```
setwd("\\\\AA.AD.EPA.GOV/ORD/RTP/USERS/E-J/jwambaug/Net MyDocuments/Research Projects/")

library(gdata)
Wetmore.data <-
read.xls("Supp_Table_8_SimCyp_IVIVE_input_output_083011.xls",stringsAsFactors=F,skip=1)
Wetmore.data.1 <- Wetmore.data[Wetmore.data[,"Concentration..uM."]==1,]
Wetmore.data.10 <- Wetmore.data[Wetmore.data[,"Concentration..uM."]==10,]
Wetmore.data.abridged <- NULL
Wetmore.data.1.CASlist <- unique(Wetmore.data.1[,"CASRN"])
Wetmore.data.10.CASlist <- unique(Wetmore.data.10[,"CASRN"])
good.cols <- c(1:19)
for (this.CAS in unique(Wetmore.data[,"CASRN"]))
{
  if (this.CAS %in% Wetmore.data.1.CASlist) Wetmore.data.abridged <-
rbind(Wetmore.data.abridged,Wetmore.data.1[Wetmore.data.1[,"CASRN"]==this.CAS,good.cols][1,])
  if (this.CAS %in% Wetmore.data.10.CASlist) Wetmore.data.abridged <-
rbind(Wetmore.data.abridged,Wetmore.data.10[Wetmore.data.10[,"CASRN"]==this.CAS,good.cols][1,])
}
Wetmore.data.abridged <- cbind(Wetmore.data.abridged,"Human")
colnames(Wetmore.data.abridged)[20] <- "Species"



Wetmore.rat.data <- read.xls("\\\\AA.AD.EPA.GOV/ORD/RTP/USERS/E-J/jwambaug/NET
MyDocuments/Research Projects/Rat RTK/toxsci_12_0787_File012.xls",skip=2,stringsAsFactors=F)
Wetmore.rat.data.1 <- Wetmore.rat.data[Wetmore.rat.data[,"Conc.uM."]==1,]
Wetmore.rat.data.10 <- Wetmore.rat.data[Wetmore.rat.data[,"Conc.uM."]==10,]
Wetmore.rat.data.abridged <- NULL
Wetmore.rat.data.1.CASlist <- unique(Wetmore.rat.data.1[,"CASRN"])
Wetmore.rat.data.10.CASlist <- unique(Wetmore.rat.data.10[,"CASRN"])
good.cols <- c(1,2,3,4,9,9,5,10,6,11,7,8,12,15,16)
for (this.CAS in unique(Wetmore.rat.data[,"CASRN"]))
{
  if (this.CAS %in% Wetmore.rat.data.1.CASlist) Wetmore.rat.data.abridged <-
rbind(Wetmore.rat.data.abridged,Wetmore.rat.data.1[Wetmore.rat.data.1[,"CASRN"]==this.CAS,good.col
s][1,])
  if (this.CAS %in% Wetmore.rat.data.10.CASlist) Wetmore.rat.data.abridged <-
rbind(Wetmore.rat.data.abridged,Wetmore.rat.data.10[Wetmore.rat.data.10[,"CASRN"]==this.CAS,good.c
ols][1,])
}

Wetmore.rat.data.abridged[,5] <- Wetmore.rat.data.abridged[,5]*100
Wetmore.rat.data.abridged <- cbind(Wetmore.rat.data.abridged,NA)
Wetmore.rat.data.abridged <- cbind(Wetmore.rat.data.abridged,NA)
Wetmore.rat.data.abridged <- cbind(Wetmore.rat.data.abridged,NA)
Wetmore.rat.data.abridged <- cbind(Wetmore.rat.data.abridged,NA)
Wetmore.rat.data.abridged <- cbind(Wetmore.rat.data.abridged,"Rat")
Wetmore.rat.data.abridged[,18] <- Wetmore.rat.data.abridged[,15]
Wetmore.rat.data.abridged[,15] <- Wetmore.rat.data.abridged[,14]
Wetmore.rat.data.abridged[,14] <- NA
colnames(Wetmore.rat.data.abridged) <- colnames(Wetmore.data.abridged)

Wetmore.data <- rbind(Wetmore.data.abridged,Wetmore.rat.data.abridged)

save(average.tissue,chem.invivo.PK.data,chem.physical_and_invitro.data,PK.physiology.data,tissue.data
,tissuelist,Wetmore.data,file="L:\\Lab\\NCCT_vLiver\\projects\\v-Liver-
```

Sim\\vLiverPBPK\\data\\Tables.RData")