

respirometry_hinal

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Load libraries

```
library(ggplot2)
library(dplyr)
library(data.table)
library(lubridate)
library(MASS)
```

Load data

WE want to load the data and calculate quick and dirty mass specific metabolism (with not accounting for hours just yet; so no rate)

```
resp<-fread("../Data/2018-09-07_Hinal_diapause_determination.csv")
dim(resp)
```

```
## [1] 871 13
```

```
head(resp)
```

```
##      Host Sample N tape licor cohort_day cohort_date day_weight day_resp
## 1: Apple      e 1  red  7000          19    9/3/18           7         8
## 2: Apple      e 2  red  7000          19    9/3/18           7         8
## 3: Apple      e 3  red  7000          19    9/3/18           7         8
## 4: Apple      e 4  red  7000          19    9/3/18           7         8
## 5: Apple      e 5  red  7000          19    9/3/18           7         8
## 6: Apple      e 6  red  7000          19    9/3/18           7         8
##      weight Respiration Respiration_time Purge_time
## 1:  5.805   0.1471650         10:21:23      16:13
## 2:  6.045   0.1719045         10:23:02
## 3:  6.481   0.1011440         10:24:38
## 4: 10.068   0.2134008         10:26:06
## 5:  6.809   0.1134154         10:27:28
## 6:  8.442   0.6372036         10:29:05
```

```

#convert purge times to units in hours
resp$purge_time<-hour(hm(resp$Purge_time))+minute(hm(resp$Purge_time))/60

## Warning in .parse_hms(..., order = "HM", quiet = quiet): Some strings
## failed to parse, or all strings are NAs

## Warning in .parse_hms(..., order = "HM", quiet = quiet): Some strings
## failed to parse, or all strings are NAs

```

calculating purge time

we need to create a sequence of purge times that are the length of the cohorts

Data manipulation and calculating resp rate

```

#figuring out sample sizes per host, tape, cohort, and resp day
#resp%>%
  # dplyr::group_by(Host,tape,cohort_date,day_resp)%>%
  #summarise(n=length(tape))

#we figured out purge time
resp.1<-resp%>%
  dplyr::group_by(Host,tape,cohort_date,day_resp)%>%
  mutate(full_purge_time=seq(from=min(purge_time,na.rm=TRUE),to=max(purge_time,na.rm=TRUE),length.out=length(tape)))

#names(resp.1)
#resp.1$full_purge_time

#### now we need total time

#resp.1$Respiration_time

resp.1$resp_time1<-hour(hms(resp.1$Respiration_time)) + minute(hms(resp.1$Respiration_time))/60+second(hms(resp.1$Respiration_time))

resp.1$total_time<- (24- resp.1$full_purge_time) +resp.1$resp_time1

#### now that we have total time in syringe, we can measure metabolic rate (CO2/time)

## we first need to subtract every value by blank

blank<-resp.1%>%
  dplyr::group_by(Host,tape,cohort_date,day_resp)%>%
  filter(Sample=="b")%>%
  summarize(blank=mean(Respiration))

# To look at the negative resp values
#filter(resp.1,Respiration<0)
#join smaller blank dataset with larger dataset
resp.2<-inner_join(resp.1,blank,by=c("Host", "tape", "cohort_date", "day_resp"))

```

```
#cbind(resp.2$Respiration,resp.2$blank)
#subtract rows!
resp.2$norm_resp<-resp.2$Respiration-resp.2$blank

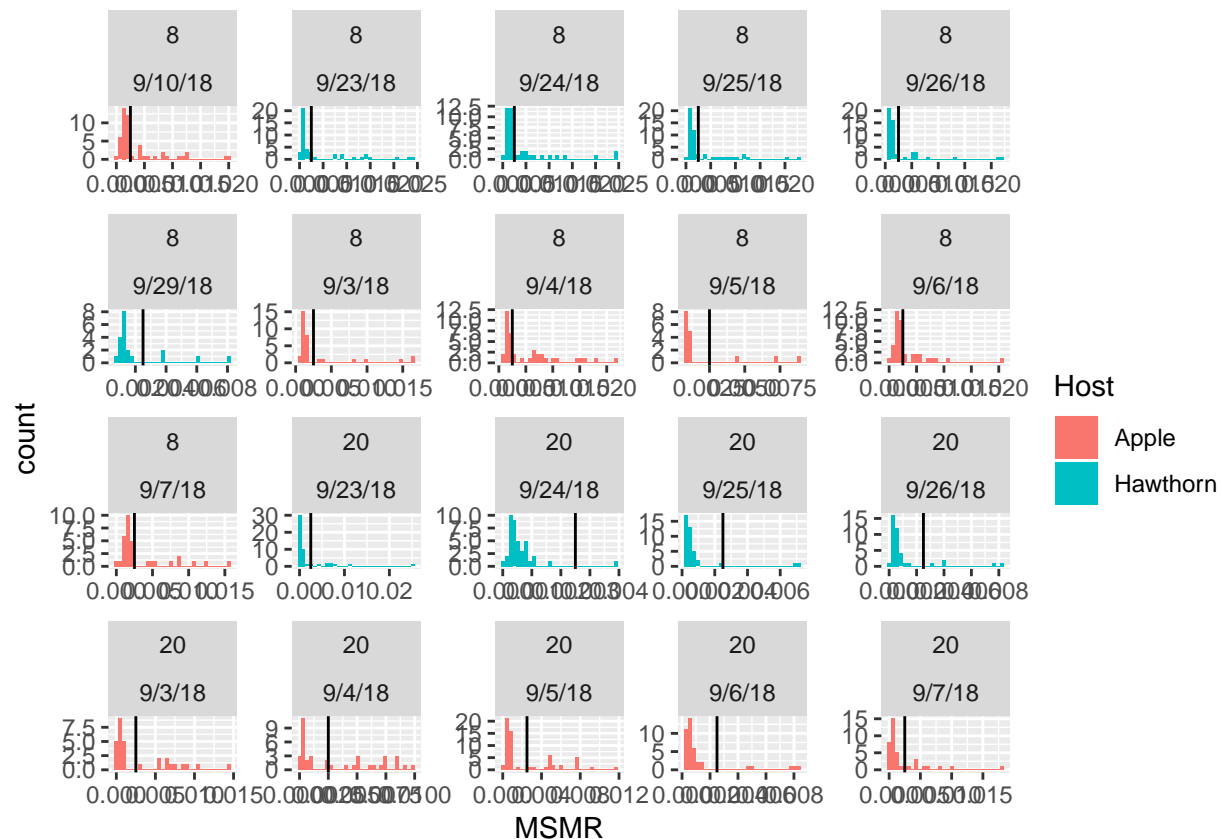
####Calculating metabolic rate and mass specific metabolic rate

resp.2$MR<- resp.2$norm_resp/resp.2$total_time # metabolic rate
resp.2$MSMR<- resp.2$norm_resp/(resp.2$total_time*resp.2$weight)# mass specific metabolic rate
resp.2<-filter(resp.2,Sample=="e")
```

Make plots of the data

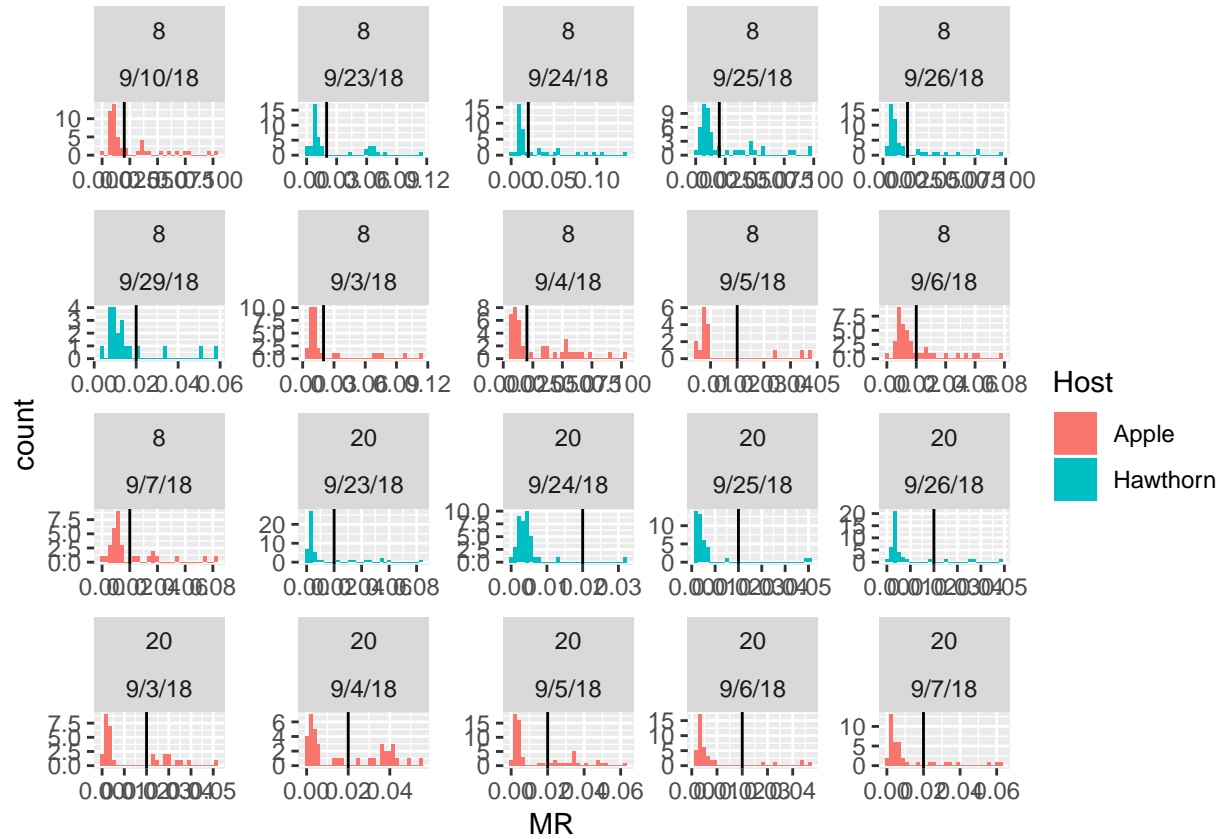
```
#mass specific metabolic rate
ggplot(resp.2,aes(x=MSMR,fill=Host))+geom_histogram(position="identity")+facet_wrap(day_resp~cohort_date,
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
#metabolic rate
ggplot(resp.2,aes(x=MR,fill=Host))+geom_histogram(position="identity")+facet_wrap(day_resp~cohort_date,
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Assigning cutoffs for diapause and non-diapause

```
# 2 cutoffs and let's see how they match
resp.2$cutoffMSMR<-ifelse(resp.2$MSMR<0.0025,"Diapause","Non-Diapause")

resp.2$cutoffMR<-ifelse(resp.2$MR<0.02,"Diapause","Non-Diapause")

table(resp.2$cutoffMR,resp.2$cutoffMSMR)

##
##           Diapause Non-Diapause
## Diapause         584          14
## Non-Diapause         1         192

#how many non-diapausers across days and host?
resp.2%>%
  group_by(Host,day_resp,cutoffMSMR)%>%
  summarise(sample.size=length(Host))%>%
  knitr::kable()
```

Host	day_resp	cutoffMSMR	sample.size
Apple	8	Diapause	142
Apple	8	Non-Diapause	68
Apple	20	Diapause	145
Apple	20	Non-Diapause	62
Hawthorn	8	Diapause	145

Host	day_resp	cutoffMSMR	sample.size
Hawthorn	8	Non-Diapause	59
Hawthorn	20	Diapause	153
Hawthorn	20	Non-Diapause	17

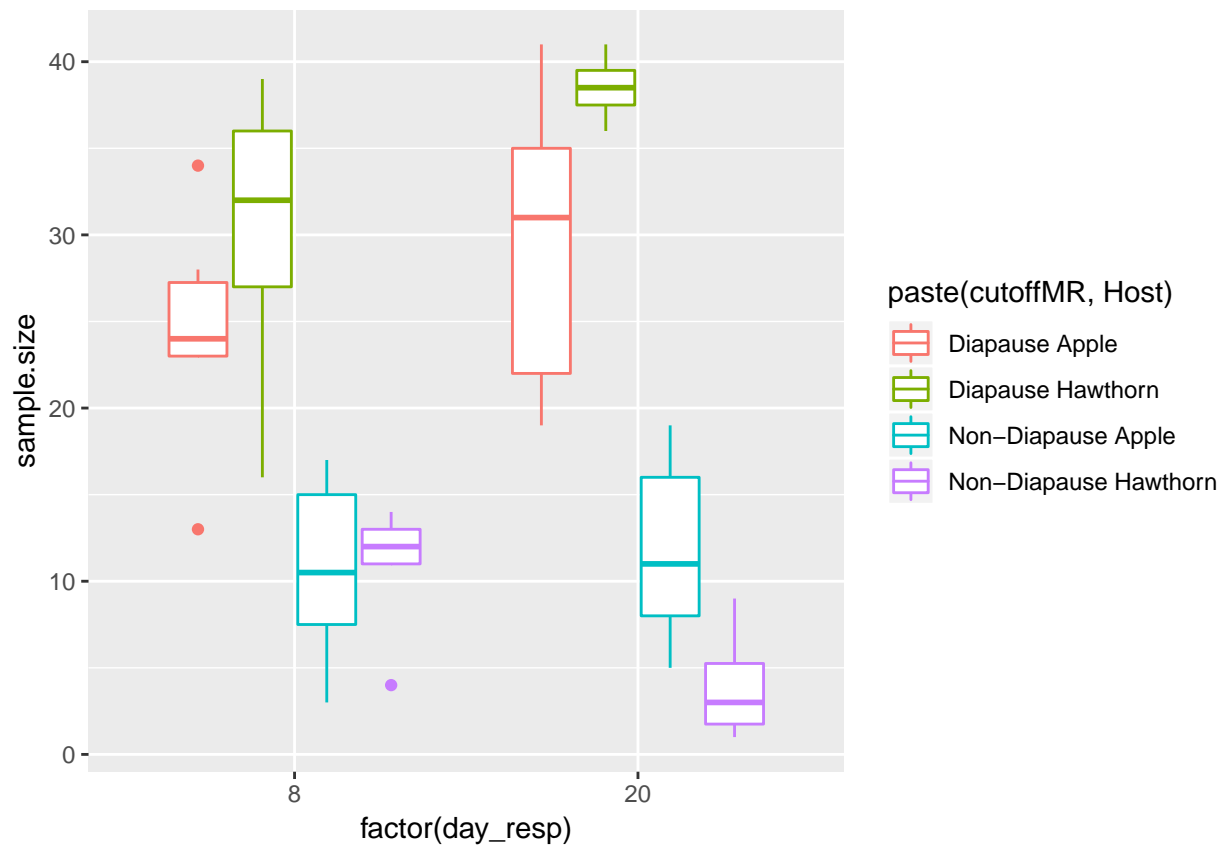
```

resp.sum<-resp.2%>%
  group_by(Host,day_resp,cohort_date,cutoffMR)%>%
  summarise(sample.size=length(Host))%>%
  data.frame()
#knitr::kable()

#resp.sum

#ggplot(resp.sum,aes(x=day_resp,y=sample.size,colour=factor(cutoffMR)))+geom_point(size=5)+geom_line(s
ggplot(resp.sum,aes(x=factor(day_resp),y=sample.size,colour=paste(cutoffMR,Host)))+geom_boxplot()

```



```

#mod1<-glm(sample.size~day_resp*cutoffMR*Host,family=poisson(link="log"),data=resp.sum)
mod1<-glm.nb(sample.size~day_resp*cutoffMR*Host,data=resp.sum)

summary(mod1)

```

```

##
## Call:
## glm.nb(formula = sample.size ~ day_resp * cutoffMR * Host, data = resp.sum,
##   init.theta = 24.16479002, link = log)
##

```

```
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.42801  -0.98863   0.05013   0.65160   1.93841
##
## Coefficients:
##              Estimate Std. Error z value
## (Intercept)      3.061229   0.211816  14.452
## day_resp         0.016327   0.014137   1.155
## cutoffMRNon-Diapause -0.761423   0.344440  -2.211
## HostHawthorn      0.173661   0.306364   0.567
## day_resp:cutoffMRNon-Diapause -0.007913   0.023053  -0.343
## day_resp:HostHawthorn  0.004461   0.020508   0.218
## cutoffMRNon-Diapause:HostHawthorn  0.568247   0.523868   1.085
## day_resp:cutoffMRNon-Diapause:HostHawthorn -0.095647   0.038001  -2.517
##              Pr(>|z|)
## (Intercept)      <2e-16 ***
## day_resp         0.2481
## cutoffMRNon-Diapause  0.0271 *
## HostHawthorn      0.5708
## day_resp:cutoffMRNon-Diapause  0.7314
## day_resp:HostHawthorn  0.8278
## cutoffMRNon-Diapause:HostHawthorn  0.2780
## day_resp:cutoffMRNon-Diapause:HostHawthorn  0.0118 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(24.1648) family taken to be 1)
##
##      Null deviance: 193.852  on 39  degrees of freedom
## Residual deviance:  48.053  on 32  degrees of freedom
## AIC: 270.67
##
## Number of Fisher Scoring iterations: 1
##
##              Theta:  24.2
##              Std. Err.:  14.5
##
## 2 x log-likelihood:  -252.671
```

Session info

```
sessionInfo()
```

```
## R version 3.5.1 (2018-07-02)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS High Sierra 10.13.4
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
```

```

## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] bindrcpp_0.2.2    MASS_7.3-50      lubridate_1.7.4  data.table_1.11.4
## [5] dplyr_0.7.6       ggplot2_3.0.0
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.18      pillar_1.3.0      compiler_3.5.1    plyr_1.8.4
## [5] highr_0.7         bindr_0.1.1       tools_3.5.1       digest_0.6.15
## [9] evaluate_0.11     tibble_1.4.2      gtable_0.2.0      pkgconfig_2.0.1
## [13] rlang_0.2.1       yaml_2.2.0        withr_2.1.2       stringr_1.3.1
## [17] knitr_1.20        rprojroot_1.3-2   grid_3.5.1        tidyselect_0.2.4
## [21] glue_1.3.0        R6_2.2.2          rmarkdown_1.10    purrr_0.2.5
## [25] magrittr_1.5      backports_1.1.2    scales_1.0.0      htmltools_0.3.6
## [29] assertthat_0.2.0  colorspace_1.3-2  labeling_0.3       stringi_1.2.4
## [33] lazyeval_0.2.1    munsell_0.5.0     crayon_1.3.4

```