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**DATA ANALYSIS SECTION**

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**CODE FOR FIGURE AVERAGE:**

Make a folder with another folder inside called: nutil\_outputs. Inside of nutil outputs, put your data in it. All your Nutil data transported in as tab delimited. (Must open the nutil data in excel and then save it as tab delimited data).

For example see: \\pn.vai.org\projects\henderson\FEEHAAN\GBA Pilot Data Analysis DONE\Individual Mouse Data\Mouse A\Right\Figure 32\nutil\_outputs

You can pull out the RMD and put it next to your nutil\_outputs and pull it out in R studio and run that code. You can also knit straight to HTML by using the HTML in that folder and clicking the knit button after running the code. It will also give you an excel sheet of your data at the end.

If you choose to copy and paste the code, you can run both together at the same time.

Packages: (If you do not have them, must download them first)

*#---------- Knitr*

setwd("C:/Users/feehaan.sultan/OneDrive - Van Andel Institute/Desktop/Mouse A/Right/Figure 32")

knitr::opts\_chunk$set(**warning**=FALSE, message=FALSE, cache=FALSE, error=FALSE, cache.lazy=FALSE)

*#knitr::opts\_knit$set(root.dir='/Volumes/projects\_secondary/bras/Lee/ASAP/Aging\_Mice\_GSE129788')*

*#options(scipen=999)*

*#options(stringsAsFactors = FALSE)*

*# Chunk Options*

*# include = FALSE, runs code, prevents code and results from appearing*

*# echo = FALSE, runs code, prevents code from appearing but not the results*

*# eval = FALSE, does not run code*

*# message = FALSE prevents messages that are generated by code from appearing*

*# warning = FALSE prevents warnings that are generated by code from appearing*

*# fig.cap = "..." adds a caption to graphical results.*

*#---------- Packages*

*#if (!requireNamespace("BiocManager", quietly = TRUE))*

*# install.packages("BiocManager")*

*#BiocManager::install("fgsea")*

*#install.packages('metap')*

suppressPackageStartupMessages({

**library**(data.table)

**library**(dplyr)

**library**(ggplot2)

**library**(knitr)

**library**(readr)

**library**(reshape2)

**library**(viridis)

})

sessionInfo()

Nutil Code:

*#---------- Set Folder*

file\_path <- "./nutil\_outputs"

*#---------- Whole\_Brain\_Average*

file\_names <- list.files(path = file\_path)

**for**(i **in** seq(length(file\_names))){

**if**(i == 1){

Whole\_Brain <- read\_delim(paste(file\_path,file\_names[i],sep="/"),

delim = "\t",

escape\_double = FALSE,

trim\_ws = TRUE) %>%

select(`Region Name`, `Region area`, `Object area`) %>%

mutate(`Object Percentage` = `Object area` / `Region area` \* 100)

} **else** {

Whole\_Brain <- rbind(Whole\_Brain,

read\_delim(paste(file\_path,file\_names[i],sep="/"),

delim = "\t",

escape\_double = FALSE,

trim\_ws = TRUE) %>%

select(`Region Name`, `Region area`, `Object area`) %>%

mutate(`Object Percentage` = `Object area` / `Region area` \* 100))

}

}

Whole\_Brain\_Avg <- Whole\_Brain %>%

group\_by(`Region Name`) %>%

summarise\_each(funs(mean, sd))

*#---------- Plot*

Whole\_Brain\_Avg %>% ggplot(aes(x=`Region area\_mean`,y=`Object area\_mean`)) +

geom\_point() +

geom\_smooth(method=lm) +

ggtitle("Whole Brain Average") +

theme\_classic() +

theme(axis.text.x = element\_text(angle = 45, vjust = 1, hjust=1)) +

theme(plot.title = element\_text(hjust=0.5, face="bold"))

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**CODE FOR WHOLE BRAIN AVERAGE:**

Make a folder with another folder inside called: nutil\_outputs. Inside of nutil outputs, you can make separate folders with all your different mice within it. All your Nutil data transported in as tab delimited. (Must open the nutil data in excel and then save it as tab delimited data).

For example see: \\pn.vai.org\projects\henderson\FEEHAAN\GBA Pilot Data Analysis DONE\Left Mouse

You can pull out the RMD and put it next to your nutil\_outputs and pull it out in R studio and run that code. You can also knit straight to HTML by using the HTML in that folder and clicking the knit button after running the code. It will also give you an excel sheet of your data at the end.

Packages: (If you do not have them, you must download them first)

*#---------- Knitr*

*# setwd("/Volumes/projects\_secondary/bras/Lee/ASAP/Aging\_Mice\_GSE129788")*

knitr::opts\_chunk$set(**warning**=FALSE, message=FALSE, cache=FALSE, error=FALSE, cache.lazy=FALSE)

*#knitr::opts\_knit$set(root.dir='/Volumes/projects\_secondary/bras/Lee/ASAP/Aging\_Mice\_GSE129788')*

*#options(scipen=999)*

*#options(stringsAsFactors = FALSE)*

*# Chunk Options*

*# include = FALSE, runs code, prevents code and results from appearing*

*# echo = FALSE, runs code, prevents code from appearing but not the results*

*# eval = FALSE, does not run code*

*# message = FALSE prevents messages that are generated by code from appearing*

*# warning = FALSE prevents warnings that are generated by code from appearing*

*# fig.cap = "..." adds a caption to graphical results.*

*#---------- Packages*

*#if (!requireNamespace("BiocManager", quietly = TRUE))*

*# install.packages("BiocManager")*

*#BiocManager::install("fgsea")*

*#install.packages('metap')*

suppressPackageStartupMessages({

**library**(data.table)

**library**(dplyr)

**library**(ggplot2)

**library**(knitr)

**library**(readr)

**library**(reshape2)

**library**(viridis)

})

sessionInfo()

Nutil Code:

*#---------- Set Folder*

file\_path <- "./nutil\_outputs"

*#---------- Whole\_Brain\_Average*

file\_names <- list.files(path = file\_path)

**for**(i **in** seq(length(file\_names))){

**if**(i == 1){

Whole\_Brain <- read\_delim(paste(file\_path,file\_names[i],sep="/"),

delim = "\t",

escape\_double = FALSE,

trim\_ws = TRUE) %>%

select(`Region Name`, `Region area`, `Object area`) %>%

mutate(`Object Percentage` = `Object area` / `Region area` \* 100)

} **else** {

Whole\_Brain <- rbind(Whole\_Brain,

read\_delim(paste(file\_path,file\_names[i],sep="/"),

delim = "\t",

escape\_double = FALSE,

trim\_ws = TRUE) %>%

select(`Region Name`, `Region area`, `Object area`) %>%

mutate(`Object Percentage` = `Object area` / `Region area` \* 100))

}

}

Whole\_Brain\_Avg <- Whole\_Brain %>%

group\_by(`Region Name`) %>%

summarise\_each(funs(mean, sd))

*#---------- Plot*

Whole\_Brain\_Avg %>% ggplot(aes(x=`Region area\_mean`,y=`Object area\_mean`)) +

geom\_point() +

geom\_smooth(method=lm) +

ggtitle("Whole Brain Average") +

theme\_classic() +

theme(axis.text.x = element\_text(angle = 45, vjust = 1, hjust=1)) +

theme(plot.title = element\_text(hjust=0.5, face="bold"))