rm(list=ls()); library(pavo);

P <- read.csv("spectra.csv", header=T); str(P)

P[,2:ncol(P)] <- P[,2:ncol(P)]

P <- as.rspec(P)

xlims <- c(300,900)

ylims <- c(0,0.8)

#select one of the four species below to run model for that species

R <- P$Slatalba\_R; str(R)

Tr.measured <- P$Slatalba\_T; str(Tr.measured)

R <- P$Nparadoxa\_R; str(R)

Tr.measured <- P$Nparadoxa\_T; str(Tr.measured)

R <- P$Omacrocarpa\_R; str(R)

Tr.measured <- P$Omacrocarpa\_T; str(Tr.measured)

R <- P$Prhoeas\_R; str(R)

Tr.measured <- P$Prhoeas\_T; str(Tr.measured)

#plot panel settings

par(mai=c(0.5,0.8,0.5,0.2))

par(mfrow=c(1,3))

par(mai=c(0.8,0.8,0.1,0.1))

par(las=1) #axis labels always horizontal

#check values at 800nm

(sum(R[[500]],Tr.measured[[500]])) #check values at 800nm

(diff\_from\_100 <- 1-(max(R)+max(Tr.measured)))

(diff\_from\_100 <- 1 - sum(R[[500]],Tr.measured[[500]]))

#Correct transmittance such that Tr + R in long wavelengths = 1. The measured spectra may not sum up to 1 at 800nm due to light that escaped horizontally.

Tr <- Tr.measured

q <- 20 #maximum in loop

wave <- P$wl

n <- nrow(P)

# Stack reflectance and transmittance

# calculate absorption and scattering parameters with reflectance and transmittance spectra (for explanations about the used calculations, see the Appendix in Stavenga & van der Kooi 2016 Planta)

df1 <- data.frame(wave)

a <- (1 + R^2 - Tr^2) / (2\*R); b <- sqrt(a^2-1) # equations 6c

Ssp <- (log((1-(a-b)\*(R))/Tr)) / b # equation 6a

Ksp <- (a-1) \* Ssp # equation 6b

Ssu <- 0 #no distinction in scattering and absorption between layers, that is, in essence the slab is one layer

Ksp.max <- max(Ksp[1:601], na.rm=T)

for (z in 1:q) {

Ksp.l <- Ksp #take the original Ksp and Ssp to take new fractions of that in each loop

Ssp.l <- Ssp

#Define the fractions to take for Ksp

Ksp.l <- Ksp.l\*z/(0.25\*q)

Ksp.l <- ifelse(Ksp.l < 0.01, 0.01, Ksp.l)

As <- Ksp.l + Ssp.l

Bs <- (Ksp.l^2 + 2 \* Ksp.l \* Ssp.l)^0.5

N <- As \* sinh(Bs) + Bs \* cosh(Bs)

r2 <- Ssp.l \* sinh(Bs) / N

t2 <- Bs / N

pig.m11 <- t2-r2^2/t2

pig.m12 <- r2/t2

pig.m21 <- -r2/t2

pig.m22 <- 1/t2

M1 <- c(pig.m11, pig.m12, pig.m21, pig.m22)

# Layer 3, mesophyll

#Tc <- numeric(length=n)

Rc1 <- numeric(length=n)

#Rc2 <- numeric(length=n)

r3 <- (Ssu/(1+Ssu))\*rep.int(1, times=n)

t3 <- 1-r3

mes.m11 <- t3-r3^2/t3

mes.m12 <- r3/t3

mes.m21 <- -r3/t3

mes.m22 <- 1/t3

M2 <- c(mes.m11, mes.m12, mes.m21, mes.m22)

for (i in 1:n) {

N1 <- numeric(4)

N2 <- numeric(4)

N1 <- matrix(data=c(pig.m11[i], pig.m12[i], pig.m21[i], pig.m22[i]), nrow=2, ncol=2, byrow=T)

N2 <- matrix(data=c(mes.m11[i], mes.m12[i], mes.m21[i], mes.m22[i]), nrow=2, ncol=2, byrow=T)

Ns <- N2%\*%N1

Rc1[i] <--Ns[2,1]/Ns[2,2] #adaxial reflectance

}

df1 <- cbind(df1, Rc1)

}

names(df1) [2:(q)] <- sprintf("Rc1\_%02d", 1:q) #give the spectra obtained in different runs a unique name

df1 <- cbind(wave,df1[,2:q])

plot(df1$Rc1\_01 ~ df1$wave, type="n", bty="L", ylab="", xlab="", ylim=c(0,0.5), xlim=c(300,800))

lines(supsmu(df1$wave, df1$Rc1\_01), lty=2)

lines(supsmu(df1$wave, df1$Rc1\_02), lty=2)

lines(supsmu(df1$wave, df1$Rc1\_03), lty=2)

lines(supsmu(df1$wave, df1$Rc1\_04), lty=2)

lines(supsmu(df1$wave, df1$Rc1\_05), lty=1)

lines(supsmu(df1$wave, df1$Rc1\_07), lty=2)

lines(supsmu(df1$wave, df1$Rc1\_12), lty=2)

lines(supsmu(df1$wave, df1$Rc1\_19), lty=2)

lines(supsmu(wave,R), col="red", lwd=2)

#lines(supsmu(wave,Tr), col="blue", lwd=2) #Transmittance spectra

############### Analyses with pavo ################

df1 <- as.rspec(df1)

df2 <- df1[1:401,]

# Incorporate background spectrum into df

back <- read.csv ("~/leaf\_average\_8spp.csv",header=T); Rb <-back$spec/100 #green leaf background used (average for eight species, but any green leaf background can be used)

df2 <- cbind (df2, Rb)

sens.apis <- read.table("sensitivity\_A.mellifera.txt", header=T) #sensitivity honeybee from van der Kooi et al 2021 Annual Review of Entomology

RNL.bee <- vismodel(df2, visual=sens.apis, achromatic = "l", illum="D65", relative=F, bkg=Rb);

RNL.bee <- coldist(RNL.bee,subset="Rb", noise="neural", achro=F, n=c(1,1,6));

sens.D.elp <- read.table("sensitivity\_D.elpenor\_ss.txt", header=T) #sensitivity Deilephila elpenor (with self-screening) from van der Kooi et al 2021 Annual Review of Entomology

RNL.moth <- vismodel(df2, visual=sens.D.elp, achromatic="l", illum="D65", relative=F, bkg=Rb);

RNL.moth <- coldist(RNL.moth, subset="Rb", noise="neural", achro=F, n=c(1,1,6))

RNL.max <- max(max(RNL.bee$dS),max(RNL.moth$dS)) #find maxima to homogenise y-axes for both RNL plots

plot(RNL.bee$dS, xlim=c(0,q), ylim=c(0,max(RNL.max)), bty="L",type="l", xlab="", ylab="", lwd=lwd.fig)

lines(RNL.moth$dS, lwd=lwd.fig, col="green")

hex.bee <- vismodel(df2, visual=sens.apis, qcatch="Ei", relative=F, vonkries=T, achromatic="l", bkg=Rb, illum="D65")

hex.bee <- colspace(hex.bee, space="hexagon")

hex.bee <- coldist(hex.bee,subset="Rb")

plot(hex.bee$dS, xlim=c(0,q), ylim=c(0,max(hex.bee$dS)), lwd=lwd.fig, bty="L",type="l", ylab="", xlab="")