ratio (PD/Nml) Scaled to Axons & VM
(subset)")
###
da_data_i_cs <- escalc(ni=nml.caudate.dopamine.n,
  mi = ratio.caudate.dopamine.adj.axon.vm.c.value,
  sdi = ratio.caudate.dopamine.adj.axon.vm.sd, data = subset_da, measure="MNLN",
  append = TRUE)
da_model_i_cs <- rma(yi, vi, data = da_data_i_cs)
###

```

