

```

#####
#####Quantification of SPE extracts
#####

#packages
library(openxlsx)
library(effects)
library(investr)

###import data
setwd("C:\\\\Users\\\\charles.chappuis\\\\OneDrive - HESSO\\\\Documents\\\\Ra&D\\\\Lefort\\\\conf_publi")

ana <- read.xlsx("data_chappuis_2023.xlsx",sheet=3)
colnames(ana) <- c("name","rep","type","levels","istd","verb","meth","phero","panis")
str(ana)

###quantification
#values of blanks are neglected as they are very low. Headspace cells and cartridges were clean.

i=3
k=1

for(i in c(1:4)){
  prodi <- ana[,c(1,2,3,4,5,i+5)]
  nam <- names(prodi)[6]
  if(nam=="verb"){
    cali <- prodi[prodi$type=="Cal",]
    cali$levels <- cali$levels*0.992*0.94 #mass and purity taken into account
    cali$rel <- cali$verb/cali$istd
    mod <- lm(rel~levels,weight=1/levels,data=cali)
    summary(mod)
  }
}

```

```

}else{}

if(nam=="meth"){
  cali <- prodi[prodi$type=="Cal",]
  cali$levels <- cali$levels*1.187*0.98
  cali$rel <- cali$meth/cali$istd
  mod <- lm(rel~levels,weight=1/levels,data=cali)
  summary(mod)
}else{}

if(nam=="phero"){
  cali <- prodi[prodi$type=="Cal",]
  cali$levels <- cali$levels*1.623*0.983
  cali$rel <- cali$phero/cali$istd
  calii <- cali[c(1:7),] #limit the calibration span, values above are useless
  mod <- lm(rel~levels+l(levels^2),weight=1/levels^2,data=calii)#
  summary(mod)
}else{}

if(nam=="panis"){
  cali <- prodi[prodi$type=="Cal",]
  cali$levels <- cali$levels*1.148*0.98
  cali$rel <- cali$panis/cali$istd
  mod <- lm(rel~levels,weight=1/levels,data=cali)
  summary(mod)
}else{}

conc <- c()
for(k in c(1:nrow(prodi))){
  prodi$rel <- prodi[,6]/prodi[,5]
  xx <- prodi$rel[k]
  pred <- invest(mod,xx,interval="none",extendInt="yes")
}

```

```
conci <- as.numeric(pred)
conc <- c(conc,conci)
}

ana$pred <- conc
colnames(ana)[9+i] <- paste(nam,"C",sep="")
}

ana
#write.table(ana,"quant_extracts_chappuis_2023.txt",sep="\t",col.names=T)

ana$verbCC <- 100*ana$verbC/(ana$levels*0.992*0.94)
ana$pheroCC <- 100*ana$pheroC/(ana$levels*1.623*0.983)
ana$methCC <- 100*ana$methC/(ana$levels*1.187*0.98)
ana$panisCC <- 100*ana$panisC/(ana$levels*1.148*0.98)

test <- ana$phero/ana$istd
(test+2.411e-04)/4.301e-05
```