f3<-paste0("../Outputs/Second derivative plots/","Individual\_",id,".jpg")

#Reading images

j1<-readJPEG(f1)

j2<-readJPEG(f2)

j3<-readJPEG(f3)

#Establishing path

mypath <- file.path("C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses/Outputs/Figure montages/", paste("Individual\_", id, ".jpg", sep = ""))

# Creating figures

jpeg(file = mypath, width=20, height=36, units="cm", res=300)

par(mar=c(1,1,1,1))

layout(matrix(1:3, ncol=1,byrow=TRUE))

plot(NA,xlim=0:1,ylim=0:1,xaxt="n",yaxt="n")

rasterImage(j1,0,0,1,1)

plot(NA,xlim=0:1,ylim=0:1,xaxt="n",yaxt="n")

rasterImage(j2, 0,0,1,1)

plot(NA,xlim=0:1,ylim=0:1,xaxt="n",yaxt="n")

rasterImage(j3, 0,0,1,1)

dev.off()

}

groups<-levels(as.factor(a$id))

map(groups, make\_grid)

derivs<-read.csv("../Outputs/derivatives.csv")

derivs<-derivs %>%

mutate(first2=first.y1\*-1)%>% #Converting the slopes to positive

filter(between(first.logtime, 30, 105)) #Triming the timeframe to the actual slope time

# Plotting to see if the conversion looks right

derivs%>%

filter(id==10) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

derivs%>%

filter(id==3) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

# Getting the row with the maximum value for each individual

ropt<-derivs %>%

group\_by(id) %>%

slice(which.max(first2))%>%

mutate(logtime=first.logtime,

ind=id)

derivs%>%

filter(id==22) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

#Merging the temperatures

topt<-difference\_left\_join(ropt,oxall, by=c("ind","logtime"), max\_dist=0.13) %>%

group\_by(ind.x, logtime.x, first.y1, first2) %>%

summarize(tempcorr2=mean(tempcorr)) %>% #averaging the tempcorr for when multiple cells are called

ungroup()

#getting the other demographic data

toptfinal<-oxall %>%

select(c("date", "trial", "channel", "ind", "stage", "weight", "ramp")) %>%

group\_by(ind)%>%

filter(row\_number()==1) %>%

right\_join(topt, by=c("ind"="ind.x")) %>%

rename(logtime=logtime.x,

tempcorr=tempcorr2,

ropt1=first.y1,

ropt2=first2) %>%

ungroup()%>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

levels(toptfinal$stage)

#Visualizing the topt and Ropt

## Temperature optima

ggplot(toptfinal, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")

ggplot(toptfinal, aes(x=stage, y=ropt2))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Maximum rate of oxygen consumption")

write.csv(toptfinal, "../Outputs/ToptandRopts.csv")

knitr::opts\_chunk$set(warning = FALSE, message = FALSE)

knitr::opts\_knit$set(root.dir = "C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses")

getwd()

library(data.table)

library(tidyr)

library(dplyr)

library(lubridate)

library(ggplot2)

library(readr)

library(stringr)

library(purrr)

library(knitr)

library(magick)

library(jpeg)

library(fuzzyjoin)

library(forcats)

notrim<-read.csv("../Outputs/ToptandRoptswithoutTrimming.csv")

poly7<-read.csv("../Outputs/ToptandRoptsTrimmedPoly7.csv")

poly10<-read.csv("../Outputs/ToptandRoptsTrimmedPoly10.csv")

View(poly10)

## Temperature optima

t1<-ggplot(notrim, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")

t1

notrim<-read.csv("../Outputs/ToptandRoptswithoutTrimming.csv") %>% %>%

notrim<-read.csv("../Outputs/ToptandRoptswithoutTrimming.csv") %>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

## Temperature optima

t1<-ggplot(notrim, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")

t1

poly7<-read.csv("../Outputs/ToptandRoptsTrimmedPoly7.csv") %>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

poly10<-read.csv("../Outputs/ToptandRoptsTrimmedPoly10.csv") %>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

t2<-ggplot(poly7, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")

t2

t3<-ggplot(poly10, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")

t3

?ggarrange

library(ggpubr)

ggarrange(t1,t2,t3, ncol=1, nrow=3)

t1<-ggplot(notrim, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")+ylim(30,55)

t1

t2<-ggplot(poly7, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")+ylim(30,55)

t2

t3<-ggplot(poly10, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")+ylim(30,55)

t3

ggarrange(t1,t2,t3, ncol=1, nrow=3)

t<-ggarrange(t1,t2,t3, ncol=1, nrow=3)

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3)

annotate\_figure(t, left = textGrob("Temperature (celsius)", rot = 90, vjust = 1, gp = gpar(cex = 1.3)),

bottom = textGrob("Stage", gp = gpar(cex = 1.3)))

library(grid)

annotate\_figure(t, left = textGrob("Temperature (celsius)", rot = 90, vjust = 1, gp = gpar(cex = 1.3)),

bottom = textGrob("Stage", gp = gpar(cex = 1.3)))

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3, labes=c("Poly7-NoTrim", "Poly7-Trim", "Poly10-Trim"))

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3, labes=c("Poly7-NoTrim", "Poly7-Trim", "Poly10-Trim"))

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3, labels=c("Poly7-NoTrim", "Poly7-Trim", "Poly10-Trim"))

annotate\_figure(t, left = textGrob("Temperature (celsius)", rot = 90, vjust = 1, gp = gpar(cex = 1.3)),

bottom = textGrob("Stage", gp = gpar(cex = 1.3)))

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3, labels=c("Poly7-NoTrim", "Poly7-Trim", "Poly10-Trim"), lebel.x=0.9)

annotate\_figure(t, left = textGrob("Temperature (celsius)", rot = 90, vjust = 1, gp = gpar(cex = 1.3)),

bottom = textGrob("Stage", gp = gpar(cex = 1.3)))

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3, labels=c("Poly7-NoTrim", "Poly7-Trim", "Poly10-Trim"), label.x=0.9)

annotate\_figure(t, left = textGrob("Temperature (celsius)", rot = 90, vjust = 1, gp = gpar(cex = 1.3)),

bottom = textGrob("Stage", gp = gpar(cex = 1.3)))

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3, labels=c("Poly7-NoTrim", "Poly7-Trim", "Poly10-Trim"), label.x=0.75)

annotate\_figure(t, left = textGrob("Temperature (celsius)", rot = 90, vjust = 1, gp = gpar(cex = 1.3)),

bottom = textGrob("Stage", gp = gpar(cex = 1.3)))

bind\_rows

?bind\_rows

notrim<-notrim%>%

select(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

notrim<-notrim%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

notrim<-read.csv("../Outputs/ToptandRoptswithoutTrimming.csv") %>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

poly7b<-poly7b%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

poly7b<-poly7%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

poly10b<-poly10%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

notrimb<-notrim%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

trimmed<-brind\_rows(notrimb, poly7b, poly10b)

trimmed<-brind\_row(notrimb, poly7b, poly10b, .id=T)

trimmed<-bind\_rows(notrimb, poly7b, poly10b, .id=T)

trimmed<-bind\_rows(notrimb, poly7b, poly10b, .id="type")

View(trimmed)

trimmed<-bind\_rows("No trim" = notrimb, "Polynomial 7"= poly7b, "Polynomial 10"= poly10b, .id="type")

trimmed<-bind\_rows("No trim-Poly 7" = notrimb, "Polynomial 7"= poly7b, "Polynomial 10"= poly10b, .id="type")

#Comparing temperature

ggplot(data=trimmed(aes(x=logtime, y=tempcorr, color=type))) + geom\_point()+theme\_classic()theme(text = element\_text(size = 15))+

#Comparing temperature

ggplot(data=trimmed(aes(x=logtime, y=tempcorr, color=type))) + geom\_point()+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Ctmax (Celsius)")+facet\_wrap(~ind)

#Comparing temperature

ggplot(data=trimmed,(aes(x=logtime, y=tempcorr, color=type))) + geom\_point()+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Ctmax (Celsius)")+facet\_wrap(~ind)

#Comparing temperature

ggplot(data=trimmed,(aes(x=logtime, y=tempcorr, color=type))) + geom\_point(size=2)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Ctmax (Celsius)")+facet\_wrap(~ind)

type

#Comparing temperature

ggplot(data=trimmed,(aes(x=logtime, y=tempcorr, color=type))) + geom\_point(size=2, shape=1)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Ctmax (Celsius)")+facet\_wrap(~ind)

#Comparing rates

ggplot(data=trimmed,(aes(x=logtime, y=ropt2, color=type))) + geom\_point(size=2, shape=1)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Ctmax (Celsius)")+facet\_wrap(~ind)

#Comparing rates

ggplot(data=trimmed,(aes(x=logtime, y=ropt2, color=type))) + geom\_point(size=2, shape=1)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Maximum rate of oxygen consumed")+facet\_wrap(~ind)

notrimb<-notrim%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

poly7b<-poly7%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

poly10b<-poly10%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

trimmed<-bind\_rows("No trim-Poly 7" = notrimb, "Polynomial 7"= poly7b, "Polynomial 10"= poly10b, .id="type")

#Comparing temperature

ggplot(data=trimmed,(aes(x=logtime, y=tempcorr, color=type))) + geom\_point(size=2, shape=1)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Ctmax (Celsius)")+facet\_wrap(~ind)

#Comparing rates

ggplot(data=trimmed,(aes(x=logtime, y=ropt2, color=type))) + geom\_point(size=2, shape=1)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Maximum rate of oxygen consumed")+facet\_wrap(~ind)

knitr::opts\_chunk$set(warning = FALSE, message = FALSE)

knitr::opts\_knit$set(root.dir = "C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses")

getwd()

library(data.table)

library(tidyr)

library(dplyr)

library(lubridate)

library(ggplot2)

library(readr)

library(stringr)

library(purrr)

library(knitr)

library(magick)

library(jpeg)

library(fuzzyjoin)

library(forcats)

library(ggpubr)

library(grid)

knitr::opts\_chunk$set(warning = FALSE, message = FALSE)

knitr::opts\_knit$set(root.dir = "C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses")

getwd()

#Calling csv file to avoid running the whole code

oxall<-read.csv("../Outputs/oxygenall.csv")

knitr::opts\_chunk$set(warning = FALSE, message = FALSE)

knitr::opts\_knit$set(root.dir = "C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses")

getwd()

library(data.table)

library(tidyr)

library(dplyr)

library(lubridate)

library(ggplot2)

library(readr)

library(stringr)

library(purrr)

library(knitr)

library(magick)

library(jpeg)

library(fuzzyjoin)

library(forcats)

library(ggpubr)

library(grid)

#Calling csv file to avoid running the whole code

oxall<-read.csv("../Outputs/oxygenall.csv")

#Calling csv file to avoid running the whole code

oxall<-read.csv("../Outputs/oxygenall.csv")

oxall<-read.csv("../Outputs/oxygenall.csv")

oxall<-read.csv("Outputs/oxygenall.csv")

ind22<-oxall %>%

filter(ind=="22")

ggplot(aes(x=logtime, y=oxymgl), data=ind22)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind22<-ind22 %>%

filter(!between(logtime, 75, 85))

ggplot(aes(x=logtime, y=oxymgl), data=ind22)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind83<-oxall %>%

filter(ind=="83")

ggplot(aes(x=logtime, y=oxymgl), data=ind83)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind83<-ind83 %>%

filter(!between(logtime, 70, 80))

ggplot(aes(x=logtime, y=oxymgl), data=ind83)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind131<-oxall %>%

filter(ind=="131")

ggplot(aes(x=logtime, y=oxymgl), data=ind131)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind131<-ind131 %>%

filter(!between(logtime, 72, 82))

ggplot(aes(x=logtime, y=oxymgl), data=ind131)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind136<-oxall %>%

filter(ind=="136")

ggplot(aes(x=logtime, y=oxymgl), data=ind136)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind136<-ind136 %>%

filter(!between(logtime, 72, 82))

ggplot(aes(x=logtime, y=oxymgl), data=ind136)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind159<-oxall %>%

filter(ind=="159")

ggplot(aes(x=logtime, y=oxymgl), data=ind159)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind159<-ind159 %>%

filter(!between(logtime, 65, 75))

ggplot(aes(x=logtime, y=oxymgl), data=ind159)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind168<-oxall %>%

filter(ind=="168")

ggplot(aes(x=logtime, y=oxymgl), data=ind168)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind168<-ind168 %>%

filter(!between(logtime, 75 ,90))

ggplot(aes(x=logtime, y=oxymgl), data=ind168)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind267<-oxall %>%

filter(ind=="267")

ggplot(aes(x=logtime, y=oxymgl), data=ind267)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind267<-ind267 %>%

filter(!between(logtime, 80, 90))

ggplot(aes(x=logtime, y=oxymgl), data=ind267)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind270<-oxall %>%

filter(ind=="270")

ggplot(aes(x=logtime, y=oxymgl), data=ind270)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind270<-ind270 %>%

filter(!between(logtime, 70, 80))

ggplot(aes(x=logtime, y=oxymgl), data=ind270)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

oxall<-oxall%>%

filter(!ind%in%c("22","83", "131", "136", "159", "168", "267", "270")) %>%

bind\_rows(ind22, ind83, ind131, ind136, ind159, ind168, ind267, ind270)

levels(as.factor(oxall$ind))

# Creating separate lists, one for each individual

dat\_list<-split(oxall, oxall$ind)

# Creating function for fitting model

r2 = function(data) {

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

output<-broom::glance(fit) #Getting adjusted r

suma<-broom::tidy(summary(fit)) #Getting parameters for model

merge(output, suma, all=TRUE)

}

a<-map\_dfr(dat\_list, r2, .id = "id") #Provides dataframe with adjusted R

write.csv(a,"../Outputs/modelfitting.csv")

# Creating separate lists, one for each individual

dat\_list<-split(oxall, oxall$ind)

# Creating function for fitting model

r2 = function(data) {

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

output<-broom::glance(fit) #Getting adjusted r

suma<-broom::tidy(summary(fit)) #Getting parameters for model

merge(output, suma, all=TRUE)

}

a<-map\_dfr(dat\_list, r2, .id = "id") #Provides dataframe with adjusted R

write.csv(a,"Outputs/modelfitting.csv")

# Getting the derivatives for each individual

#a2<-split(a, a$id)

r4=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7f.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7f.data)<-"y1"

d7f.data$logtime<-x

d7b<-D(d7, "x")

d7s.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7s.data)<-"y1"

d7s.data$logtime<-x

deriv<-list("first"=d7f.data, "second"=d7s.data)

}

a3<-map\_dfr(dat\_list, r4, .id = "id") #Creates the list with the values of the derivatives

## Saving the second derivatives into a single dataframe

write.csv(a3, "../Outputs/derivatives.csv")

# Getting the inflection points: the points where there was a change in the "slope"

r5=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

id<-data[1,11]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

inflection<-polyroot(c((a2 \*2), (a3 \*3 \* 2 ),(a4\* 4 \* 3 ), (a5 \*5 \* 4) , (a6 \* 6 \* 5 ), (a7 \* 7 \* 6 ),(a8 \*8\*7), (a9\*9\*8), (a10\*10\*9)))

inflec<-as.data.frame(inflection)

inflec$id<-data[1,1]

as.data.frame(inflec)

}

a4<-map\_dfr(dat\_list, r5, .id = "id") # List of dataframes containing the inflection points

## Merging points into a single dataframe

options(scipen=999) #Removing scientific notation

inflections<-a4%>%

bind\_rows() %>%

mutate(real=Re(inflection), #Extracting the real number from the complex expression

values=format(real, scientific=FALSE, big.mark=","), #Coverting the real number to printed decimal expression

rounded=round(real, digits=2), #rounding the real number

imagine=round(Im(inflection), digits=2)) %>% #Extracting te imaginary number

filter(between(real, 10, 115))

write.csv(inflections, "../Outputs/inflections.csv")

derivs<-read.csv("../Outputs/derivatives.csv")

derivs<-derivs %>%

mutate(first2=first.y1\*-1)%>% #Converting the slopes to positive

filter(between(first.logtime, 30, 105)) #Triming the timeframe to the actual slope time

derivs<-a3

derivs<-derivs %>%

mutate(first2=first.y1\*-1)%>% #Converting the slopes to positive

filter(between(first.logtime, 30, 105)) #Triming the timeframe to the actual slope time

derivs<-read.csv("Outputs/derivatives.csv")

derivs<-derivs %>%

mutate(first2=first.y1\*-1)%>% #Converting the slopes to positive

filter(between(first.logtime, 30, 105)) #Triming the timeframe to the actual slope time

# Plotting to see if the conversion looks right

derivs%>%

filter(id==10) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

derivs%>%

filter(id==22) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

derivs%>%

filter(id==22) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

# Getting the row with the maximum value for each individual

ropt<-derivs %>%

group\_by(id) %>%

slice(which.max(first2))%>%

mutate(logtime=first.logtime,

ind=id)

#Merging the temperatures

topt<-difference\_left\_join(ropt,oxall, by=c("ind","logtime"), max\_dist=0.13) %>%

group\_by(ind.x, logtime.x, first.y1, first2) %>%

summarize(tempcorr2=mean(tempcorr)) %>% #averaging the tempcorr for when multiple cells are called

ungroup()

#getting the other demographic data

toptfinal<-oxall %>%

select(c("date", "trial", "channel", "ind", "stage", "weight", "ramp")) %>%

group\_by(ind)%>%

filter(row\_number()==1) %>%

right\_join(topt, by=c("ind"="ind.x")) %>%

rename(logtime=logtime.x,

tempcorr=tempcorr2,

ropt1=first.y1,

ropt2=first2) %>%

ungroup()%>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

levels(toptfinal$stage)

#Visualizing the topt and Ropt

## Temperature optima

ggplot(toptfinal, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")

## Optimal rate

ggplot(toptfinal, aes(x=stage, y=ropt2))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Maximum rate of oxygen consumption")

write.csv(toptfinal, "../Outputs/ToptandRopts.csv")

notrim<-read.csv("Outputs/ToptandRoptswithoutTrimming.csv") %>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

poly7<-read.csv("Outputs/ToptandRoptsTrimmedPoly7.csv") %>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

poly10<-read.csv("Outputs/ToptandRoptsTrimmedPoly10.csv") %>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female",

"Male" )))

## Temperature optima

t1<-ggplot(notrim, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")+ylim(30,55)

t1

t2<-ggplot(poly7, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")+ylim(30,55)

t2

t3<-ggplot(poly10, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")+ylim(30,55)

t3

t<-ggarrange(t1+ rremove("ylab") + rremove("xlab"),t2+ rremove("ylab") + rremove("xlab"),t3+ rremove("ylab") + rremove("xlab"), ncol=1, nrow=3, labels=c("Poly7-NoTrim", "Poly7-Trim", "Poly10-Trim"), label.x=0.75)

annotate\_figure(t, left = textGrob("Temperature (celsius)", rot = 90, vjust = 1, gp = gpar(cex = 1.3)),

bottom = textGrob("Stage", gp = gpar(cex = 1.3)))

notrimb<-notrim%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

poly7b<-poly7%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

poly10b<-poly10%>%

filter(ind %in% c("22", "83", "131", "136", "159", "168", "267", "270"))

trimmed<-bind\_rows("No trim-Poly 7" = notrimb, "Polynomial 7"= poly7b, "Polynomial 10"= poly10b, .id="type")

#Comparing temperature

ggplot(data=trimmed,(aes(x=logtime, y=tempcorr, color=type))) + geom\_point(size=2, shape=1)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Ctmax (Celsius)")+facet\_wrap(~ind)

#Comparing rates

ggplot(data=trimmed,(aes(x=logtime, y=ropt2, color=type))) + geom\_point(size=2, shape=1)+theme\_classic()+theme(text = element\_text(size = 15))+

xlab("Time (min)")+

ylab("Maximum rate of oxygen consumed")+facet\_wrap(~ind)

---

title: "Oxygen estimation"

author: "Laura Segura Hernández"

date: "2022-08-07"

output:

html\_document:

df\_print: paged

theme: cerulean

toc: true

toc\_depth: 4

number\_sections: true

toc\_float: false

---

```{r setup, include=FALSE}

knitr::opts\_chunk$set(warning = FALSE, message = FALSE)

knitr::opts\_knit$set(root.dir = "C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses")

getwd()

```

# Libraries

```{r}

library(data.table)

library(tidyr)

library(dplyr)

library(lubridate)

library(ggplot2)

library(readr)

library(stringr)

library(purrr)

library(knitr)

library(magick)

library(jpeg)

library(fuzzyjoin)

library(forcats)

library(ggpubr)

library(grid)

```

# Organizing data

## Getting objects from Temperature Analyses

```{r}

load("Outputs/Temperature analyses.RData")

```

## Calling and arranging data

### Trial 2

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 2/" #MODIFY FOR EACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial2",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t2a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t2b<-t2a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=2,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~250, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~239,

str\_detect(id, "ch2")~311,

str\_detect(id, "ch3")~65,

str\_detect(id, "ch4")~136,

str\_detect(id, "ch5")~168,

str\_detect(id, "ch6")~294,

str\_detect(id, "ch7")~322,

str\_detect(id, "ch8")~022,

str\_detect(id, "ch9")~258,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Female",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Tritonymph",

str\_detect(id, "ch2")~"Protonymph",

str\_detect(id, "ch3")~"Female",

str\_detect(id, "ch4")~"Deutonymph",

str\_detect(id, "ch5")~"Male",

str\_detect(id, "ch6")~"Protonymph",

str\_detect(id, "ch7")~"Tritonymph",

str\_detect(id, "ch8")~"Deutonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Male"),

weight=case\_when(str\_detect(id, "ch10")~1.269, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.792,

str\_detect(id, "ch2")~0.189,

str\_detect(id, "ch3")~1.714,

str\_detect(id, "ch4")~0.330,

str\_detect(id, "ch5")~1.219,

str\_detect(id, "ch6")~0.240,

str\_detect(id, "ch7")~0.749,

str\_detect(id, "ch8")~0.339,

#str\_detect(id, "ch9")~1.001,

TRUE~1.001),

atm=round(33.864\*28.81)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==2) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t2<- full\_join(t2b, temp2, by="datetime2", suffix=c("",".temp"))

head(t2) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox2<-t2 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox2) #MODIFY FOR EACH TRIAL

ggplot(ox2, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8.5,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 3

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 3/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial3",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t3a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t3b<-t3a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=3,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~010, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~231,

str\_detect(id, "ch2")~029,

str\_detect(id, "ch3")~087,

str\_detect(id, "ch4")~166,

str\_detect(id, "ch5")~300,

str\_detect(id, "ch6")~121,

str\_detect(id, "ch7")~014,

str\_detect(id, "ch8")~271,

str\_detect(id, "ch9")~143,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Female",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Tritonymph",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"Protonymph",

str\_detect(id, "ch4")~"Female",

str\_detect(id, "ch5")~"Deutonymph",

str\_detect(id, "ch6")~"Protonymph",

str\_detect(id, "ch7")~"Deutonymph",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Male"),

weight=case\_when(str\_detect(id, "ch10")~1.228, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.931,

str\_detect(id, "ch2")~0.924,

str\_detect(id, "ch3")~0.251,

str\_detect(id, "ch4")~1.376,

str\_detect(id, "ch5")~0.289,

str\_detect(id, "ch6")~0.189,

str\_detect(id, "ch7")~0.347,

str\_detect(id, "ch8")~0.647,

#str\_detect(id, "ch9")~1.001,

TRUE~1.021),

atm=round(33.864\*28.81)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==3) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t3<- full\_join(t3b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t3) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox3<-t3 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox3) #MODIFY FOR EACH TRIAL

ggplot(ox3, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(7,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 4

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 4/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial4",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t4a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t4b<-t4a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=4,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~213, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~337,

str\_detect(id, "ch2")~051,

str\_detect(id, "ch3")~109,

str\_detect(id, "ch4")~245,

str\_detect(id, "ch5")~037,

str\_detect(id, "ch6")~131,

str\_detect(id, "ch7")~005,

str\_detect(id, "ch8")~194,

str\_detect(id, "ch9")~154,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Protonymph",

str\_detect(id, "ch2")~"Deutonymph",

str\_detect(id, "ch3")~"Tritonymph",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Female",

str\_detect(id, "ch6")~"Tritonymph",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Male",

#str\_detect(id, "ch9")~"Male",

TRUE~"Protonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.241, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.163,

str\_detect(id, "ch2")~0.350,

str\_detect(id, "ch3")~0.730,

str\_detect(id, "ch4")~0.963,

str\_detect(id, "ch5")~1.332,

str\_detect(id, "ch6")~0.509,

str\_detect(id, "ch7")~1.582,

str\_detect(id, "ch8")~0.999,

#str\_detect(id, "ch9")~1.001,

TRUE~0.109),

atm=round(33.864\*28.90)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==4) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t4<- full\_join(t4b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t4) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox4<-t4 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox4) #MODIFY FOR EACH TRIAL

ggplot(ox4, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 5

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 5/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial5",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t5a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t5b<-t5a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=5,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~324, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~024,

str\_detect(id, "ch2")~253,

str\_detect(id, "ch3")~025,

str\_detect(id, "ch4")~003,

str\_detect(id, "ch5")~290,

str\_detect(id, "ch6")~244,

str\_detect(id, "ch7")~257,

str\_detect(id, "ch8")~032,

str\_detect(id, "ch9")~159,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Protonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Female",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"Tritonymph",

str\_detect(id, "ch4")~"Deutonymph",

str\_detect(id, "ch5")~"Protonymph",

str\_detect(id, "ch6")~"Female",

str\_detect(id, "ch7")~"Male",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Deutonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.158, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~1.472,

str\_detect(id, "ch2")~0.900,

str\_detect(id, "ch3")~0.688,

str\_detect(id, "ch4")~0.328,

str\_detect(id, "ch5")~0.166,

str\_detect(id, "ch6")~1.454,

str\_detect(id, "ch7")~0.946,

str\_detect(id, "ch8")~0.613,

#str\_detect(id, "ch9")~1.001,

TRUE~0.278),

atm=round(33.864\*28.84)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==5) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t5<- full\_join(t5b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t5) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox5<-t5 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox5) #MODIFY FOR EACH TRIAL

ggplot(ox5, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 6

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 6/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial6",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t6a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t6b<-t6a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=6,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~267, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~288,

str\_detect(id, "ch2")~030,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~287,

str\_detect(id, "ch5")~218,

str\_detect(id, "ch6")~238,

str\_detect(id, "ch7")~165,

str\_detect(id, "ch8")~298,

str\_detect(id, "ch9")~066,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Deutonymph",

str\_detect(id, "ch2")~"Female",

str\_detect(id, "ch3")~"NA",

str\_detect(id, "ch4")~"Tritonymph",

str\_detect(id, "ch5")~"Tritonymph",

str\_detect(id, "ch6")~"Male",

str\_detect(id, "ch7")~"Protonymph",

str\_detect(id, "ch8")~"Protonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Female"),

weight=case\_when(str\_detect(id, "ch10")~0.221, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.257,

str\_detect(id, "ch2")~1.583,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~0.583,

str\_detect(id, "ch5")~0.715,

str\_detect(id, "ch6")~0.794,

str\_detect(id, "ch7")~0.142,

str\_detect(id, "ch8")~0.201,

#str\_detect(id, "ch9")~1.001,

TRUE~2.208),

atm=round(33.864\*28.81)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==6) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t6<- full\_join(t6b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t6) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox6<-t6 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox6) #MODIFY FOR EACH TRIAL

ggplot(ox6, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 7

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 7/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial7",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t7a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t7b<-t7a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=7,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~274, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~235,

str\_detect(id, "ch2")~216,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~237,

str\_detect(id, "ch5")~175,

str\_detect(id, "ch6")~246,

str\_detect(id, "ch7")~232,

str\_detect(id, "ch8")~269,

str\_detect(id, "ch9")~043,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Male",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"NA",

str\_detect(id, "ch4")~"Female",

str\_detect(id, "ch5")~"Protonymph",

str\_detect(id, "ch6")~"Female",

str\_detect(id, "ch7")~"Tritonymph",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Protonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.324, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.900,

str\_detect(id, "ch2")~1.126,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~1.345,

str\_detect(id, "ch5")~0.213,

str\_detect(id, "ch6")~1.937,

str\_detect(id, "ch7")~0.748,

str\_detect(id, "ch8")~0.622,

#str\_detect(id, "ch9")~1.001,

TRUE~0.139),

atm=round(33.864\*28.78)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==7) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t7<- full\_join(t7b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t7) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox7<-t7 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox7) #MODIFY FOR EACH TRIAL

ggplot(ox7, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 8

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 8/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial8",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t8a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t8b<-t8a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=8,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~345, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~301,

str\_detect(id, "ch2")~107,

str\_detect(id, "ch3")~54,

str\_detect(id, "ch4")~270,

str\_detect(id, "ch5")~85,

str\_detect(id, "ch6")~36,

str\_detect(id, "ch7")~112,

str\_detect(id, "ch8")~138,

str\_detect(id, "ch9")~80,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Tritonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Protonymph",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"Tritonymph",

str\_detect(id, "ch4")~"Deutonymph",

str\_detect(id, "ch5")~"Female",

str\_detect(id, "ch6")~"Protonymph",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Deutonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Male"),

weight=case\_when(str\_detect(id, "ch10")~0.863, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.176,

str\_detect(id, "ch2")~0.648,

str\_detect(id, "ch3")~0.858,

str\_detect(id, "ch4")~0.325,

str\_detect(id, "ch5")~1.863,

str\_detect(id, "ch6")~0.146,

str\_detect(id, "ch7")~1.522,

str\_detect(id, "ch8")~0.329,

#str\_detect(id, "ch9")~1.001,

TRUE~1.199),

atm=round(33.864\*28.72)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==8) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t8<- full\_join(t8b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t8) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox8<-t8 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox8) #MODIFY FOR EACH TRIAL

ggplot(ox8, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 9

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 9/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial9",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t9a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t9b<-t9a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=9,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~007, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~242,

str\_detect(id, "ch2")~035,

str\_detect(id, "ch3")~146,

str\_detect(id, "ch4")~153,

str\_detect(id, "ch5")~334,

str\_detect(id, "ch6")~264,

str\_detect(id, "ch7")~1000,

str\_detect(id, "ch8")~004,

str\_detect(id, "ch9")~228,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Male",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Female",

str\_detect(id, "ch2")~"Protonymph",

str\_detect(id, "ch3")~"Male",

str\_detect(id, "ch4")~"Tritonymph",

str\_detect(id, "ch5")~"Deutonymph",

str\_detect(id, "ch6")~"Deutonymph",

str\_detect(id, "ch7")~"NA",

str\_detect(id, "ch8")~"Female",

#str\_detect(id, "ch9")~"Male",

TRUE~"Tritonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.983, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~1.775,

str\_detect(id, "ch2")~0.185,

str\_detect(id, "ch3")~1.118,

str\_detect(id, "ch4")~0.551,

str\_detect(id, "ch5")~0.302,

str\_detect(id, "ch6")~0.342,

str\_detect(id, "ch7")~1000,

str\_detect(id, "ch8")~1.425,

#str\_detect(id, "ch9")~1.001,

TRUE~0.569),

atm=round(33.864\*28.66)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==9) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t9<- full\_join(t9b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t9) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox9<-t9 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox9) #MODIFY FOR EACH TRIAL

ggplot(ox9, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 10

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 10/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial10",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t10a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t10b<-t10a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=10,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~179, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~048,

str\_detect(id, "ch2")~158,

str\_detect(id, "ch3")~079,

str\_detect(id, "ch4")~145,

str\_detect(id, "ch5")~057,

str\_detect(id, "ch6")~251,

str\_detect(id, "ch7")~248,

str\_detect(id, "ch8")~314,

str\_detect(id, "ch9")~212,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Tritonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Deutonymph",

str\_detect(id, "ch2")~"Female",

str\_detect(id, "ch3")~"Female",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Tritonymph",

str\_detect(id, "ch6")~"Male",

str\_detect(id, "ch7")~"Male",

str\_detect(id, "ch8")~"Deutonymph",

#str\_detect(id, "ch9")~"",

TRUE~"Female"),

weight=case\_when(str\_detect(id, "ch10")~0.653, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.451,

str\_detect(id, "ch2")~1.178,

str\_detect(id, "ch3")~1.781,

str\_detect(id, "ch4")~0.929,

str\_detect(id, "ch5")~0.866,

str\_detect(id, "ch6")~0.941,

str\_detect(id, "ch7")~0.864,

str\_detect(id, "ch8")~0.188,

#str\_detect(id, "ch9")~1.001,

TRUE~1.582),

atm=round(33.864\*28.64)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==10) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t10<- full\_join(t10b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t10) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox10<-t10 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox10) #MODIFY FOR EACH TRIAL

ggplot(ox10, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 11

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 11/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial11",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t11a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t11b<-t11a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=11,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~141, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~272,

str\_detect(id, "ch2")~305,

str\_detect(id, "ch3")~326,

str\_detect(id, "ch4")~224,

str\_detect(id, "ch5")~173,

str\_detect(id, "ch6")~214,

str\_detect(id, "ch7")~082,

str\_detect(id, "ch8")~113,

str\_detect(id, "ch9")~329,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Female",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Tritonymph",

str\_detect(id, "ch2")~"Deutonymph",

str\_detect(id, "ch3")~"Deutonymph",

str\_detect(id, "ch4")~"Female",

str\_detect(id, "ch5")~"Tritonymph",

str\_detect(id, "ch6")~"Deutonymph",

str\_detect(id, "ch7")~"Male",

str\_detect(id, "ch8")~"Male",

#str\_detect(id, "ch9")~"",

TRUE~"Tritonymph"),

weight=case\_when(str\_detect(id, "ch10")~1.853, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.675,

str\_detect(id, "ch2")~0.312,

str\_detect(id, "ch3")~0.283,

str\_detect(id, "ch4")~1.785,

str\_detect(id, "ch5")~0.566,

str\_detect(id, "ch6")~0.184,

str\_detect(id, "ch7")~1.095,

str\_detect(id, "ch8")~1.046,

#str\_detect(id, "ch9")~1.001,

TRUE~0.591),

atm=round(33.864\*28.55)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==11) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t11<- full\_join(t11b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t11) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox11<-t11 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox11) #MODIFY FOR EACH TRIAL

ggplot(ox11, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 12

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 12/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial12",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t12a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t12b<-t12a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=12,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~339, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~256,

str\_detect(id, "ch2")~341,

str\_detect(id, "ch3")~18,

str\_detect(id, "ch4")~83,

str\_detect(id, "ch5")~50,

str\_detect(id, "ch6")~201,

str\_detect(id, "ch7")~211,

str\_detect(id, "ch8")~317,

str\_detect(id, "ch9")~335,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Female",

str\_detect(id, "ch2")~"Tritonymph",

str\_detect(id, "ch3")~"Male",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Male",

str\_detect(id, "ch6")~"Female",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"",

TRUE~"Deutonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.314, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~1.450,

str\_detect(id, "ch2")~0.790,

str\_detect(id, "ch3")~1.23,

str\_detect(id, "ch4")~1.015,

str\_detect(id, "ch5")~1.229,

str\_detect(id, "ch6")~1.49,

str\_detect(id, "ch7")~1.500,

str\_detect(id, "ch8")~0.905,

#str\_detect(id, "ch9")~1.001,

TRUE~0.268),

atm=round(33.864\*28.58)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==12) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t12<- full\_join(t12b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t12) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox12<-t12 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox12) #MODIFY FOR EACH TRIAL

ggplot(ox12, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 13

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 13/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial13",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t13a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t13b<-t13a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=13,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~1000, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~296,

str\_detect(id, "ch2")~263,

str\_detect(id, "ch3")~156,

str\_detect(id, "ch4")~073,

str\_detect(id, "ch5")~171,

str\_detect(id, "ch6")~002,

str\_detect(id, "ch7")~247,

str\_detect(id, "ch8")~233,

str\_detect(id, "ch9")~028,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"NA",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Deutonymph",

str\_detect(id, "ch2")~"Tritonymph",

str\_detect(id, "ch3")~"Male",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Deutonymph",

str\_detect(id, "ch6")~"Tritonymph",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Female",

#str\_detect(id, "ch9")~"",

TRUE~"Tritonymph"),

weight=case\_when(str\_detect(id, "ch10")~1000, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.272,

str\_detect(id, "ch2")~0.764,

str\_detect(id, "ch3")~0.656,

str\_detect(id, "ch4")~1.18,

str\_detect(id, "ch5")~0.361,

str\_detect(id, "ch6")~0.767,

str\_detect(id, "ch7")~1.256,

str\_detect(id, "ch8")~1.693,

#str\_detect(id, "ch9")~1.001,

TRUE~0.866),

atm=round(33.864\*28.55)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==13) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t13<- full\_join(t13b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t13) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox13<-t13 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox13) #MODIFY FOR EACH TRIAL

ggplot(ox13, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

Go back to each trial and annotate the best beginning and end of trial, and change it in the temperature data, then re-run this analysis again, to only get the curves that actual pertain to the trial (i.e. get it from the start and also remove the tail when it warms up again at the end)

# Merging trials into a single dataframe FALTA

```{r, eval=F}

oxall<-bind\_rows(ox2,ox3,ox4,ox5,ox6,ox7,ox8,ox9,ox10,ox11,ox12,ox13) #%>%

#filter(!ind%in%c("22","83", "131", "136", "159", "168", "267", "270")) # Cambiar por individuos ahogados

#FALTA REMOVER INDIVIDUOS AHOGADOS

write.csv(oxall,"Outputs/oxygenall\_aftercodedeletion.csv")

```

# Trying which function to use

```{r}

# Filtering for a single individuals to just see the fit

func<-ox7%>%

filter(ind==232) %>%

group\_by(logtime) %>%

filter(duplicated(logtime|n()==2))

#Trying different curves

fit2<-lm(oxymgl~poly(logtime, 2, raw=TRUE), data=func)

fit3<-lm(oxymgl~poly(logtime, 3, raw=TRUE), data=func)

fit4<-lm(oxymgl~poly(logtime, 4, raw=TRUE), data=func)

fit5<-lm(oxymgl~poly(logtime, 5, raw=TRUE), data=func)

fit6<-lm(oxymgl~poly(logtime, 6, raw=TRUE), data=func)

fit7<-lm(oxymgl~poly(logtime, 7, raw=TRUE), data=func)

fit8<-lm(oxymgl~poly(logtime, 8, raw=TRUE), data=func)

fit9<-lm(oxymgl~poly(logtime, 9, raw=TRUE), data=func)

fit10<-lm(oxymgl~poly(logtime, 10, raw=TRUE), data=func)

# CReating a dataframe to build the prediction

logtime <- seq(1, 125, length=125)

# Plotting each predicted function line to the real data

plot(func$logtime, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit2, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit3, data.frame(x=logtime)), col='purple')

lines(logtime, predict(fit4, data.frame(x=logtime)), col='blue')

lines(logtime, predict(fit5, data.frame(x=logtime)), col='orange')

lines(logtime, predict(fit6, data.frame(x=logtime)), col='green')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit8, data.frame(x=logtime)), col='yellow')

lines(logtime, predict(fit9, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit10, data.frame(x=logtime)), col='grey')

#calculated adjusted R-squared of each model

# The adjusted r squared is the percent of the variance of Y intact after subtracting the error of the model. The more the R Squared value the better the model is for that data frame.

summary(fit2)$adj.r.squared

summary(fit3)$adj.r.squared

summary(fit4)$adj.r.squared

summary(fit5)$adj.r.squared

summary(fit6)$adj.r.squared

summary(fit7)$adj.r.squared

summary(fit8)$adj.r.squared

summary(fit9)$adj.r.squared

summary(fit10)$adj.r.squared

coef7<-as.data.frame(fit7$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1] #cambiar a A

x<-func$logtime

form7<-expression((a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

ggplot(aes(x=logtime, y=oxymgl), data=func)+geom\_point()

plot(x, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='red')

#Primera derivada: tasa con la que consume oxigeno

d7b.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()

#Segunda derivada: cruce con y=0 son los punto de cambio, puntos de inflexion donde la pendiente cambia hacia arriva o hacia abajo

d7b.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()+scale\_x\_continuous(breaks=c(0,10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120))

# Finding the values at which the second derivative=0

f=function(x) eval(d7b)

uniroot(f, c(0,125))

inflection<-polyroot(c((a2 \*2), (a3 \*3 \* 2 ),(a4\* 4 \* 3 ), (a5 \*5 \* 4) , (a6 \* 6 \* 5 ), (a7 \* 7 \* 6 )))

inflec<-as.data.frame(inflection)

```

# Trying which function to use on a different individual

```{r}

# Filtering for a single individuals to just see the fit

func<-ox3%>%

filter(ind=="87")# %>%

#group\_by(logtime) %>%

#filter(duplicated(logtime|n()==2))

#Trying different curves

fit2<-lm(oxymgl~poly(logtime, 2, raw=TRUE), data=func)

fit3<-lm(oxymgl~poly(logtime, 3, raw=TRUE), data=func)

fit4<-lm(oxymgl~poly(logtime, 4, raw=TRUE), data=func)

fit5<-lm(oxymgl~poly(logtime, 5, raw=TRUE), data=func)

fit6<-lm(oxymgl~poly(logtime, 6, raw=TRUE), data=func)

fit7<-lm(oxymgl~poly(logtime, 7, raw=TRUE), data=func)

fit8<-lm(oxymgl~poly(logtime, 8, raw=TRUE), data=func)

fit9<-lm(oxymgl~poly(logtime, 9, raw=TRUE), data=func)

fit10<-lm(oxymgl~poly(logtime, 10, raw=TRUE), data=func)

# CReating a dataframe to build the prediction

logtime <- seq(1, 125, length=125)

# Plotting each predicted function line to the real data

plot(func$logtime, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit2, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit3, data.frame(x=logtime)), col='purple')

lines(logtime, predict(fit4, data.frame(x=logtime)), col='blue')

lines(logtime, predict(fit5, data.frame(x=logtime)), col='orange')

lines(logtime, predict(fit6, data.frame(x=logtime)), col='green')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit8, data.frame(x=logtime)), col='yellow')

lines(logtime, predict(fit9, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit10, data.frame(x=logtime)), col='grey')

#calculated adjusted R-squared of each model

# The adjusted r squared is the percent of the variance of Y intact after subtracting the error of the model. The more the R Squared value the better the model is for that data frame.

summary(fit2)$adj.r.squared

summary(fit3)$adj.r.squared

summary(fit4)$adj.r.squared

summary(fit5)$adj.r.squared

summary(fit6)$adj.r.squared

summary(fit7)$adj.r.squared

summary(fit8)$adj.r.squared

summary(fit9)$adj.r.squared

summary(fit10)$adj.r.squared

coef7<-as.data.frame(fit7$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1] #cambiar a A

x<-func$logtime

form7<-expression((a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

ggplot(aes(x=logtime, y=oxymgl), data=func)+geom\_point()

plot(x, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='red')

#Primera derivada: tasa con la que consume oxigeno

d7b.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()

#Segunda derivada: cruce con y=0 son los punto de cambio, puntos de inflexion donde la pendiente cambia hacia arriba o hacia abajo

d7b.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()+scale\_x\_continuous(breaks=c(0,10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120))

# Finding the values at which the second derivative=0

#f=function(x) eval(d7b)

#uniroot(f, c(0,125))

inflection<-polyroot(c((a2 \*2), (a3 \*3 \* 2 ),(a4\* 4 \* 3 ), (a5 \*5 \* 4) , (a6 \* 6 \* 5 ), (a7 \* 7 \* 6 )))

inflection

inflec<-as.data.frame(inflection)

#inflec$inflection<-as.numeric\*inflec$inflection

```

# Calling the csv file to avoid running the whole code

```{r}

#Calling csv file to avoid running the whole code

oxall<-read.csv("../Outputs/oxygenall.csv")

```

# Cutting out traces with weird patterns

## Individual 22

```{r}

ind22<-oxall %>%

filter(ind=="22")

ggplot(aes(x=logtime, y=oxymgl), data=ind22)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind22<-ind22 %>%

filter(!between(logtime, 75, 85))

ggplot(aes(x=logtime, y=oxymgl), data=ind22)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 83

```{r}

ind83<-oxall %>%

filter(ind=="83")

ggplot(aes(x=logtime, y=oxymgl), data=ind83)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind83<-ind83 %>%

filter(!between(logtime, 70, 80))

ggplot(aes(x=logtime, y=oxymgl), data=ind83)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 131

```{r}

ind131<-oxall %>%

filter(ind=="131")

ggplot(aes(x=logtime, y=oxymgl), data=ind131)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind131<-ind131 %>%

filter(!between(logtime, 72, 82))

ggplot(aes(x=logtime, y=oxymgl), data=ind131)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 136

```{r}

ind136<-oxall %>%

filter(ind=="136")

ggplot(aes(x=logtime, y=oxymgl), data=ind136)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind136<-ind136 %>%

filter(!between(logtime, 72, 82))

ggplot(aes(x=logtime, y=oxymgl), data=ind136)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 159

```{r}

ind159<-oxall %>%

filter(ind=="159")

ggplot(aes(x=logtime, y=oxymgl), data=ind159)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind159<-ind159 %>%

filter(!between(logtime, 65, 75))

ggplot(aes(x=logtime, y=oxymgl), data=ind159)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 168

```{r}

ind168<-oxall %>%

filter(ind=="168")

ggplot(aes(x=logtime, y=oxymgl), data=ind168)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind168<-ind168 %>%

filter(!between(logtime, 75 ,90))

ggplot(aes(x=logtime, y=oxymgl), data=ind168)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 267

```{r}

ind267<-oxall %>%

filter(ind=="267")

ggplot(aes(x=logtime, y=oxymgl), data=ind267)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind267<-ind267 %>%

filter(!between(logtime, 80, 90))

ggplot(aes(x=logtime, y=oxymgl), data=ind267)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 270

```{r}

ind270<-oxall %>%

filter(ind=="270")

ggplot(aes(x=logtime, y=oxymgl), data=ind270)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind270<-ind270 %>%

filter(!between(logtime, 70, 80))

ggplot(aes(x=logtime, y=oxymgl), data=ind270)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Creating new dataset with trimmed individuals

```{r}

oxall<-oxall%>%

filter(!ind%in%c("22","83", "131", "136", "159", "168", "267", "270")) %>%

bind\_rows(ind22, ind83, ind131, ind136, ind159, ind168, ind267, ind270) %>%

filter\_all(all\_vars(!is.infinite(.)))

levels(as.factor(oxall$ind))

```

# Creating a loop to get data for all individuals

Steps needed:

1. Fit the polynomial function to each individual

2. See the r.adjusted for each individual

3. Extract the coefficient of the function for each individual

4. Get the first and second derivatives

5. Get the inflection points

6. Clean the inflection points

7. Check the inflection points with the data

8. Merge the inflection points with the data set (get at least ID, stage)

9. Do statistical comparison

## 1. Adjusting a polynomial function to each individual

```{r}

# Creating separate lists, one for each individual

dat\_list<-split(oxall, oxall$ind)

# Creating function for fitting model

# Creating function for fitting model

r2 = function(data) {

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

output<-broom::glance(fit) #Getting adjusted r

suma<-broom::tidy(summary(fit)) #Getting parameters for model

merge(output, suma, all=TRUE)

}

a<-map\_dfr(dat\_list, r2, .id = "id") #Provides dataframe with adjusted R

write.csv(a,"./Outputs/modelfitting.csv")

```

## 2. Plotting the function to the data of each individual

```{r}

# Creating plots to see the fit

r3 = function(data) {

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

id<-data[1,10]

mypath <- file.path("Outputs/Function fit/",paste("Individual\_", id, ".jpg", sep = ""))

jpeg(file = mypath, width=20, height=12, units="cm", res=300)

plot(data$logtime, data$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)', main=paste("Function fit: Ind", id), cex.lab=1.5, cex.axis=1.25)

lines(data$logtime, predict(fit, data.frame(logtime=data$logtime)), col='red',lwd=2)

dev.off()

}

map\_dfr(dat\_list, r3, .id = "id")

```

## 3. Getting the first and second derivative for each individual

```{r}

# Getting the derivatives for each individual

#a2<-split(a, a$id)

r4=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7f.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7f.data)<-"y1"

d7f.data$logtime<-x

d7b<-D(d7, "x")

d7s.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7s.data)<-"y1"

d7s.data$logtime<-x

deriv<-list("first"=d7f.data, "second"=d7s.data)

}

a3<-map\_dfr(dat\_list, r4, .id = "id") #Creates the list with the values of the derivatives

## Saving the second derivatives into a single dataframe

write.csv(a3, "./Outputs/derivatives.csv")

```

```{r}

# Plotting the first derivative

r4first=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

id<-data[1,10]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7f.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7f.data)<-"y1"

d7f.data$logtime<-x

mypath <- file.path("Outputs/First derivative plots/",paste("Individual\_", id, ".jpg", sep = ""))

jpeg(file = mypath, width=20, height=12, units="cm", res=300)

plot(d7f.data$logtime, d7f.data$y1\*-1, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)', main=paste("First derivative: Ind ", id), cex.lab=1.5, cex.axis=1.25, ylim=c(-0.04,0.04))

dev.off()

}

map(dat\_list, r4first)

```

```{r}

# Plotting the second derivative

r4second=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

id<-data[1,10]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

d7s.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7s.data)<-"y1"

d7s.data$logtime<-x

mypath <- file.path("Outputs/Second derivative plots/",paste("Individual\_", id, ".jpg", sep = ""))

jpeg(file = mypath, width=20, height=12, units="cm", res=300)

plot(d7s.data$logtime, d7s.data$y1, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)', main=paste("Second derivative: Ind", id), cex.lab=1.5, cex.axis=1.25, ylim=c(-0.004,0.004))

abline(h=0,col="orange", lty=2, lwd=2)

dev.off()

}

map(dat\_list, r4second)

```

```{r}

# Getting the inflection points: the points where there was a change in the "slope"

r5=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

id<-data[1,11]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

inflection<-polyroot(c((a2 \*2), (a3 \*3 \* 2 ),(a4\* 4 \* 3 ), (a5 \*5 \* 4) , (a6 \* 6 \* 5 ), (a7 \* 7 \* 6 ),(a8 \*8\*7), (a9\*9\*8), (a10\*10\*9)))

inflec<-as.data.frame(inflection)

inflec$id<-data[1,1]

as.data.frame(inflec)

}

a4<-map\_dfr(dat\_list, r5, .id = "id") # List of dataframes containing the inflection points

## Merging points into a single dataframe

options(scipen=999) #Removing scientific notation

inflections<-a4%>%

bind\_rows() %>%

mutate(real=Re(inflection), #Extracting the real number from the complex expression

values=format(real, scientific=FALSE, big.mark=","), #Coverting the real number to printed decimal expression

rounded=round(real, digits=2), #rounding the real number

imagine=round(Im(inflection), digits=2)) %>% #Extracting te imaginary number

filter(between(real, 10, 115))

write.csv(inflections, "./Outputs/inflections.csv")

```

# Making combine figures for the function fit, first and second derivatives

```{r}

make\_grid <- function(group){

f1<-paste0("Outputs/Function fit/Individual\_",group,".jpg")

f2<-paste0("Outputs/First derivative plots/","Individual\_",group,".jpg")

f3<-paste0("Outputs/Second derivative plots/","Individual\_",group,".jpg")

imgs\_url<-c(f1, f2, f3)

imgs <- image\_read(imgs\_url)

montage<-image\_montage(imgs, tile = '1x3', geometry\_size\_percent(150))

#image\_write(montage, path = paste("Outputs/Figure montages/","Individual\_", group[i], ".png"), format = "png")

}

groups<-as.data.frame(levels(as.factor(a$id)))

colnames(groups)<-"id"

#groups<-levels(as.factor(a$id))

for(id in groups) {

montage<-make\_grid(id)

image\_write(montage, path = paste("Outputs/Figure montages/","Individual\_", id, ".png"), format = "png")

}

groups[2]

map(groups, make\_grid)

```

plot1<-ggplot(data1,aes(x=logtime, y=oxymgl)+geom\_point( pch=19)+ xlab('Logtime')+ ylab('Oxygen(mg/l)')+main(paste("Individual ", id)) +theme\_classic()+theme(size=18)

lines(data$logtime, predict(fit, data.frame(logtime=data$logtime)), col='red',lwd=1.2)

revisaar si el numero imaginario no tiene un valor despreciable y no esta replicado, ahi si es de cuidado

FINAL CODE

---

title: "Oxygen estimation"

author: "Laura Segura Hernández"

date: "2022-08-07"

output:

html\_document:

df\_print: paged

theme: cerulean

toc: true

toc\_depth: 4

number\_sections: true

toc\_float: false

---

```{r setup, include=FALSE}

knitr::opts\_chunk$set(warning = FALSE, message = FALSE)

knitr::opts\_knit$set(root.dir = "C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses")

getwd()

```

# Libraries

```{r}

library(data.table)

library(tidyr)

library(dplyr)

library(lubridate)

library(ggplot2)

library(readr)

library(stringr)

library(purrr)

library(knitr)

library(magick)

library(jpeg)

library(fuzzyjoin)

library(forcats)

library(ggpubr)

library(grid)

```

# Organizing data

## Getting objects from Temperature Analyses

```{r}

load("Outputs/Temperature analyses.RData")

```

## Calling and arranging data

### Trial 2

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 2/" #MODIFY FOR EACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial2",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t2a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t2b<-t2a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=2,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~250, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~239,

str\_detect(id, "ch2")~311,

str\_detect(id, "ch3")~65,

str\_detect(id, "ch4")~136,

str\_detect(id, "ch5")~168,

str\_detect(id, "ch6")~294,

str\_detect(id, "ch7")~322,

str\_detect(id, "ch8")~022,

str\_detect(id, "ch9")~258,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Female",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Tritonymph",

str\_detect(id, "ch2")~"Protonymph",

str\_detect(id, "ch3")~"Female",

str\_detect(id, "ch4")~"Deutonymph",

str\_detect(id, "ch5")~"Male",

str\_detect(id, "ch6")~"Protonymph",

str\_detect(id, "ch7")~"Tritonymph",

str\_detect(id, "ch8")~"Deutonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Male"),

weight=case\_when(str\_detect(id, "ch10")~1.269, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.792,

str\_detect(id, "ch2")~0.189,

str\_detect(id, "ch3")~1.714,

str\_detect(id, "ch4")~0.330,

str\_detect(id, "ch5")~1.219,

str\_detect(id, "ch6")~0.240,

str\_detect(id, "ch7")~0.749,

str\_detect(id, "ch8")~0.339,

#str\_detect(id, "ch9")~1.001,

TRUE~1.001),

atm=round(33.864\*28.81)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==2) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t2<- full\_join(t2b, temp2, by="datetime2", suffix=c("",".temp"))

head(t2) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox2<-t2 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox2) #MODIFY FOR EACH TRIAL

ggplot(ox2, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8.5,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 3

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 3/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial3",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t3a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t3b<-t3a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=3,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~010, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~231,

str\_detect(id, "ch2")~029,

str\_detect(id, "ch3")~087,

str\_detect(id, "ch4")~166,

str\_detect(id, "ch5")~300,

str\_detect(id, "ch6")~121,

str\_detect(id, "ch7")~014,

str\_detect(id, "ch8")~271,

str\_detect(id, "ch9")~143,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Female",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Tritonymph",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"Protonymph",

str\_detect(id, "ch4")~"Female",

str\_detect(id, "ch5")~"Deutonymph",

str\_detect(id, "ch6")~"Protonymph",

str\_detect(id, "ch7")~"Deutonymph",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Male"),

weight=case\_when(str\_detect(id, "ch10")~1.228, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.931,

str\_detect(id, "ch2")~0.924,

str\_detect(id, "ch3")~0.251,

str\_detect(id, "ch4")~1.376,

str\_detect(id, "ch5")~0.289,

str\_detect(id, "ch6")~0.189,

str\_detect(id, "ch7")~0.347,

str\_detect(id, "ch8")~0.647,

#str\_detect(id, "ch9")~1.001,

TRUE~1.021),

atm=round(33.864\*28.81)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==3) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t3<- full\_join(t3b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t3) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox3<-t3 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox3) #MODIFY FOR EACH TRIAL

ggplot(ox3, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(7,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 4

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 4/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial4",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t4a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t4b<-t4a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=4,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~213, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~337,

str\_detect(id, "ch2")~051,

str\_detect(id, "ch3")~109,

str\_detect(id, "ch4")~245,

str\_detect(id, "ch5")~037,

str\_detect(id, "ch6")~131,

str\_detect(id, "ch7")~005,

str\_detect(id, "ch8")~194,

str\_detect(id, "ch9")~154,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Protonymph",

str\_detect(id, "ch2")~"Deutonymph",

str\_detect(id, "ch3")~"Tritonymph",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Female",

str\_detect(id, "ch6")~"Tritonymph",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Male",

#str\_detect(id, "ch9")~"Male",

TRUE~"Protonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.241, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.163,

str\_detect(id, "ch2")~0.350,

str\_detect(id, "ch3")~0.730,

str\_detect(id, "ch4")~0.963,

str\_detect(id, "ch5")~1.332,

str\_detect(id, "ch6")~0.509,

str\_detect(id, "ch7")~1.582,

str\_detect(id, "ch8")~0.999,

#str\_detect(id, "ch9")~1.001,

TRUE~0.109),

atm=round(33.864\*28.90)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==4) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t4<- full\_join(t4b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t4) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox4<-t4 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox4) #MODIFY FOR EACH TRIAL

ggplot(ox4, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 5

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 5/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial5",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t5a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t5b<-t5a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=5,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~324, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~024,

str\_detect(id, "ch2")~253,

str\_detect(id, "ch3")~025,

str\_detect(id, "ch4")~003,

str\_detect(id, "ch5")~290,

str\_detect(id, "ch6")~244,

str\_detect(id, "ch7")~257,

str\_detect(id, "ch8")~032,

str\_detect(id, "ch9")~159,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Protonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Female",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"Tritonymph",

str\_detect(id, "ch4")~"Deutonymph",

str\_detect(id, "ch5")~"Protonymph",

str\_detect(id, "ch6")~"Female",

str\_detect(id, "ch7")~"Male",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Deutonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.158, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~1.472,

str\_detect(id, "ch2")~0.900,

str\_detect(id, "ch3")~0.688,

str\_detect(id, "ch4")~0.328,

str\_detect(id, "ch5")~0.166,

str\_detect(id, "ch6")~1.454,

str\_detect(id, "ch7")~0.946,

str\_detect(id, "ch8")~0.613,

#str\_detect(id, "ch9")~1.001,

TRUE~0.278),

atm=round(33.864\*28.84)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==5) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t5<- full\_join(t5b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t5) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox5<-t5 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox5) #MODIFY FOR EACH TRIAL

ggplot(ox5, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 6

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 6/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial6",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t6a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t6b<-t6a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=6,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~267, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~288,

str\_detect(id, "ch2")~030,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~287,

str\_detect(id, "ch5")~218,

str\_detect(id, "ch6")~238,

str\_detect(id, "ch7")~165,

str\_detect(id, "ch8")~298,

str\_detect(id, "ch9")~066,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Deutonymph",

str\_detect(id, "ch2")~"Female",

str\_detect(id, "ch3")~"NA",

str\_detect(id, "ch4")~"Tritonymph",

str\_detect(id, "ch5")~"Tritonymph",

str\_detect(id, "ch6")~"Male",

str\_detect(id, "ch7")~"Protonymph",

str\_detect(id, "ch8")~"Protonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Female"),

weight=case\_when(str\_detect(id, "ch10")~0.221, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.257,

str\_detect(id, "ch2")~1.583,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~0.583,

str\_detect(id, "ch5")~0.715,

str\_detect(id, "ch6")~0.794,

str\_detect(id, "ch7")~0.142,

str\_detect(id, "ch8")~0.201,

#str\_detect(id, "ch9")~1.001,

TRUE~2.208),

atm=round(33.864\*28.81)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==6) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t6<- full\_join(t6b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t6) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox6<-t6 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox6) #MODIFY FOR EACH TRIAL

ggplot(ox6, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 7

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 7/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial7",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t7a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t7b<-t7a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=7,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~274, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~235,

str\_detect(id, "ch2")~216,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~237,

str\_detect(id, "ch5")~175,

str\_detect(id, "ch6")~246,

str\_detect(id, "ch7")~232,

str\_detect(id, "ch8")~269,

str\_detect(id, "ch9")~043,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Male",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"NA",

str\_detect(id, "ch4")~"Female",

str\_detect(id, "ch5")~"Protonymph",

str\_detect(id, "ch6")~"Female",

str\_detect(id, "ch7")~"Tritonymph",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Protonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.324, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.900,

str\_detect(id, "ch2")~1.126,

str\_detect(id, "ch3")~1000,

str\_detect(id, "ch4")~1.345,

str\_detect(id, "ch5")~0.213,

str\_detect(id, "ch6")~1.937,

str\_detect(id, "ch7")~0.748,

str\_detect(id, "ch8")~0.622,

#str\_detect(id, "ch9")~1.001,

TRUE~0.139),

atm=round(33.864\*28.78)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==7) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t7<- full\_join(t7b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t7) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox7<-t7 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox7) #MODIFY FOR EACH TRIAL

ggplot(ox7, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 8

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 8/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial8",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t8a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t8b<-t8a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=8,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~345, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~301,

str\_detect(id, "ch2")~107,

str\_detect(id, "ch3")~54,

str\_detect(id, "ch4")~270,

str\_detect(id, "ch5")~85,

str\_detect(id, "ch6")~36,

str\_detect(id, "ch7")~112,

str\_detect(id, "ch8")~138,

str\_detect(id, "ch9")~80,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Tritonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Protonymph",

str\_detect(id, "ch2")~"Male",

str\_detect(id, "ch3")~"Tritonymph",

str\_detect(id, "ch4")~"Deutonymph",

str\_detect(id, "ch5")~"Female",

str\_detect(id, "ch6")~"Protonymph",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Deutonymph",

#str\_detect(id, "ch9")~"Male",

TRUE~"Male"),

weight=case\_when(str\_detect(id, "ch10")~0.863, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.176,

str\_detect(id, "ch2")~0.648,

str\_detect(id, "ch3")~0.858,

str\_detect(id, "ch4")~0.325,

str\_detect(id, "ch5")~1.863,

str\_detect(id, "ch6")~0.146,

str\_detect(id, "ch7")~1.522,

str\_detect(id, "ch8")~0.329,

#str\_detect(id, "ch9")~1.001,

TRUE~1.199),

atm=round(33.864\*28.72)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==8) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t8<- full\_join(t8b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t8) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox8<-t8 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox8) #MODIFY FOR EACH TRIAL

ggplot(ox8, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 9

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 9/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial9",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t9a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t9b<-t9a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=9,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~007, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~242,

str\_detect(id, "ch2")~035,

str\_detect(id, "ch3")~146,

str\_detect(id, "ch4")~153,

str\_detect(id, "ch5")~334,

str\_detect(id, "ch6")~264,

str\_detect(id, "ch7")~1000,

str\_detect(id, "ch8")~004,

str\_detect(id, "ch9")~228,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Male",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Female",

str\_detect(id, "ch2")~"Protonymph",

str\_detect(id, "ch3")~"Male",

str\_detect(id, "ch4")~"Tritonymph",

str\_detect(id, "ch5")~"Deutonymph",

str\_detect(id, "ch6")~"Deutonymph",

str\_detect(id, "ch7")~"NA",

str\_detect(id, "ch8")~"Female",

#str\_detect(id, "ch9")~"Male",

TRUE~"Tritonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.983, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~1.775,

str\_detect(id, "ch2")~0.185,

str\_detect(id, "ch3")~1.118,

str\_detect(id, "ch4")~0.551,

str\_detect(id, "ch5")~0.302,

str\_detect(id, "ch6")~0.342,

str\_detect(id, "ch7")~1000,

str\_detect(id, "ch8")~1.425,

#str\_detect(id, "ch9")~1.001,

TRUE~0.569),

atm=round(33.864\*28.66)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==9) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t9<- full\_join(t9b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t9) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox9<-t9 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox9) #MODIFY FOR EACH TRIAL

ggplot(ox9, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 10

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 10/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial10",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t10a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t10b<-t10a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=10,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~179, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~048,

str\_detect(id, "ch2")~158,

str\_detect(id, "ch3")~079,

str\_detect(id, "ch4")~145,

str\_detect(id, "ch5")~057,

str\_detect(id, "ch6")~251,

str\_detect(id, "ch7")~248,

str\_detect(id, "ch8")~314,

str\_detect(id, "ch9")~212,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Tritonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Deutonymph",

str\_detect(id, "ch2")~"Female",

str\_detect(id, "ch3")~"Female",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Tritonymph",

str\_detect(id, "ch6")~"Male",

str\_detect(id, "ch7")~"Male",

str\_detect(id, "ch8")~"Deutonymph",

#str\_detect(id, "ch9")~"",

TRUE~"Female"),

weight=case\_when(str\_detect(id, "ch10")~0.653, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.451,

str\_detect(id, "ch2")~1.178,

str\_detect(id, "ch3")~1.781,

str\_detect(id, "ch4")~0.929,

str\_detect(id, "ch5")~0.866,

str\_detect(id, "ch6")~0.941,

str\_detect(id, "ch7")~0.864,

str\_detect(id, "ch8")~0.188,

#str\_detect(id, "ch9")~1.001,

TRUE~1.582),

atm=round(33.864\*28.64)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==10) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t10<- full\_join(t10b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t10) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox10<-t10 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox10) #MODIFY FOR EACH TRIAL

ggplot(ox10, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 11

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 11/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial11",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t11a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t11b<-t11a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=11,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~141, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~272,

str\_detect(id, "ch2")~305,

str\_detect(id, "ch3")~326,

str\_detect(id, "ch4")~224,

str\_detect(id, "ch5")~173,

str\_detect(id, "ch6")~214,

str\_detect(id, "ch7")~082,

str\_detect(id, "ch8")~113,

str\_detect(id, "ch9")~329,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Female",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Tritonymph",

str\_detect(id, "ch2")~"Deutonymph",

str\_detect(id, "ch3")~"Deutonymph",

str\_detect(id, "ch4")~"Female",

str\_detect(id, "ch5")~"Tritonymph",

str\_detect(id, "ch6")~"Deutonymph",

str\_detect(id, "ch7")~"Male",

str\_detect(id, "ch8")~"Male",

#str\_detect(id, "ch9")~"",

TRUE~"Tritonymph"),

weight=case\_when(str\_detect(id, "ch10")~1.853, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.675,

str\_detect(id, "ch2")~0.312,

str\_detect(id, "ch3")~0.283,

str\_detect(id, "ch4")~1.785,

str\_detect(id, "ch5")~0.566,

str\_detect(id, "ch6")~0.184,

str\_detect(id, "ch7")~1.095,

str\_detect(id, "ch8")~1.046,

#str\_detect(id, "ch9")~1.001,

TRUE~0.591),

atm=round(33.864\*28.55)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==11) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t11<- full\_join(t11b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t11) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox11<-t11 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox11) #MODIFY FOR EACH TRIAL

ggplot(ox11, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 12

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 12/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial12",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t12a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t12b<-t12a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=12,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~339, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~256,

str\_detect(id, "ch2")~341,

str\_detect(id, "ch3")~18,

str\_detect(id, "ch4")~83,

str\_detect(id, "ch5")~50,

str\_detect(id, "ch6")~201,

str\_detect(id, "ch7")~211,

str\_detect(id, "ch8")~317,

str\_detect(id, "ch9")~335,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"Deutonymph",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Female",

str\_detect(id, "ch2")~"Tritonymph",

str\_detect(id, "ch3")~"Male",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Male",

str\_detect(id, "ch6")~"Female",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Tritonymph",

#str\_detect(id, "ch9")~"",

TRUE~"Deutonymph"),

weight=case\_when(str\_detect(id, "ch10")~0.314, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~1.450,

str\_detect(id, "ch2")~0.790,

str\_detect(id, "ch3")~1.23,

str\_detect(id, "ch4")~1.015,

str\_detect(id, "ch5")~1.229,

str\_detect(id, "ch6")~1.49,

str\_detect(id, "ch7")~1.500,

str\_detect(id, "ch8")~0.905,

#str\_detect(id, "ch9")~1.001,

TRUE~0.268),

atm=round(33.864\*28.58)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==12) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t12<- full\_join(t12b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t12) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox12<-t12 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox12) #MODIFY FOR EACH TRIAL

ggplot(ox12, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

### Trial 13

```{r}

# creating vector for columns names

cnames<-c("date", "time", "logtime", "oxygen", "phase", "amplitude", "temperature")

# creating vector for path

path<-"Data/Oxygen/Trial 13/" #MODIFY FOR EEACH TRIAL

# Creating list of file names

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

# Renaming files to remove the "-"

newname <- sub('-','', list) ## new name

file.rename(file.path(path,list), file.path(path, newname)) ## renaming it.

# Creating list of file names again

list <- list.files(path = path, pattern=".\*txt") # creates the list of all the txt files in the directory

#Reading all files at once

for (i in list) {

filename <- paste0( "frame",sub(pattern = "(.\*)\\..\*$", replacement = "\\1", basename(i)))

wd <- paste0(path, i)

assign(filename, read.delim2(wd,sep=";", skip=38, header=F, col.names=cnames)) #CHECK FOR EACH TRIALS IF THE SAME NUMBRE OF ROWS APPLIES

}

# Merging all into a single table

pattern<-grep("framepstrial13",names(.GlobalEnv),value=TRUE) #MODIFY FOR EACH TRIAL

list2<-do.call("list",mget(pattern))

t13a<-bind\_rows(list2, .id="id") #MODIFY FOR EACH TRIAL

# Adding and modifying data to phase files

t13b<-t13a %>% #MODIFY FOR EACH TRIAL

select(c("id", "date", "time", "logtime", "phase")) %>%

mutate(trial=13,#MODIFY FOR EACH TRIAL

date=mdy(date), #formatting date

datetime=paste0(date," ", time), #copying date and time together

datetime=as\_datetime(datetime, format="%Y-%m-%d %I:%M:%S %p")-minutes(9), #adjusting pc time to real time

datetime2=round\_date(datetime, unit="minute"),

channel=case\_when(str\_detect(id, "ch10")~10, # Assigning channels

str\_detect(id, "ch1")~1,

str\_detect(id, "ch2")~2,

str\_detect(id, "ch3")~3,

str\_detect(id, "ch4")~4,

str\_detect(id, "ch5")~5,

str\_detect(id, "ch6")~6,

str\_detect(id, "ch7")~7,

str\_detect(id, "ch8")~8,

str\_detect(id, "ch9")~9,

TRUE~0),

ind=case\_when(str\_detect(id, "ch10")~1000, # Assigning individuals MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~296,

str\_detect(id, "ch2")~263,

str\_detect(id, "ch3")~156,

str\_detect(id, "ch4")~073,

str\_detect(id, "ch5")~171,

str\_detect(id, "ch6")~002,

str\_detect(id, "ch7")~247,

str\_detect(id, "ch8")~233,

str\_detect(id, "ch9")~028,

TRUE~0),

stage=case\_when(str\_detect(id, "ch10")~"NA",#Assigning stage MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~"Deutonymph",

str\_detect(id, "ch2")~"Tritonymph",

str\_detect(id, "ch3")~"Male",

str\_detect(id, "ch4")~"Male",

str\_detect(id, "ch5")~"Deutonymph",

str\_detect(id, "ch6")~"Tritonymph",

str\_detect(id, "ch7")~"Female",

str\_detect(id, "ch8")~"Female",

#str\_detect(id, "ch9")~"",

TRUE~"Tritonymph"),

weight=case\_when(str\_detect(id, "ch10")~1000, # Assigning weights MODIFY FOR EACH TRIAL

str\_detect(id, "ch1")~0.272,

str\_detect(id, "ch2")~0.764,

str\_detect(id, "ch3")~0.656,

str\_detect(id, "ch4")~1.18,

str\_detect(id, "ch5")~0.361,

str\_detect(id, "ch6")~0.767,

str\_detect(id, "ch7")~1.256,

str\_detect(id, "ch8")~1.693,

#str\_detect(id, "ch9")~1.001,

TRUE~0.866),

atm=round(33.864\*28.55)) #MODIFY FOR EACH TRIAL: 33.864 \* pressure in inHg

# Getting temperature for this trial

temp2<-all\_corr %>%

filter(trial==13) %>% #MODIFY FOR EACH TRIAL

select(c("datetime2","datetime", "tempcorr", "ramp"))

#Merging phase and temperature data

t13<- full\_join(t13b, temp2, by="datetime2", suffix=c("",".temp")) #MODIFY FOR EACH TRIAL

head(t13) #MODIFY FOR EACH TRIAL

#Estimating Oxygen

f<-pi/180

f

ox13<-t13 %>% #MODIFY FOR EACH TRIAL

na.omit() %>%

filter(ind < 900) %>%

mutate(phase=as.numeric(phase),

ind=as.factor(ind),

logtime=as.numeric(logtime),

phaseangle=62.14-0.08915\*tempcorr,

sternvolmer=0.04899+4.965\*10^(-4)\*tempcorr,

bunsen=(48.998-1.335\*tempcorr+2.755\*10^(-2)\*tempcorr^2-3.22\*10^(-4)\*tempcorr^3+1.598\*10^(-6)\*tempcorr^4)\*10^(-3),

tempK=tempcorr+273,

watervapor=exp(52.57-(6690.9/tempK)-4.681\*log(tempK)),

oxysat=(tan((pi/180)\*phaseangle)-tan((pi/180)\*phase))/tan((pi/180)\*phase)\*sternvolmer,

oxymgl=(atm-watervapor)/1013\*oxysat\*0.2095\*bunsen\*1000\*(32/22.414)\*10)

head(ox13) #MODIFY FOR EACH TRIAL

ggplot(ox13, aes(x=logtime, y=oxymgl,group=ind, color=stage))+ #MODIFY FOR EACH TRIAL

geom\_line()+

theme\_classic()+

theme(text = element\_text(size = 15))+

ylim(8,12) +

facet\_wrap(~ind)+

xlab("Time logged (min)")+

ylab("Oxygen (mg/L")

```

Go back to each trial and annotate the best beginning and end of trial, and change it in the temperature data, then re-run this analysis again, to only get the curves that actual pertain to the trial (i.e. get it from the start and also remove the tail when it warms up again at the end)

# Merging trials into a single dataframe FALTA

```{r, eval=F}

oxall<-bind\_rows(ox2,ox3,ox4,ox5,ox6,ox7,ox8,ox9,ox10,ox11,ox12,ox13) #%>%

#filter(!ind%in%c("22","83", "131", "136", "159", "168", "267", "270")) # Cambiar por individuos ahogados

#FALTA REMOVER INDIVIDUOS AHOGADOS

write.csv(oxall,"Outputs/oxygenall\_aftercodedeletion.csv")

```

# Trying which function to use

```{r}

# Filtering for a single individuals to just see the fit

func<-ox7%>%

filter(ind==232) %>%

group\_by(logtime) %>%

filter(duplicated(logtime|n()==2))

#Trying different curves

fit2<-lm(oxymgl~poly(logtime, 2, raw=TRUE), data=func)

fit3<-lm(oxymgl~poly(logtime, 3, raw=TRUE), data=func)

fit4<-lm(oxymgl~poly(logtime, 4, raw=TRUE), data=func)

fit5<-lm(oxymgl~poly(logtime, 5, raw=TRUE), data=func)

fit6<-lm(oxymgl~poly(logtime, 6, raw=TRUE), data=func)

fit7<-lm(oxymgl~poly(logtime, 7, raw=TRUE), data=func)

fit8<-lm(oxymgl~poly(logtime, 8, raw=TRUE), data=func)

fit9<-lm(oxymgl~poly(logtime, 9, raw=TRUE), data=func)

fit10<-lm(oxymgl~poly(logtime, 10, raw=TRUE), data=func)

# CReating a dataframe to build the prediction

logtime <- seq(1, 125, length=125)

# Plotting each predicted function line to the real data

plot(func$logtime, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit2, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit3, data.frame(x=logtime)), col='purple')

lines(logtime, predict(fit4, data.frame(x=logtime)), col='blue')

lines(logtime, predict(fit5, data.frame(x=logtime)), col='orange')

lines(logtime, predict(fit6, data.frame(x=logtime)), col='green')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit8, data.frame(x=logtime)), col='yellow')

lines(logtime, predict(fit9, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit10, data.frame(x=logtime)), col='grey')

#calculated adjusted R-squared of each model

# The adjusted r squared is the percent of the variance of Y intact after subtracting the error of the model. The more the R Squared value the better the model is for that data frame.

summary(fit2)$adj.r.squared

summary(fit3)$adj.r.squared

summary(fit4)$adj.r.squared

summary(fit5)$adj.r.squared

summary(fit6)$adj.r.squared

summary(fit7)$adj.r.squared

summary(fit8)$adj.r.squared

summary(fit9)$adj.r.squared

summary(fit10)$adj.r.squared

coef7<-as.data.frame(fit7$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1] #cambiar a A

x<-func$logtime

form7<-expression((a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

ggplot(aes(x=logtime, y=oxymgl), data=func)+geom\_point()

plot(x, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='red')

#Primera derivada: tasa con la que consume oxigeno

d7b.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()

#Segunda derivada: cruce con y=0 son los punto de cambio, puntos de inflexion donde la pendiente cambia hacia arriva o hacia abajo

d7b.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()+scale\_x\_continuous(breaks=c(0,10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120))

# Finding the values at which the second derivative=0

f=function(x) eval(d7b)

uniroot(f, c(0,125))

inflection<-polyroot(c((a2 \*2), (a3 \*3 \* 2 ),(a4\* 4 \* 3 ), (a5 \*5 \* 4) , (a6 \* 6 \* 5 ), (a7 \* 7 \* 6 )))

inflec<-as.data.frame(inflection)

```

# Trying which function to use on a different individual

```{r}

# Filtering for a single individuals to just see the fit

func<-ox3%>%

filter(ind=="87")# %>%

#group\_by(logtime) %>%

#filter(duplicated(logtime|n()==2))

#Trying different curves

fit2<-lm(oxymgl~poly(logtime, 2, raw=TRUE), data=func)

fit3<-lm(oxymgl~poly(logtime, 3, raw=TRUE), data=func)

fit4<-lm(oxymgl~poly(logtime, 4, raw=TRUE), data=func)

fit5<-lm(oxymgl~poly(logtime, 5, raw=TRUE), data=func)

fit6<-lm(oxymgl~poly(logtime, 6, raw=TRUE), data=func)

fit7<-lm(oxymgl~poly(logtime, 7, raw=TRUE), data=func)

fit8<-lm(oxymgl~poly(logtime, 8, raw=TRUE), data=func)

fit9<-lm(oxymgl~poly(logtime, 9, raw=TRUE), data=func)

fit10<-lm(oxymgl~poly(logtime, 10, raw=TRUE), data=func)

# CReating a dataframe to build the prediction

logtime <- seq(1, 125, length=125)

# Plotting each predicted function line to the real data

plot(func$logtime, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit2, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit3, data.frame(x=logtime)), col='purple')

lines(logtime, predict(fit4, data.frame(x=logtime)), col='blue')

lines(logtime, predict(fit5, data.frame(x=logtime)), col='orange')

lines(logtime, predict(fit6, data.frame(x=logtime)), col='green')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='grey')

lines(logtime, predict(fit8, data.frame(x=logtime)), col='yellow')

lines(logtime, predict(fit9, data.frame(x=logtime)), col='red')

lines(logtime, predict(fit10, data.frame(x=logtime)), col='grey')

#calculated adjusted R-squared of each model

# The adjusted r squared is the percent of the variance of Y intact after subtracting the error of the model. The more the R Squared value the better the model is for that data frame.

summary(fit2)$adj.r.squared

summary(fit3)$adj.r.squared

summary(fit4)$adj.r.squared

summary(fit5)$adj.r.squared

summary(fit6)$adj.r.squared

summary(fit7)$adj.r.squared

summary(fit8)$adj.r.squared

summary(fit9)$adj.r.squared

summary(fit10)$adj.r.squared

coef7<-as.data.frame(fit7$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1] #cambiar a A

x<-func$logtime

form7<-expression((a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

ggplot(aes(x=logtime, y=oxymgl), data=func)+geom\_point()

plot(x, func$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)')

lines(logtime, predict(fit7, data.frame(x=logtime)), col='red')

#Primera derivada: tasa con la que consume oxigeno

d7b.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()

#Segunda derivada: cruce con y=0 son los punto de cambio, puntos de inflexion donde la pendiente cambia hacia arriba o hacia abajo

d7b.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7b.data)<-"y1"

d7b.data$logtime<-func$logtime

ggplot(aes(x=logtime, y=y1), data=d7b.data)+geom\_point()+scale\_x\_continuous(breaks=c(0,10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120))

# Finding the values at which the second derivative=0

#f=function(x) eval(d7b)

#uniroot(f, c(0,125))

inflection<-polyroot(c((a2 \*2), (a3 \*3 \* 2 ),(a4\* 4 \* 3 ), (a5 \*5 \* 4) , (a6 \* 6 \* 5 ), (a7 \* 7 \* 6 )))

inflection

inflec<-as.data.frame(inflection)

#inflec$inflection<-as.numeric\*inflec$inflection

```

# Calling the csv file to avoid running the whole code

```{r}

#Calling csv file to avoid running the whole code

oxall<-read.csv("../Outputs/oxygenall.csv")

oxall<-read.csv("./Outputs/oxygenall\_aftercodedeletion.csv")

```

# Cutting out traces with weird patterns

## Individual 22

```{r}

ind22<-oxall %>%

filter(ind=="22")

ggplot(aes(x=logtime, y=oxymgl), data=ind22)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind22<-ind22 %>%

filter(!between(logtime, 75, 85))

ggplot(aes(x=logtime, y=oxymgl), data=ind22)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 83

```{r}

ind83<-oxall %>%

filter(ind=="83")

ggplot(aes(x=logtime, y=oxymgl), data=ind83)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind83<-ind83 %>%

filter(!between(logtime, 70, 80))

ggplot(aes(x=logtime, y=oxymgl), data=ind83)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 131

```{r}

ind131<-oxall %>%

filter(ind=="131")

ggplot(aes(x=logtime, y=oxymgl), data=ind131)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind131<-ind131 %>%

filter(!between(logtime, 72, 82))

ggplot(aes(x=logtime, y=oxymgl), data=ind131)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 136

```{r}

ind136<-oxall %>%

filter(ind=="136")

ggplot(aes(x=logtime, y=oxymgl), data=ind136)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind136<-ind136 %>%

filter(!between(logtime, 72, 82))

ggplot(aes(x=logtime, y=oxymgl), data=ind136)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 159

```{r}

ind159<-oxall %>%

filter(ind=="159")

ggplot(aes(x=logtime, y=oxymgl), data=ind159)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind159<-ind159 %>%

filter(!between(logtime, 65, 75))

ggplot(aes(x=logtime, y=oxymgl), data=ind159)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 168

```{r}

ind168<-oxall %>%

filter(ind=="168")

ggplot(aes(x=logtime, y=oxymgl), data=ind168)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind168<-ind168 %>%

filter(!between(logtime, 75 ,90))

ggplot(aes(x=logtime, y=oxymgl), data=ind168)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 267

```{r}

ind267<-oxall %>%

filter(ind=="267")

ggplot(aes(x=logtime, y=oxymgl), data=ind267)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind267<-ind267 %>%

filter(!between(logtime, 80, 90))

ggplot(aes(x=logtime, y=oxymgl), data=ind267)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Individual 270

```{r}

ind270<-oxall %>%

filter(ind=="270")

ggplot(aes(x=logtime, y=oxymgl), data=ind270)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

ind270<-ind270 %>%

filter(!between(logtime, 70, 80))

ggplot(aes(x=logtime, y=oxymgl), data=ind270)+geom\_point() +theme\_classic() + theme(text=element\_text(size=15))+scale\_x\_continuous(breaks = seq(0, 120, by = 5))

```

## Creating new dataset with trimmed individuals

```{r}

oxall<-oxall%>%

filter(!ind%in%c("22","83", "131", "136", "159", "168", "267", "270")) %>%

bind\_rows(ind22, ind83, ind131, ind136, ind159, ind168, ind267, ind270) %>%

filter\_all(all\_vars(!is.infinite(.)))

levels(as.factor(oxall$ind))

```

# Creating a loop to get data for all individuals

Steps needed:

1. Fit the polynomial function to each individual

2. See the r.adjusted for each individual

3. Extract the coefficient of the function for each individual

4. Get the first and second derivatives

5. Get the inflection points

6. Clean the inflection points

7. Check the inflection points with the data

8. Merge the inflection points with the data set (get at least ID, stage)

9. Do statistical comparison

## 1. Adjusting a polynomial function to each individual

```{r}

# Creating separate lists, one for each individual

dat\_list<-split(oxall, oxall$ind)

# Creating function for fitting model

# Creating function for fitting model

r2 = function(data) {

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

output<-broom::glance(fit) #Getting adjusted r

suma<-broom::tidy(summary(fit)) #Getting parameters for model

merge(output, suma, all=TRUE)

}

a<-map\_dfr(dat\_list, r2, .id = "id") #Provides dataframe with adjusted R

write.csv(a,"./Outputs/modelfitting.csv")

```

## 2. Plotting the function to the data of each individual

```{r}

# Creating plots to see the fit

r3 = function(data) {

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

id<-data[1,10]

mypath <- file.path("Outputs/Function fit/",paste("Individual\_", id, ".jpg", sep = ""))

jpeg(file = mypath, width=20, height=12, units="cm", res=300)

plot(data$logtime, data$oxymgl, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)', main=paste("Function fit: Ind", id), cex.lab=1.5, cex.axis=1.25)

lines(data$logtime, predict(fit, data.frame(logtime=data$logtime)), col='red',lwd=2)

dev.off()

}

map\_dfr(dat\_list, r3, .id = "id")

```

## 3. Getting the first and second derivative for each individual

```{r}

# Getting the derivatives for each individual

#a2<-split(a, a$id)

r4=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7f.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7f.data)<-"y1"

d7f.data$logtime<-x

d7b<-D(d7, "x")

d7s.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7s.data)<-"y1"

d7s.data$logtime<-x

deriv<-list("first"=d7f.data, "second"=d7s.data)

}

a3<-map\_dfr(dat\_list, r4, .id = "id") #Creates the list with the values of the derivatives

## Saving the second derivatives into a single dataframe

write.csv(a3, "./Outputs/derivatives.csv")

```

## 4. Plotting the first derivative

```{r}

# Plotting the first derivative

r4first=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

id<-data[1,10]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7f.data<-as.data.frame(eval(d7, envir=as.data.frame(x)))

colnames(d7f.data)<-"y1"

d7f.data$logtime<-x

mypath <- file.path("Outputs/First derivative plots/",paste("Individual\_", id, ".jpg", sep = ""))

jpeg(file = mypath, width=20, height=12, units="cm", res=300)

plot(d7f.data$logtime, d7f.data$y1\*-1, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)', main=paste("First derivative: Ind ", id), cex.lab=1.5, cex.axis=1.25, ylim=c(-0.04,0.04))

dev.off()

}

map(dat\_list, r4first)

```

## 5. Plotting the second derivative

```{r}

# Plotting the second derivative

r4second=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

id<-data[1,10]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

d7s.data<-as.data.frame(eval(d7b, envir=as.data.frame(x)))

colnames(d7s.data)<-"y1"

d7s.data$logtime<-x

mypath <- file.path("Outputs/Second derivative plots/",paste("Individual\_", id, ".jpg", sep = ""))

jpeg(file = mypath, width=20, height=12, units="cm", res=300)

plot(d7s.data$logtime, d7s.data$y1, pch=19, xlab='Logtime', ylab='Oxygen(mg/l)', main=paste("Second derivative: Ind", id), cex.lab=1.5, cex.axis=1.25, ylim=c(-0.004,0.004))

abline(h=0,col="orange", lty=2, lwd=2)

dev.off()

}

map(dat\_list, r4second)

```

```{r}

# Getting the inflection points: the points where there was a change in the "slope"

r5=function(data){

fit = lm(oxymgl~poly(logtime, 10, raw=TRUE), data = data)

coef7<-as.data.frame(fit$coefficients)

a0<-coef7[1,1]

a1<-coef7[2,1]

a2<-coef7[3,1]

a3<-coef7[4,1]

a4<-coef7[5,1]

a5<-coef7[6,1]

a6<-coef7[7,1]

a7<-coef7[8,1]

a8<-coef7[9,1]

a9<-coef7[10,1]

a10<-coef7[11,1]

id<-data[1,11]

#x<-ox3$logtime #Values from raw data

x <- seq(0, 125, by=0.20)

form7<-expression((a10\*x^10)+(a9\*x^9)+(a8\*x^8)+(a7\*x^7)+(a6\*x^6)+(a5\*x^5)+(a4\*x^4)+(a3\*x^3)+(a2\*x^2)+(a1\*x^1)+(a0\*x^0))

d7<-D(form7, "x")

d7b<-D(d7, "x")

inflection<-polyroot(c((a2 \*2), (a3 \*3 \* 2 ),(a4\* 4 \* 3 ), (a5 \*5 \* 4) , (a6 \* 6 \* 5 ), (a7 \* 7 \* 6 ),(a8 \*8\*7), (a9\*9\*8), (a10\*10\*9)))

inflec<-as.data.frame(inflection)

inflec$id<-data[1,1]

as.data.frame(inflec)

}

a4<-map\_dfr(dat\_list, r5, .id = "id") # List of dataframes containing the inflection points

## Merging points into a single dataframe

options(scipen=999) #Removing scientific notation

inflections<-a4%>%

bind\_rows() %>%

mutate(real=Re(inflection), #Extracting the real number from the complex expression

values=format(real, scientific=FALSE, big.mark=","), #Coverting the real number to printed decimal expression

rounded=round(real, digits=2), #rounding the real number

imagine=round(Im(inflection), digits=2)) %>% #Extracting te imaginary number

filter(between(real, 10, 115))

write.csv(inflections, "./Outputs/inflections.csv")

```

## 6. Making combined figures for the function fit, first and second derivatives

```{r}

# AS a function

make\_grid <- function(id){

#Establishing paths

f1<-paste0("Outputs/Function fit/Individual\_",id,".jpg")

f2<-paste0("Outputs/First derivative plots/","Individual\_",id,".jpg")

f3<-paste0("Outputs/Second derivative plots/","Individual\_",id,".jpg")

#Reading images

j1<-readJPEG(f1)

j2<-readJPEG(f2)

j3<-readJPEG(f3)

#Establishing path

mypath <- file.path("C:/Users/laus1/OneDrive - University of Nebraska-Lincoln/UNL/PhD Tesis/Methods/Thermolimit/Thermolimit data analyses/Outputs/Figure montages/", paste("Individual\_", id, ".jpg", sep = ""))

# Creating figures

jpeg(file = mypath, width=20, height=36, units="cm", res=300)

par(mar=c(1,1,1,1))

layout(matrix(1:3, ncol=1,byrow=TRUE))

plot(NA,xlim=0:1,ylim=0:1,xaxt="n",yaxt="n")

rasterImage(j1,0,0,1,1)

plot(NA,xlim=0:1,ylim=0:1,xaxt="n",yaxt="n")

rasterImage(j2, 0,0,1,1)

plot(NA,xlim=0:1,ylim=0:1,xaxt="n",yaxt="n")

rasterImage(j3, 0,0,1,1)

dev.off()

}

groups<-levels(as.factor(a$id))

map(groups, make\_grid)

```

# Obtaining the maximum rate of oxygen consumption (Ropt)

```{r}

derivs<-read.csv("Outputs/derivatives.csv")

derivs<-derivs %>%

mutate(first2=first.y1\*-1)%>% #Converting the slopes to positive

filter(between(first.logtime, 30, 105)) #Triming the timeframe to the actual slope time

# Plotting to see if the conversion looks right

derivs%>%

filter(id==10) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

derivs%>%

filter(id==3) %>%

ggplot(aes(x=first.logtime, y=first2))+geom\_line()

# Getting the row with the maximum value for each individual

ropt<-derivs %>%

group\_by(id) %>%

slice(which.max(first2))%>%

mutate(logtime=first.logtime,

ind=id)

```

# Getting the temperatures associated with the Ropt (Topt)

```{r}

#Merging the temperatures

topt<-difference\_left\_join(ropt,oxall, by=c("ind","logtime"), max\_dist=0.13) %>%

group\_by(ind.x, logtime.x, first.y1, first2) %>%

summarize(tempcorr2=mean(tempcorr)) %>% #averaging the tempcorr for when multiple cells are called

ungroup()

#getting the other demographic data

toptfinal<-oxall %>%

select(c("date", "trial", "channel", "ind", "stage", "weight", "ramp")) %>%

group\_by(ind)%>%

filter(row\_number()==1) %>%

right\_join(topt, by=c("ind"="ind.x")) %>%

rename(logtime=logtime.x,

tempcorr=tempcorr2,

ropt1=first.y1,

ropt2=first2) %>%

ungroup()%>%

mutate(stage=fct\_relevel(stage, levels=c("Protonymph", "Deutonymph", "Tritonymph", "Female", "Male" )))

levels(toptfinal$stage)

#Visualizing the topt and Ropt

## Temperature optima

ggplot(toptfinal, aes(x=stage, y=tempcorr))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Ctmax (Celsius)")

ggplot(toptfinal, aes(x=stage, y=ropt2))+geom\_boxplot() +theme\_classic() +

theme(text = element\_text(size = 15))+

xlab("Stage")+

ylab("Maximum rate of oxygen consumption")

write.csv(toptfinal, "Outputs/ToptandRopts.csv")

```

plot1<-ggplot(data1,aes(x=logtime, y=oxymgl)+geom\_point( pch=19)+ xlab('Logtime')+ ylab('Oxygen(mg/l)')+main(paste("Individual ", id)) +theme\_classic()+theme(size=18)

lines(data$logtime, predict(fit, data.frame(logtime=data$logtime)), col='red',lwd=1.2)

revisaar si el numero imaginario no tiene un valor despreciable y no esta replicado, ahi si es de cuidado