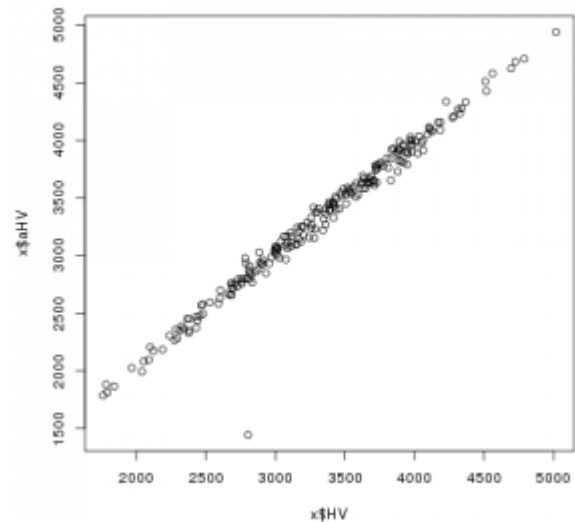


# How to correct by Intracranial Volume (ICV)



I'm going to suppose you did the pipeline thing over your MRI images and you already have the *study\_mri.csv* file. The Freesurfer version I'm using makes an estimation of Intracranial volume and the pipeline scripts put it as *EstimatedTotalIntraCranialVol\_eTIV* into the results file. First do this for a real CSV file:

```
$ sed 's/;/,/g' ab255_mri.csv > ab255_mri_rc.csv
```

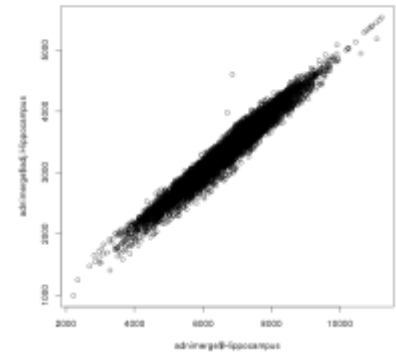
Let's say we want to get the hippocampus volume (HV) corrected by ICV. Then we must get Left and Right HV and calculate its medium value.  **$HV = 0.5*(HVR+HVL)$**

Now first step is to fit a straight line for HV vs ICV and the ICV mean value ( $\langle ICV \rangle$ ). The adjusted HV will be  **$aHV = HV - b*(ICV - \langle ICV \rangle)$** , with  $b$  as the regression coefficient of HV vs ICV.

Now we need to get the data. Let's try it in R.

```
x <- read.csv("ab255_mri_rc.csv")
x$HV = 0.5*(x$"Right.Hippocampus"+x$"Left.Hippocampus")
a <- lm(x$HV~x$"EstimatedTotalIntraCranialVol_eTIV")
b=a$coefficients[[2]]
x$aHV = x$HV - b*(x$EstimatedTotalIntraCranialVol_eTIV -
mean(x$EstimatedTotalIntraCranialVol_eTIV, na.rm=TRUE))
write.csv(x, file="ab255_mri_aHV.csv")
```

## For ADNIMERGE package



```
library("ADNIMERGE")
a <- lm(adnimage$Hippocampus~adnimage$ICV)
adnimage$adj.Hippocampus = adnimage$Hippocampus -
a$coefficients[[2]]*(adnimage$ICV - mean(adnimage$ICV, na.rm=T))
```

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