```
library(gdata)
setwd("\\\\Aa/ord/RTP/Data/Lab/NCCT_vLiver/projects/v-Liver-Chems")
setwd("/Volumes/NCCT_vLiver/projects/v-Liver-Chems")

in.vivo.data <- read.xls("HT-PBPK compounds-102212.xlsx",stringsAsFactors=FALSE,sheet=3)
in.vivo.data[1,is.na(in.vivo.data[1,])] <- ""

PK.data.in.vivo <- NULL
this.col <- 1
while (this.col <= length(colnames(in.vivo.data)))
{
  if (in.vivo.data[1,this.col]!="")
  {
    this.chem <- colnames(in.vivo.data)[this.col]
    this.species <- in.vivo.data[2,this.col]
    this.reference <- in.vivo.data[1,this.col]
    this.weight <- in.vivo.data[3,this.col]
    this.weight.units <- in.vivo.data[4,this.col]
    this.time.units <- in.vivo.data[6,this.col]
    this.first.col <- this.col
    this.col <- this.col + 1
    this.media <- ""
    this.media.units <- ""
    while (in.vivo.data[1,this.col]=="")
    {
      this.row.index <- 8
      while(is.na(in.vivo.data[this.row.index,this.col]))
      {
        this.row.index <- this.row.index + 1
        if (this.row.index > dim(in.vivo.data)[1]) break()
      }
      if (this.row.index > dim(in.vivo.data)[1]) break()
      this.dose <- in.vivo.data[3,this.col]
      this.dose.units <- in.vivo.data[4,this.col]
      if (in.vivo.data[5,this.col]!="") this.media <- in.vivo.data[5,this.col]
      if (in.vivo.data[6,this.col]!="") this.media.units <- in.vivo.data[6,this.col]
      this.row.stub <- data.frame(this.chem,stringsAsFactors=FALSE)
      this.row.stub <- cbind(this.row.stub,data.frame(this.reference,stringsAsFactors=FALSE))
      this.row.stub <- cbind(this.row.stub,data.frame(this.species,stringsAsFactors=FALSE))
      this.row.stub <- cbind(this.row.stub,data.frame(this.weight,stringsAsFactors=FALSE))
      this.row.stub <- cbind(this.row.stub,data.frame(this.weight.units,stringsAsFactors=FALSE))
      this.row.stub <- cbind(this.row.stub,data.frame(this.dose,stringsAsFactors=FALSE))
      this.row.stub <- cbind(this.row.stub,data.frame(this.dose.units,stringsAsFactors=FALSE))
      while (in.vivo.data[this.row.index,this.col] != "")
      {
        this.time <- in.vivo.data[this.row.index,this.first.col]
        this.value <- in.vivo.data[this.row.index,this.col]
        this.row <- cbind(this.row.stub,data.frame(this.time,stringsAsFactors=FALSE))
        this.row <- cbind(this.row,data.frame(this.time.units,stringsAsFactors=FALSE))
        this.row <- cbind(this.row,data.frame(this.media,stringsAsFactors=FALSE))
        this.row <- cbind(this.row,data.frame(this.media.units,stringsAsFactors=FALSE))
        this.row <- cbind(this.row,data.frame(this.value,stringsAsFactors=FALSE))
        colnames(this.row) <- c("Compound","Reference","Species","Species Weight","Species Weight
Units","Dose","Dose Units and Type","Time","Time Units","Media","Media Units","Value")
        PK.data.in.vivo <- rbind(PK.data.in.vivo,this.row)
        print(paste(this.row.index,this.col))
```

```
      this.row.index <- this.row.index + 1
      while(is.na(in.vivo.data[this.row.index,this.col]))
      {
        this.row.index <- this.row.index + 1
        if (this.row.index > dim(in.vivo.data)[1]) break()
      }
      if (this.row.index > dim(in.vivo.data)[1]) break()
    }
    this.col <- this.col + 1
    if (this.col > dim(in.vivo.data)[2]) break()
  }
 }
 this.col <- this.col + 1
}
```

add checks for exceeding dimensions both row and columns