#The following code calculates weighted mean Hg concentration and total number of samples (across studies) by scientific name. To calculate by common name, substitute “Species” in place of “ScientificName”.

fish<-read.csv("/Users/roxannekarimi2/Desktop/SeafoodHgFishBaseMergeOct2014.csv",header=T)

attach(fish)

names(fish)

var1= by(fish$scrap, ScientificName, sum, na.rm=T)

var2= by(fish$Samples, ScientificName, sum, na.rm=T)

weighted\_mean= var1/var2

N= by(fish$Samples, ScientificName, sum, na.rm=T)

cbind(weighted\_mean, N)