

## R script for analyzing data of automated image analysis.

```
## loading results of Fiji analysis
Frame <- read.table("Results.csv", header = TRUE, sep = ",", quote = "")
Frame$imageType <- c("PASint", "PASarea", "H_int", "tissueArea")
## create dataframe with all relevant data
PAS <- data.frame(mouseID = substring(Frame$Label[Frame$imageType=="PASint"], 1,4),
  mouseGenotype = substring(Frame$Label[Frame$imageType=="PASint"], 10,11),
  mouseTransplantation = substring(Frame$Label[Frame$imageType=="PASint"], 16,19),
  mouseDiabetic = substring(Frame$Label[Frame$imageType=="PASint"], 21,24),
  mouseAge = substring(Frame$Label[Frame$imageType=="PASint"], 13,14),
  CCF = substring(Frame$Label[Frame$imageType=="PASint"], 26,29),
  Tumor = substring(Frame$Label[Frame$imageType=="PASint"], 31,34),
  ImageID = substring(Frame$Label[Frame$imageType=="PASint"], 6,6),
  PASvisual = substring(Frame$Label[Frame$imageType=="PASint"], 8,8),
  PASintensity = 255-Frame$Mean[Frame$imageType=="PASint"],
  ImageArea = Frame$Area[Frame$imageType=="PASarea"],
  PASarea = Frame$X.Area[Frame$imageType=="PASarea"],
  H_Intensity = 255-Frame$Mean[Frame$imageType=="H_int"],
  TissueArea = Frame$X.Area[Frame$imageType=="tissueArea"])
## count pixels of tissue
PAS$tissuePixels <- PAS$ImageArea*PAS$TissueArea/100
## count pixels of PAS
PAS$PASPixels <- PAS$ImageArea*PAS$PASArea/100
## count PAS/tissue x 100 -> PAS in %
PAS$PASquant <- PAS$PASPixels/PAS$tissuePixels*100

## summarise PAS
library(plyr)
PAS_sum <- ddply(PAS, ~mouseID, summarise, meanPASArea=mean(PASArea), sdPASArea=sd(PASArea),
  meanTissueArea=mean(TissueArea), sdTissueArea=sd(TissueArea), meantissuePixels=mean(tissuePixels),
  sdtissuePixels=sd(tissuePixels), meanPASPixels=mean(PASPixels), sdPASPixels=sd(PASPixels),
  meanPASquant=mean(PASquant), sdPASquant=sd(PASquant), meanPASintensity=mean(PASintensity),
  sdPASintensity=sd(PASintensity))
## remove unique data
PAS_unique <- subset(PAS, select = c("mouseID", "mouseGenotype", "mouseTransplantation", "mouseDiabetic",
  "mouseAge", "CCF", "Tumor", "PASvisual"))
## remove redundant data
PAS_unique <- PAS_unique[!duplicated(PAS_unique),]
## merge PAS_unique and PAS_sum
PASframe <- merge(PAS_unique, PAS_sum, by="mouseID")

## delete all other frames
rm(Frame)
rm(PAS)
rm(PAS_sum)
rm(PAS_unique)
```