viability_selection_mr_lifespan

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Libraries

```
library(dplyr) #data parsing library
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(data.table) #data parsing library mainly for reading and writing out
```

```
##
## Attaching package: 'data.table'
```

```
## The following objects are masked from 'package:dplyr':
##
##     between, first, last
```

```
library(ggplot2) #data visualization library
library(lubridate) #package to deal with time variables
```

```
##
## Attaching package: 'lubridate'
```

```
## The following objects are masked from 'package:data.table':
##
##     hour, isoweek, mday, minute, month, quarter, second, wday,
##     week, yday, year
```

```
## The following object is masked from 'package:base':
##
##     date
```

```
library(curl) #incorporate URLs
library(DiagrammeR) #figure aesthetics
library(MASS) #Functions and datasets to support
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```
library(BBmisc) #Miscellaneous functions
```

```
##
## Attaching package: 'BBmisc'
```

```
## The following objects are masked from 'package:dplyr':
##
##     coalesce, collapse
```

```
## The following object is masked from 'package:base':
##
##     isFALSE
```

```
library(survival) #survival data analysis
library(survminer) #survival data analysis
```

```
## Loading required package: ggpubr
```

```
## Loading required package: magrittr
```

```
library(gridExtra) #figure aesthetics
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

Download data and do preliminary parsing

Data are publicly available via github

```
data<- fread("https://raw.githubusercontent.com/adnguyen/Circadian_rhythm_runs_seasonal_timing/master/Da

#look at summary of data
#glimpse(data)
```

Calculating metabolic rates

Metabolic Rate = CO2 production/ hours Mass Specific Metabolic Rate = CO2 production/hrs per mass **Problem** with purge_time_1: only start and stop times except for apple cohort 1 **Solution** create time sequence for each cohort from start to end and merge into master data sheet

Day 11 Cohort

Creating the time sequence

```
#glimpse(data$purge_time_1)
#hm(data$purge_time_1)
data$day10purge <- lubridate::hour(hm(data$purge_time_1))+lubridate::minute(hm(data$purge_time_1))/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
```

```
#Obtaining start and end (min and max) of purges and smaple size for each host, cohort day, and tape
param <- data%>%
  group_by(cohort_day, tape)%>%
  summarise(max=max(day10purge, na.rm=TRUE), min=min(day10purge, na.rm=TRUE), n=length(cohort_day))

#goal: for this section, we want a sequence of times for day 10 purge
data2 <- data%>%
  group_by(cohort_day, tape)%>%
  mutate(.,day10purge.trans=seq(from = min(day10purge, na.rm=TRUE), to = max(day10purge, na.rm=TRUE), le
#glimpse(data2)

#cohort 2&3 for apple have the right sequence of purge times so they(day10purge) need to be replaced in
```

```
  #extract number of rows we want to replace
data2[1:500,]%>%
  filter(cohort_day < 4)
```

```
## # A tibble: 211 x 46
## # Groups:   cohort_day, tape [4]
##    Ind_ID tape  Site_name mass_day10 purge_time_1 purge1 collection_date
##     <int> <chr> <chr>          <dbl> <chr>         <dbl> <chr>
##  1      1 blue  OG              6.94 13:38            NA 2017-08-21
##  2      2 blue  Ferris         11.2  13:39            NA 2017-08-21
##  3      3 blue  Ferris          6.72 13:39            NA 2017-08-21
##  4      4 blue  Ferris         10.7  13:40            NA 2017-08-21
##  5      5 blue  OG              3.85 13:41            NA 2017-08-21
##  6      6 blue  OG              7.58 13:37            NA 2017-08-21
##  7      7 blue  OG              6.41 13:35            NA 2017-08-21
##  8      8 blue  OG              9.36 13:57            NA 2017-08-21
##  9      9 blue  Ferris          7.98 13:41            NA 2017-08-21
## 10     10 blue  OG              4.89 13:36            NA 2017-08-21
## # ... with 201 more rows, and 39 more variables: day10 <chr>,
## #   cohort_date <chr>, cohort_day <int>, Host <chr>, `Li-cor_1` <int>,
## #   resp_time_1 <chr>, resp_day11 <dbl>, mass_day14 <dbl>,
## #   purge_time_2 <chr>, resp_time_2 <chr>, resp_day15 <dbl>,
## #   Li_cor2 <int>, treatment_day15 <chr>, exit_fridge_date <chr>,
## #   Eclosion_reference_date <chr>, notes <chr>, Resp_code <int>,
## #   treatment <chr>, uniqueID <chr>, eclosion_date <chr>,
## #   eclosion_days <int>, well_id <chr>, organism <chr>,
## #   Trikinetics_position <int>, Trik_monitor <int>,
## #   Trikinetics_entry_LD_time <chr>, Trikinetic_exit_date <chr>,
## #   Trikinetics_exit_LD_time <chr>, notes_2 <chr>,
## #   Free_run_trik_monitor <int>, Free_run_trik_position <int>,
## #   Free_run_entry_date <chr>, Free_run_entry_time <chr>,
## #   Free_run_exit_date <chr>, Free_run_exit_time <chr>, notes_3 <chr>,
## #   Adult_death_date <chr>, day10purge <dbl>, day10purge.trans <dbl>
```

```
data2[1:211,46]<- data2[1:211,45]
#data2[1:211,46]
```

Calculating start and end time for total amount of hours of CO2 production

```
#glimpse(data$resp_time_1)
#hms(data$resp_time_1)
data2$day10resp <- lubridate::hour(hms(data$resp_time_1))+lubridate::minute(hms(data$resp_time_1))/60
```

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

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

```
#reformatting to obtain positive values
data2$total_time_day10 <- (24 - data2$day10purge.trans) + data2$day10resp
```

Metabolic Rate Calculation

```
#getting denominator for mass-specific mr
data2$total_time_day10 * data$mass_day10
```

```
##    [1]        NA 229.83250 138.29942 220.81140  79.33293 156.94947
##    [7] 133.28352 191.35817 165.41053 102.06075 134.06937 198.97133
##   [13] 202.73053 174.27900 131.12400 153.31475 148.76400 137.45385
##   [19] 129.41402 124.37533 247.19317 137.31037 196.51778 186.87757
##   [25] 129.05108 191.59152 205.04187 159.63547 130.04567 174.42242
##   [31] 137.74995 171.24340 218.04005 204.34300 102.53520 167.59402
##   [37] 232.00425 206.99625 179.07500 104.12440 141.08700 147.13358
##   [43] 164.42125        NA 239.80840 207.43060 114.60095 168.56820
##   [49]        NA        NA 138.67740 196.90170 314.60017 142.91760
##   [55] 125.05880 113.25457 153.11313 140.15320 157.46640 229.13875
##   [61] 185.82117 133.44450 197.32320 145.49050 215.34893 196.72853
##   [67]  91.35700 165.46533 184.50458 151.48130 178.31283 209.33055
##   [73] 260.69035 164.04410 167.20608 179.64780 110.27360 261.05570
##   [79] 194.20050 214.30920 172.98820 225.70182 220.81920 176.24658
##   [85] 177.44417 146.92125 168.89110 229.35780        NA 186.92440
##   [91] 170.11611        NA 128.57202  72.88260 129.32833 128.61440
##   [97]  89.01920 159.33793  86.82412 112.69375 165.06190 115.35067
##  [103] 143.17950 115.47800 141.54450 117.52545 117.51428 114.32415
##  [109] 156.78033 118.28022 111.65880 107.33050 124.35120 142.86957
##  [115] 115.84625 150.19747 106.20518 117.50745 136.12157 102.05720
##  [121] 136.71595 123.43413 150.84300 120.24693 192.83600 148.08917
##  [127] 114.25620 155.41110 108.33290 122.71523 131.52720 124.16267
##  [133] 147.12793 103.73120 122.45975 189.97560 109.16353 185.47000
##  [139] 121.58408 114.76355 125.13542  85.46352 133.69167 176.58013
##  [145] 138.70560 127.59480 151.10165 189.68912 132.43253 121.99575
##  [151]        NA        NA 193.45755 125.64170 110.72000 104.15253
##  [157]  78.77340 156.23440 129.20732  91.36055 117.78230  83.02500
##  [163]  82.20875 165.95030 108.15933 147.41160 169.86240  78.14333
##  [169] 135.53155 105.65013 143.00550 146.07200 101.76903 163.52660
##  [175] 162.97340 113.43645  83.53340 103.07733 119.24325  92.65200
##  [181] 170.67317 116.43350 144.11613  99.21625 169.68645 122.85743
##  [187] 111.16300 143.25410  97.37500 146.13020 122.15800 112.01815
##  [193] 135.50570 116.38575 177.36157 110.93057 104.31200 118.35383
##  [199] 191.13900 147.22565 118.82573 140.15750 105.29482 137.67000
##  [205] 177.13395 157.43030 149.01320 112.64150 172.85580        NA
##  [211]        NA 160.98160 137.55440 184.14926 174.98031 191.56902
##  [217] 130.26728 221.11751 147.21585 185.66552  61.81770 183.90629
##  [223] 118.60771 145.96979 145.70552 128.39497 234.65451 130.91413
##  [229] 171.66903 172.36607 146.29393 227.10513 160.57917 125.69158
##  [235] 154.60008 181.70051 197.00156 184.72090 124.79015 191.41764
##  [241] 148.67394 100.12418 151.71858 162.62494  99.69210 182.48331
##  [247] 147.77721 131.76176 223.66187 220.85404 162.32503 164.41431
##  [253] 138.83681 144.21126 167.93866 117.94359 137.90120 208.16427
##  [259] 117.60693 142.84450 173.28354 125.29670 197.13775 249.00363
##  [265]  87.93122 129.72116 181.50986 221.52903 177.11113 199.71484
##  [271] 143.59812 137.42575 130.97763 100.38239 101.96694 194.29634
##  [277] 238.28225 110.63830 189.79042  83.82351 114.96796 182.28144
##  [283] 129.95645 151.67436 154.74247 186.75853 235.60695        NA
##  [289]        NA 104.58910 114.40759 174.24962 149.94311 166.28462
```

```
##  [295] 104.87402 151.05469 108.79407 171.44309 218.38588 119.94811
##  [301] 158.76229 129.99138 180.47169 177.65541 104.29854  84.95010
##  [307] 176.21938 153.05964 137.85460 177.45286 116.44867 118.43806
##  [313] 134.50245 104.22427 152.81204 104.58031 188.10263  97.42360
##  [319] 124.80878 104.22246 179.31408  92.35752 103.95750 226.67892
##  [325] 143.04624 124.33558 220.15066 156.17497 185.22211 173.20529
##  [331]  68.47136 130.34693 167.66992 179.35920 122.53376 169.45778
##  [337] 156.86031 149.63238 223.31825 211.39354 120.14077  85.23373
##  [343] 101.25868 206.39688 139.01981 131.60096  94.97724  90.01493
##  [349] 148.91532 130.76857 169.55661 114.06377 125.39011 202.57852
##  [355] 139.68017 115.63470 125.80445 162.43486 203.74528 156.70339
##  [361] 122.19424 222.66181 147.45711 133.81049 125.63435        NA
##  [367]        NA 114.17120 152.02211 104.25936 180.07640 132.07403
##  [373] 145.75529 105.82967 180.42481 110.82069 139.22719 169.03201
##  [379] 115.78122 102.40206 106.62088 116.57799 149.53794 169.14195
##  [385] 141.70102  94.36315 111.54938 119.39799 164.12316 146.61286
##  [391] 155.96672 102.18130 133.86163 144.72199 113.36554 101.47485
##  [397] 118.34672 150.56059 101.83648 185.19999 122.23608 112.50406
##  [403] 129.96509 148.46465 136.77738 143.86682 145.42596 141.68891
##  [409] 115.95627 147.09597 121.32930 169.93489 147.72194 190.94451
##  [415] 118.29552 143.88231 198.47243 160.72151 161.24418 135.63606
##  [421] 221.81741 119.11098 114.86218 175.14436  99.21399 135.86251
##  [427] 186.36390 109.93696 162.30509 117.68008 166.70285 182.91869
##  [433] 164.85652 130.94903 131.43494 149.60601 127.62350 172.15866
##  [439] 113.35145 179.60115        NA        NA 129.04167  94.89798
##  [445] 135.26804 127.54211 141.51345  90.80238 173.95637 109.27991
##  [451] 153.63981 123.73701  96.88159 111.12977 108.14407 110.95517
##  [457] 125.67430 149.81600 102.16825  71.88306 126.76443 138.24708
##  [463] 142.71816 213.94819 124.31272 154.43764 111.51000 162.63898
##  [469] 140.57957 148.70665 113.75937 161.47634 102.55418  96.53827
##  [475] 161.16447 105.12363 159.67721 112.51355 128.71857 173.07352
##  [481] 143.56650 150.14673 147.38431 164.34063 143.20026  96.61558
##  [487] 176.89015 100.25656 175.56435  97.15781 138.86573 217.30523
##  [493] 119.30236 166.43456 131.89045 167.86442 175.93598  76.46047
##  [499] 105.75255 162.04308  95.74179 115.32514 108.68151 163.93181
##  [505]  97.50559 115.76844 218.95465  86.14281 189.65865 168.06256
##  [511] 144.51311 115.73658 103.61306 107.44191 120.21442  66.77178
##  [517] 112.55024        NA        NA  89.60792 135.99274  92.13925
##  [523]  83.90501 157.98976 143.46973 171.59371 128.85333 103.59508
##  [529]  89.02023 115.16380  84.68511 121.06293 101.38043 125.89552
##  [535] 149.35228 173.32581 107.94427 126.61853  91.03290 170.07970
##  [541] 106.17546  97.83041  76.80043  79.13677  76.23361 114.29979
##  [547]  87.89238 115.97241 200.81198  68.92276 184.30115 152.07273
##  [553] 122.83428  76.83550  54.82412 137.34469 158.10355 132.63194
##  [559] 113.30461 103.90424 131.39523 147.56714 122.57605  88.43900
##  [565] 186.60155 118.16147 110.56058 107.71312 154.63522 167.39581
##  [571]  90.92231 120.61385  97.77491 133.09700 134.84764 103.58501
##  [577] 210.43972  71.55708 138.55393  73.76099 115.49332 122.25481
##  [583] 156.69138 147.05874  71.82052 155.03377 131.96618  86.10923
##  [589] 190.51437  99.85836 111.52131 130.28281 201.18865 143.14706
##  [595] 119.45067        NA        NA 119.63500 115.70564 109.97769
##  [601]  84.11150 101.91854 105.80700 163.05083 132.14667 102.83111
##  [607] 112.81900 116.16443  69.97429 108.60400  77.91131 141.63023
##  [613] 153.76575 142.90833 158.54578 113.14422 129.22849 170.06278
```

```
##  [619] 103.38693 116.48976 120.22496 146.42750  98.04133  70.30732
##  [625] 118.30453 101.47312 100.05735 166.76587 182.14980 183.72667
##  [631] 102.60067  89.87078 125.54669 130.33670 107.27396  82.26349
##  [637] 130.84605 131.12493 105.87344 104.90987 154.93172  89.75972
##  [643]  54.86287  99.81554  83.38311 163.82750 168.12778 101.39176
##  [649] 178.41390 109.99351 134.92269  89.47950 100.63481  95.05394
##  [655]  83.93600  94.05100 122.40880 119.65520  95.13611 114.65067
##  [661] 188.32515 112.86920  91.53478 100.66680 177.23608  89.49252
##  [667] 139.70125 116.36451 103.77651  88.98170 112.40042 151.29811
##  [673] 150.25650  88.40724        NA        NA 185.94333 139.95375
##  [679] 131.52484 122.28105 147.64440 171.40194 167.60189 194.89025
##  [685] 181.64644 222.23556 115.13557  86.41585 164.32688  97.10026
##  [691]  91.82586 155.65060  93.46918 228.55036 173.21986 114.20893
##  [697] 189.69403 138.66261 213.11254  94.14771 138.83520 230.59548
##  [703] 152.68302 163.90062 155.20642 188.87217 120.67228        NA
##  [709]        NA 194.23015 255.76490 150.58549 197.82436 202.23543
##  [715] 138.55750 205.08268 260.08189 146.71509 169.98730 149.46466
##  [721] 162.13095 206.64901  89.99596 153.69833 134.64714 126.56377
##  [727] 178.32049 221.48969 153.32440 149.49620 139.70537 187.19701
##  [733] 194.29798 162.31713 155.51597 159.06149 117.90465 298.18559
##  [739] 156.94160  81.61460 124.55479 154.51687 203.50478 107.76720
##  [745] 144.78826 239.55233 123.30920 105.00450 205.05270 198.74050
##  [751] 245.93819 137.16900 100.04887 185.18833 158.71118 194.40355
##  [757] 122.42304 131.01622 195.41531 170.31976 103.96842 195.76287
##  [763]  72.91833 122.18592 149.02107 110.17400 149.69059  84.25531
##  [769] 128.07301  97.24834 116.89326 133.64101 207.95864 198.31675
##  [775] 134.35809 179.77615 158.39652 144.35674 146.46266 208.63462
##  [781] 136.01120 125.82232 243.24489 133.93615 183.81389 155.97689
##  [787] 146.62580 147.93977 155.32271 106.80806 125.03218 139.03290
##  [793] 134.70249 112.61489 198.54930 192.39418  91.57236 151.66250
##  [799] 135.29763 204.36869 131.55925 167.30835 133.11269 133.93418
##  [805] 183.91530 159.39016 245.42675 125.04043 110.31178  64.38848
##  [811] 166.83944  98.92447 113.26006 159.85266 141.63854        NA
##  [817]        NA 242.00267 187.95620 184.30204  90.76780 239.19784
##  [823] 151.60813 155.08402 160.51899 181.45933 125.11891 197.46458
##  [829] 122.67061 182.10020 154.05487 159.32617 212.98948 205.17475
##  [835] 201.18759 116.55287 103.23271 181.79849  74.35889 116.77060
##  [841] 133.41942 209.18082 121.80952 197.57476 235.08032 179.93054
##  [847] 216.40576 205.43619 112.58999 107.09379  90.20766  83.85344
##  [853] 174.02456 164.27322 184.31481 114.06429 150.08956 144.48600
##  [859] 116.34581 117.47332 183.57523 175.96135 174.25034 174.71819
##  [865] 128.04229 184.17562 105.07557 149.20299  74.10898 180.54654
##  [871] 144.42138 108.81461 122.08972 154.36449 143.73694 120.96534
##  [877] 140.39208 151.42382 122.01917  84.88125 194.25631 197.88847
##  [883]  85.62919 110.78646 145.61374 128.43631 157.28490 106.14017
##  [889] 168.42726 164.13566 165.71969 114.48578 112.56015        NA
##  [895]        NA 188.87733 142.77008 100.51128 156.74864 176.45575
##  [901] 170.19481 139.29622 107.68737  55.87789 131.84202  74.13450
##  [907] 122.45263 106.23768  92.04438 142.71279 118.74113  68.81785
##  [913] 102.82762 136.37363 122.26594 104.88081 116.65928  58.99633
##  [919] 133.89875 111.78581 135.08548 197.05147 135.45937 111.61904
##  [925] 175.19706  92.00232 129.38189 207.19922  85.93670 110.57158
##  [931]  97.82292 132.69178  91.53976 187.05555  97.78618 234.27203
##  [937] 138.92104 124.97691  92.23114 154.30114 140.15043 165.45698
```

```
##  [943] 134.03450 120.69978 155.56993 167.73295 158.65154 185.67999
##  [949] 134.32867 223.33826 127.07675 100.76959 127.16367 199.24956
##  [955] 174.79408 168.92368 138.27653 137.85677 137.01765 125.33659
##  [961] 132.06652 216.36658 163.19895 130.90068 126.21964 111.30702
##  [967] 125.10399 164.65189 143.44467 161.58900        NA        NA
##  [973] 161.40020 174.14401 147.90829 158.13235 205.00830 125.58432
##  [979] 156.68621 118.60232 194.05737 175.16424  74.65430 125.86896
##  [985] 103.24228 135.42213 107.47118 103.72129 177.16409 117.41503
##  [991] 164.38699 144.11543 138.89903 181.89089  86.55914 183.17073
##  [997] 229.89745 224.88473 201.08884 245.96768 197.49885 123.18913
## [1003] 166.93640 140.75071 206.67424 123.09466 115.00619 236.09784
## [1009] 190.81831 186.80620 183.37529 178.06876 123.25473 121.81579
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## [1039] 195.18495        NA 125.96601 190.89313        NA 135.69220
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## [1051] 139.08702 212.86140 149.18889 107.26954 128.97442 136.60285
## [1057] 174.45017 129.57646 102.74794  80.74769 128.87995 116.41035
## [1063] 170.49681  82.17580 190.45479 114.25144 131.26973  86.99943
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## [1225] 115.45929 112.96324 178.08848 138.19074 208.48416 129.94223
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## [1279] 245.84774 149.92279 146.18557 148.78407 120.69537 147.61535
## [1285] 103.04634 163.31440 228.86843 181.84956  94.65262 147.40825
## [1291]        NA        NA 167.41060 139.91920 177.49981 224.01475
## [1297] 193.41696 138.99619 171.99369 237.28411 226.08175 234.10107
## [1303] 224.96252  76.53008 148.76576 129.32995 207.15345 179.11304
## [1309] 137.60457 121.85052 169.57946 160.39995 163.95529 183.09422
## [1315] 202.27354 152.36843 152.40566 136.38287 159.67222 129.36755
## [1321] 209.50420 125.34959 118.65316 128.99707 130.78535 156.07044
## [1327] 179.40675 132.51138        NA        NA 122.93398 176.52255
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## [1339] 140.96983 264.11051 154.52414 201.45797 293.41517 109.00732
## [1345] 166.77159 144.01834 130.03841 161.62988  88.87576 199.54329
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## [1357] 157.37313 188.97673 289.72767 115.52040 106.97229 258.29933
## [1363]        NA        NA 181.21833 269.44909  76.11165 182.23958
## [1369] 295.94153 228.57671 257.07097 162.91631 114.13193 184.46888
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## [1411] 187.71644 223.54463 199.39100  77.97282 152.39923 248.14182
## [1417] 140.61874 220.11266 112.58019 143.82033 282.24373 191.37258
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## [1429] 114.61053 189.86335        NA        NA 117.04825 175.52945
## [1435] 183.29962  92.76235 142.52697 282.45317 150.12132 226.61818
## [1441] 192.51811 197.23011 139.58596 143.47117  63.31617 295.51770
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## [1507] 133.34522 166.00527 184.10000 164.72538 168.18218 117.46247
## [1513] 230.91246 148.86109 241.87710 124.80000 126.04622 226.17288
## [1519] 141.98321 211.59838 162.37694 182.63900 106.95641 216.76707
## [1525] 228.16920 222.12979 109.03537 226.84534 155.39157 184.90230
## [1531] 124.49999 148.65269 136.98108 176.25465 199.14195 154.42257
## [1537] 214.56905        NA        NA 191.59569 150.94633 165.19561
## [1543] 113.30868 167.63394  87.97359 179.01035 219.64297 183.29902
## [1549] 147.69612 170.90734 192.00438 114.68039 169.89503 173.17221
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```

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## [1591]  83.97080 174.13751 205.55791 123.29382 138.50174 168.35341
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## [1627]  75.35852 118.80559        NA        NA 284.63086 248.41157
## [1633] 342.87828 268.42123 168.89510 167.94445        NA 135.95820
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## [1879] 153.41239 225.50421 151.69722        NA        NA 258.86433
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## [1897]        NA        NA 241.96603 239.51537 137.91522 199.50657
## [1903]        NA        NA 212.69424 196.33720 133.97971        NA
## [1909]        NA
```

```
#Metabolic Rate for day 11
data2$MR11<- data$resp_day11/(data2$total_time_day10)

#Mass specific Metabolic Rate for day 11
data2$msMR11<- data$resp_day11/(data2$total_time_day10 * data$mass_day10)
```

Controlling for blank controls

```
#Assign the blanks to an object
data3 <- data2%>%
  group_by(cohort_day, tape)%>%
  filter(Site_name=="Blank")%>%
  summarise(mean.blank=mean(MR11,na.rm=TRUE))

#check columns
#glimpse(data3)
data3$mean.blank
```

```
##  [1] 0.0011257856 0.0006226170 0.0003137692 0.0038187342 0.0006020381
##  [6] 0.0005606454 0.0067232397 0.0010034398 0.0004597089 0.0003777458
## [11] 0.0004217324 0.0008299999 0.0010143259 0.0006680801 0.0012768032
## [16] 0.0005854209 0.0010247606 0.0006378185 0.0011384133 0.0005885973
## [21] 0.0004956928 0.0143301474 0.0009422219 0.0008234242 0.0010247213
## [26] 0.0009524855 0.0006771652 0.0006364143 0.0007423115 0.0004865312
## [31] 0.0051276472 0.0004456934 0.0003163145 0.0009844019 0.0006993465
## [36] 0.0004824640 0.0009931376 0.0002493671
```

```
#merge data3 and data2 by cohort day and tape and create a mean blanks column
data4 <- inner_join(data2, data3, by=c("cohort_day", "tape"))
data4$mean.blank
```

```
##    [1] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##    [6] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [11] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [16] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [21] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [26] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [31] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [36] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [41] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
##   [46] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0006226170
##   [51] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0006226170
##   [56] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0006226170
##   [61] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0006226170
##   [66] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0006226170
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##   [76] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0006226170
##   [81] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0006226170
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## [1531] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0006226170
## [1536] 0.0006226170 0.0006226170 0.0006226170 0.0006226170 0.0011257856
## [1541] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
## [1546] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
## [1551] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
## [1556] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
## [1561] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
## [1566] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0011257856
## [1571] 0.0011257856 0.0011257856 0.0011257856 0.0011257856 0.0038187342
## [1576] 0.0038187342 0.0038187342 0.0038187342 0.0038187342 0.0038187342
## [1581] 0.0038187342 0.0038187342 0.0038187342 0.0038187342 0.0038187342
## [1586] 0.0038187342 0.0038187342 0.0038187342 0.0038187342 0.0038187342
## [1591] 0.0038187342 0.0038187342 0.0038187342 0.0038187342 0.0038187342
## [1596] 0.0038187342 0.0038187342 0.0038187342 0.0038187342 0.0038187342
## [1601] 0.0038187342 0.0038187342 0.0003137692 0.0003137692 0.0003137692
## [1606] 0.0003137692 0.0003137692 0.0003137692 0.0003137692 0.0003137692
## [1611] 0.0003137692 0.0003137692 0.0003137692 0.0003137692 0.0003137692
## [1616] 0.0003137692 0.0003137692 0.0003137692 0.0003137692 0.0003137692
## [1621] 0.0003137692 0.0003137692 0.0003137692 0.0003137692 0.0003137692
## [1626] 0.0003137692 0.0003137692 0.0003137692 0.0003137692 0.0003137692
## [1631] 0.0005606454 0.0005606454 0.0005606454 0.0005606454 0.0005606454
## [1636] 0.0005606454 0.0005606454 0.0005606454 0.0005606454 0.0005606454
## [1641] 0.0005606454 0.0005606454 0.0005606454 0.0005606454 0.0005606454
## [1646] 0.0005606454 0.0005606454 0.0005606454 0.0005606454 0.0005606454
## [1651] 0.0005606454 0.0005606454 0.0005606454 0.0005606454 0.0005606454
## [1656] 0.0005606454 0.0006020381 0.0006020381 0.0006020381 0.0006020381
## [1661] 0.0006020381 0.0006020381 0.0006020381 0.0006020381 0.0006020381
## [1666] 0.0006020381 0.0006020381 0.0006020381 0.0006020381 0.0006020381
## [1671] 0.0006020381 0.0006020381 0.0006020381 0.0006020381 0.0006020381
## [1676] 0.0006020381 0.0006020381 0.0006020381 0.0006020381 0.0006020381
## [1681] 0.0006020381 0.0006020381 0.0006020381 0.0010034398 0.0010034398
## [1686] 0.0010034398 0.0010034398 0.0010034398 0.0010034398 0.0010034398
## [1691] 0.0010034398 0.0010034398 0.0010034398 0.0010034398 0.0010034398
## [1696] 0.0010034398 0.0010034398 0.0010034398 0.0010034398 0.0010034398
## [1701] 0.0010034398 0.0010034398 0.0010034398 0.0010034398 0.0010034398
## [1706] 0.0010034398 0.0010034398 0.0004597089 0.0004597089 0.0004597089
## [1711] 0.0004597089 0.0004597089 0.0004597089 0.0004597089 0.0004597089
## [1716] 0.0004597089 0.0004597089 0.0004597089 0.0004597089 0.0004597089
## [1721] 0.0004597089 0.0004597089 0.0004597089 0.0004597089 0.0004597089
## [1726] 0.0004597089 0.0004597089 0.0004597089 0.0004597089 0.0004597089
```

```
## [1731] 0.0004597089 0.0008299999 0.0008299999 0.0008299999 0.0008299999
## [1736] 0.0008299999 0.0008299999 0.0008299999 0.0008299999 0.0008299999
## [1741] 0.0008299999 0.0008299999 0.0008299999 0.0008299999 0.0008299999
## [1746] 0.0008299999 0.0008299999 0.0008299999 0.0008299999 0.0008299999
## [1751] 0.0008299999 0.0008299999 0.0008299999 0.0008299999 0.0008299999
## [1756] 0.0008299999 0.0008299999 0.0008299999 0.0008299999 0.0008299999
## [1761] 0.0008299999 0.0008299999 0.0008299999 0.0004217324 0.0004217324
## [1766] 0.0004217324 0.0004217324 0.0004217324 0.0004217324 0.0004217324
## [1771] 0.0004217324 0.0004217324 0.0004217324 0.0004217324 0.0004217324
## [1776] 0.0004217324 0.0004217324 0.0004217324 0.0004217324 0.0004217324
## [1781] 0.0004217324 0.0004217324 0.0004217324 0.0004217324 0.0004217324
## [1786] 0.0004217324 0.0004217324 0.0004217324 0.0004217324 0.0004217324
## [1791] 0.0004217324 0.0004217324 0.0004217324 0.0004217324 0.0004217324
## [1796] 0.0006680801 0.0006680801 0.0006680801 0.0006680801 0.0006680801
## [1801] 0.0006680801 0.0006680801 0.0006680801 0.0006680801 0.0006680801
## [1806] 0.0006680801 0.0006680801 0.0006680801 0.0006680801 0.0006680801
## [1811] 0.0006680801 0.0006680801 0.0006680801 0.0006680801 0.0010143259
## [1816] 0.0010143259 0.0010143259 0.0010143259 0.0010143259 0.0010143259
## [1821] 0.0010143259 0.0010143259 0.0010143259 0.0010143259 0.0010143259
## [1826] 0.0010143259 0.0010143259 0.0010143259 0.0010143259 0.0010143259
## [1831] 0.0010143259 0.0010143259 0.0005854209 0.0005854209 0.0005854209
## [1836] 0.0005854209 0.0005854209 0.0005854209 0.0005854209 0.0005854209
## [1841] 0.0005854209 0.0005854209 0.0005854209 0.0005854209 0.0005854209
## [1846] 0.0005854209 0.0005854209 0.0005854209 0.0005854209 0.0005854209
## [1851] 0.0005854209 0.0005854209 0.0012768032 0.0012768032 0.0012768032
## [1856] 0.0012768032 0.0012768032 0.0012768032 0.0012768032 0.0012768032
## [1861] 0.0012768032 0.0012768032 0.0012768032 0.0012768032 0.0012768032
## [1866] 0.0012768032 0.0012768032 0.0012768032 0.0012768032 0.0012768032
## [1871] 0.0012768032 0.0006378185 0.0006378185 0.0006378185 0.0006378185
## [1876] 0.0006378185 0.0006378185 0.0010247606 0.0010247606 0.0010247606
## [1881] 0.0010247606 0.0010247606 0.0010247606 0.0011384133 0.0011384133
## [1886] 0.0011384133 0.0011384133 0.0011384133 0.0011384133 0.0011384133
## [1891] 0.0011384133 0.0004956928 0.0004956928 0.0004956928 0.0004956928
## [1896] 0.0004956928 0.0004956928 0.0004956928 0.0008234242 0.0008234242
## [1901] 0.0008234242 0.0008234242 0.0008234242 0.0008234242 0.0009524855
## [1906] 0.0009524855 0.0009524855 0.0009524855 0.0009524855
```

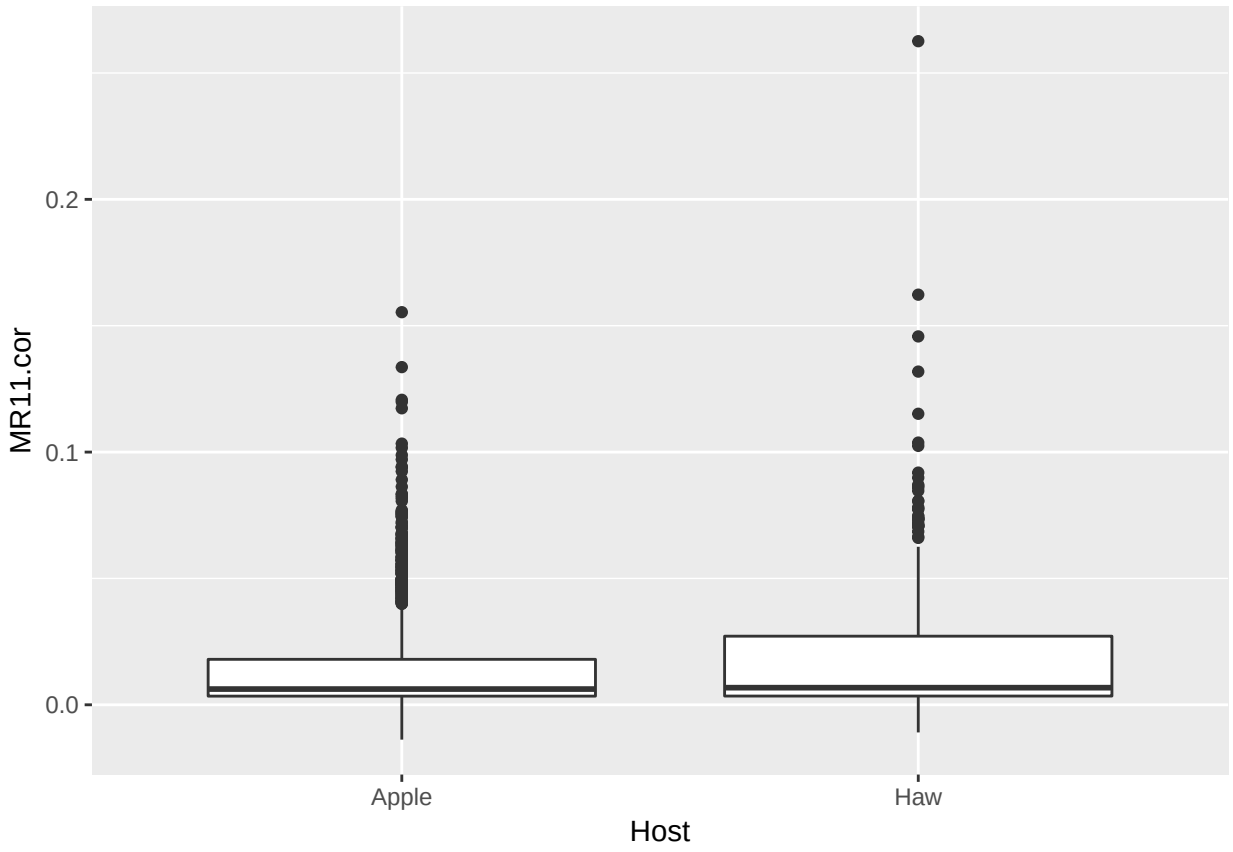
```
#do some corrections
data5 <- data4%>%
  mutate(MR11.cor = MR11 - mean.blank, msMR11.cor = msMR11 - mean.blank)
#glimpse(data5)

data5.neg <- data5%>%
  filter(MR11.cor<0)
```

Figure of Metabolic Rate between Hosts

```
#Boxplot
ggplot(data5, aes(x=Host, y=MR11.cor))+geom_boxplot()
```

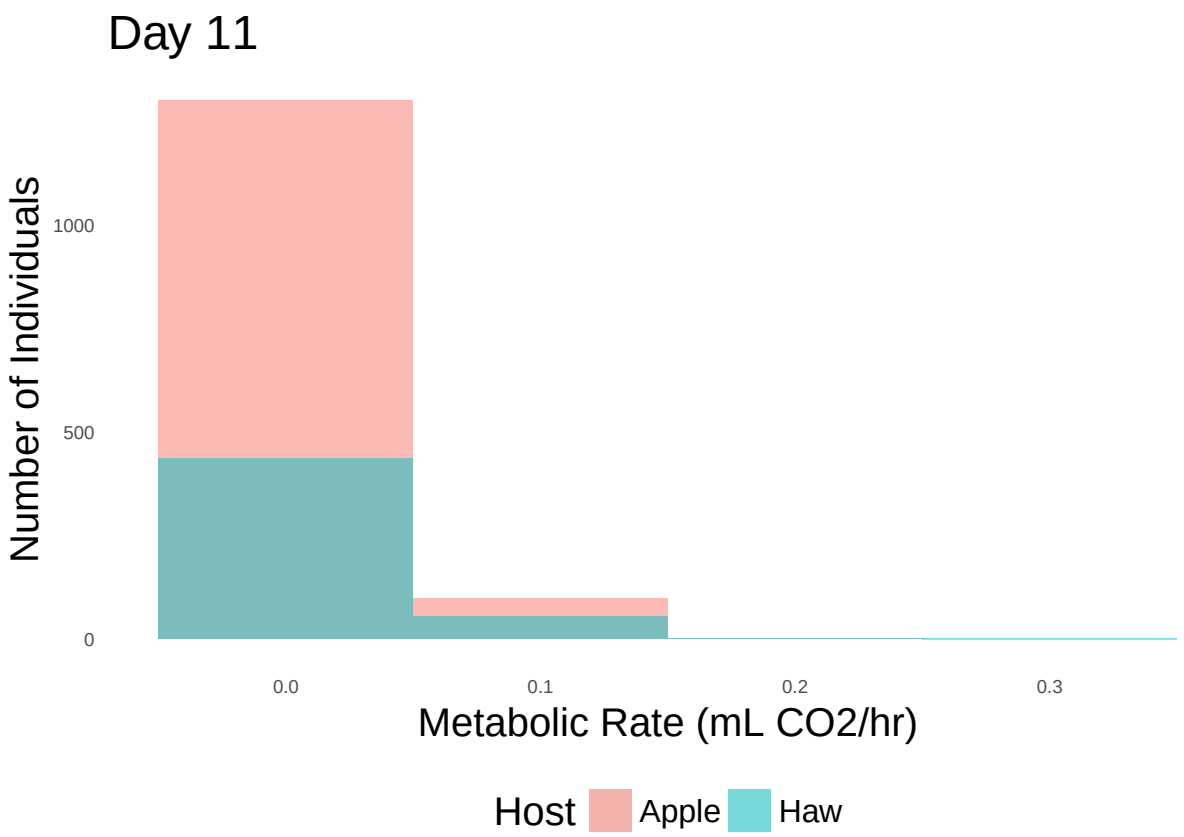
```
## Warning: Removed 13 rows containing non-finite values (stat_boxplot).
```




```
#Histogram
setup<-theme_bw()+theme(axis.text.x=element_blank(),
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.text.y=element_blank(),
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s

ggplot(data5, aes(x=MR11.cor, fill=Host))+geom_histogram(position = "identity", alpha=.5, binwidth = .1
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Warning: Removed 13 rows containing non-finite values (stat_bin).
```



Calculate eclosion days

```
data5$neweclosions<-difftime(as.Date(data5$eclosion_date), as.Date(data5$Eclosion_reference_date),units=

data5$neweclosions <- as.numeric(data5$neweclosions)
```

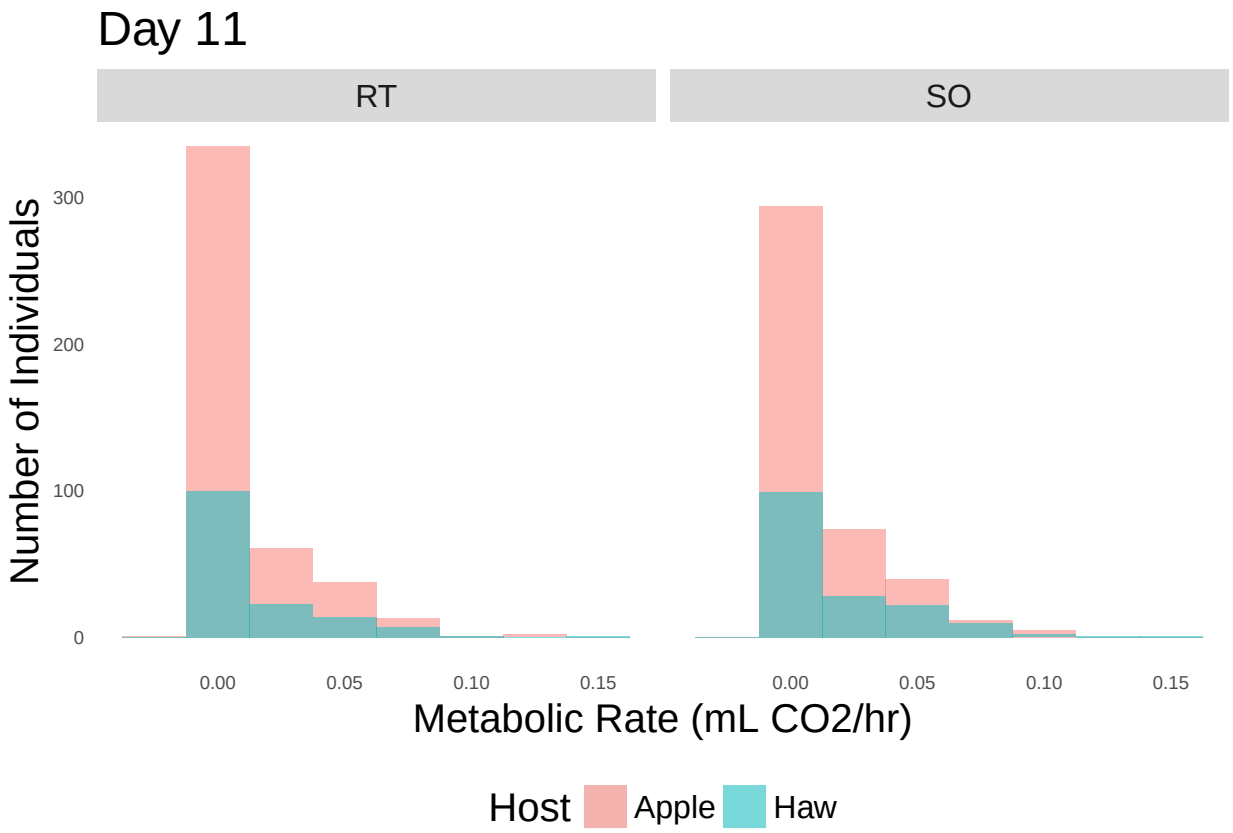
Figures of eclosion and metabolic rate data

```
data5.treatsub<-data5%>%
  filter(treatment!="GC"&treatment!="")

data5.treatsub$neweclosions<-as.numeric(data5.treatsub$neweclosions)

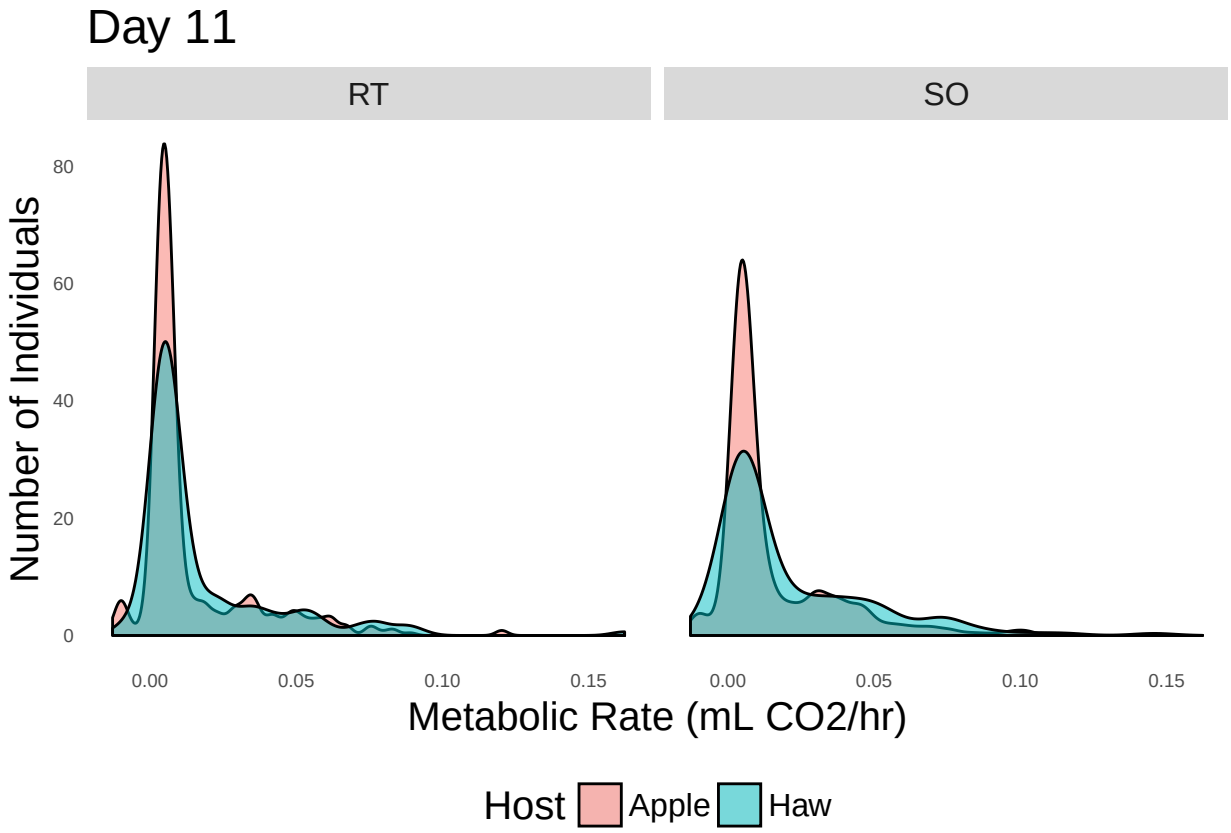
#Histogram comparison between MR of RT & SO
ggplot(data5.treatsub, aes(x=MR11.cor, fill=Host))+geom_histogram(position = "identity", alpha=.5, binwi
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(si
```

```
## Warning: Removed 4 rows containing non-finite values (stat_bin).
```



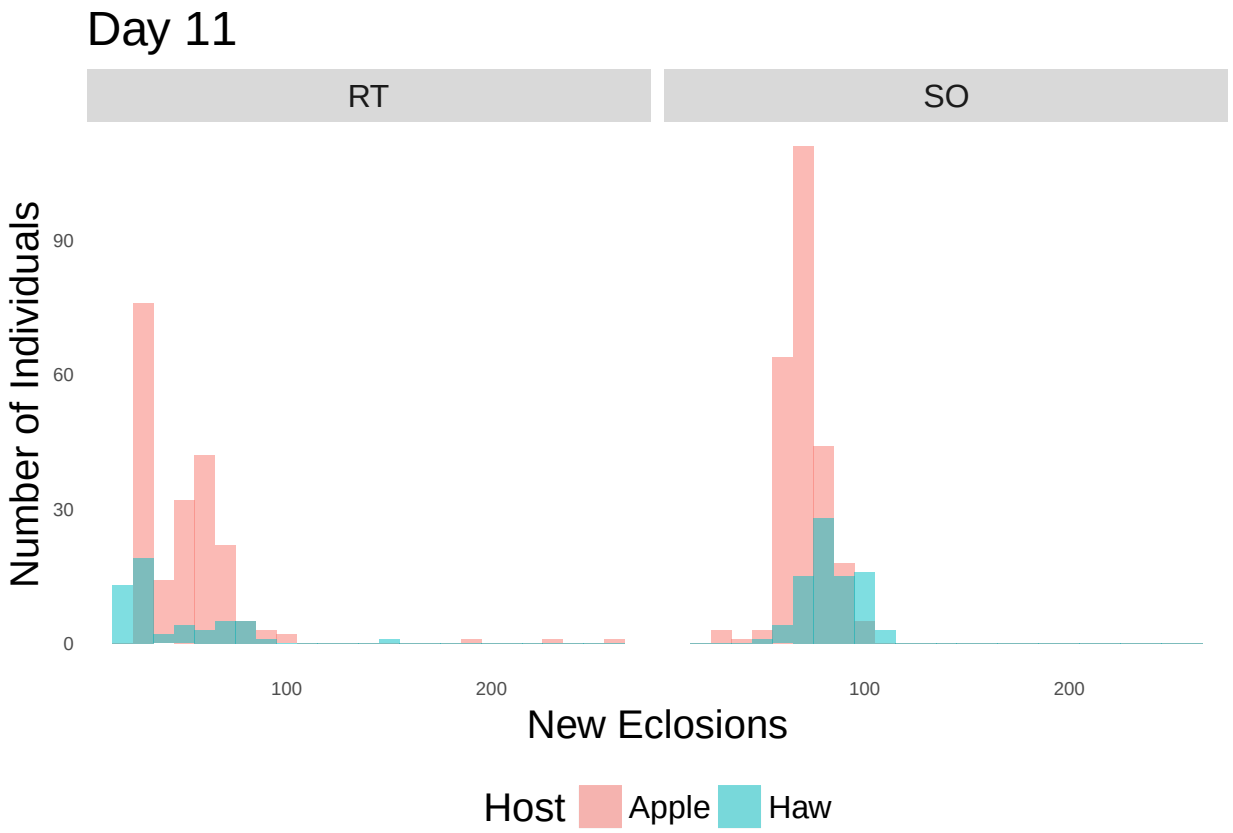

```
#Density comparison between MR of RT & SO
ggplot(data5.treatsub, aes(x=MR11.cor, fill=Host))+geom_density(position = "identity", alpha=.5)+facet_
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Warning: Removed 4 rows containing non-finite values (stat_density).
```



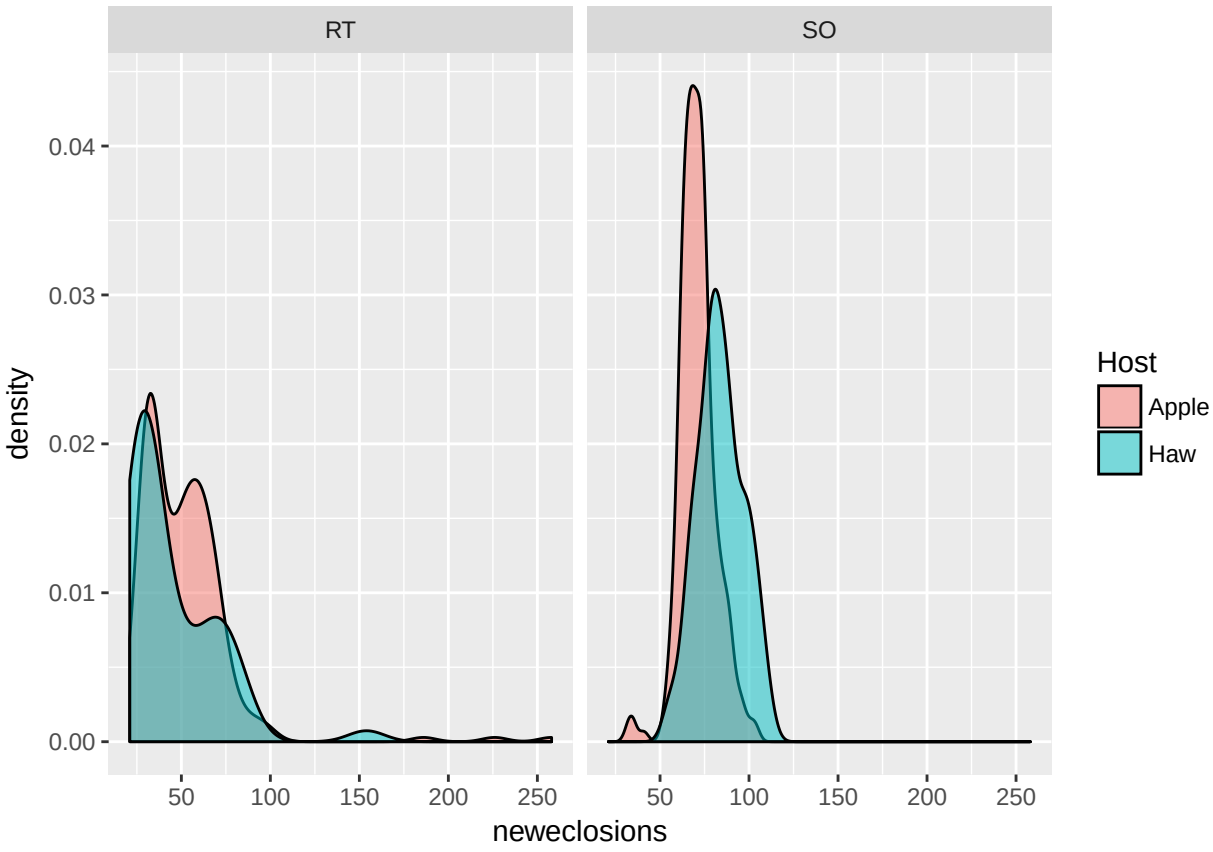

```
#Histogram comparison between eclosion date of RT & SO
ggplot(data5.treatsub, aes(x=neweclosions, fill=Host))+geom_histogram(position = "identity", alpha=.5, l
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(si
```

```
## Warning: Removed 606 rows containing non-finite values (stat_bin).
```




```
#Density comparison between eclosion date of RT & SO
ggplot(data5.treatsub, aes(x=neweclosions, fill=Host))+geom_density(position = "identity", alpha=.5)+fa
```

```
## Warning: Removed 606 rows containing non-finite values (stat_density).
```



Test differences in eclosion timing between host and experiment (ANOVA)

Using ANOVA which tests differences between two or more means * The null hypothesis would be that the two means are equal * Significance would indicate two means are not equal One Way ANOVA compares two means from two independent groups, in this case eclosion date and host (specific to SO and RT)

Two Way ANOVA compares means of two independent variables affecting one dependent variable, in this case the effect of Host and treatment (interacting) on eclosion

```
#Focus only on RT and SO treatments
data5.treatsub<-data5%>%
  filter(treatment!="GC"&treatment!="")

#Two Way ANOVA
mod1<- aov(neweclosions ~ Host*treatment, data=data5.treatsub)
summary(mod1)
```

```
##                 Df Sum Sq Mean Sq F value   Pr(>F)
## Host             1   3685    3685   9.705  0.00193 **
## treatment        1  82798   82798 218.056  < 2e-16 ***
## Host:treatment   1   9903    9903  26.080 4.45e-07 ***
## Residuals      579 219851     380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 606 observations deleted due to missingness
```

```
#narrow down to SO & RT
data5.SO<-data5.treatsub%>%
  filter(treatment=="SO")

data5.RT<-data5.treatsub%>%
  filter(treatment=="RT")

#One Way ANOVA for RT & SO
mod2RT<-aov(neweclosions~Host, data=data5.RT)
summary(mod2RT)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Host          1   2143  2142.9    2.97  0.086 .
## Residuals   250 180353   721.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 346 observations deleted due to missingness
```

```
mod2SO<-aov(neweclosions~Host, data=data5.SO)
summary(mod2SO)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Host          1  10064   10064   83.83 <2e-16 ***
## Residuals   329  39499     120
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 260 observations deleted due to missingness
```

```
#how balanced it is
data5.RT%>%
  group_by(Host)%>%
  summarise(n=length(Host))
```

```
## # A tibble: 2 x 2
##   Host      n
##   <chr> <int>
## 1 Apple   452
## 2 Haw     146
```

Both the one way and two way ANOVA tests showed significance between the two means (meaning they are not equal). The two way ANOVA suggests that there is a difference in number of days to eclosion based on treatment type - favorable conditions vs. simulated overwintering. Therefore, a one way ANOVA was done for each treatment to test whether there is any significance between host type and days to eclosion. The one way ANOVA showed significance for both treatments; however, the simulated overwintering samples had a lower p value, which indicates more signigicance.

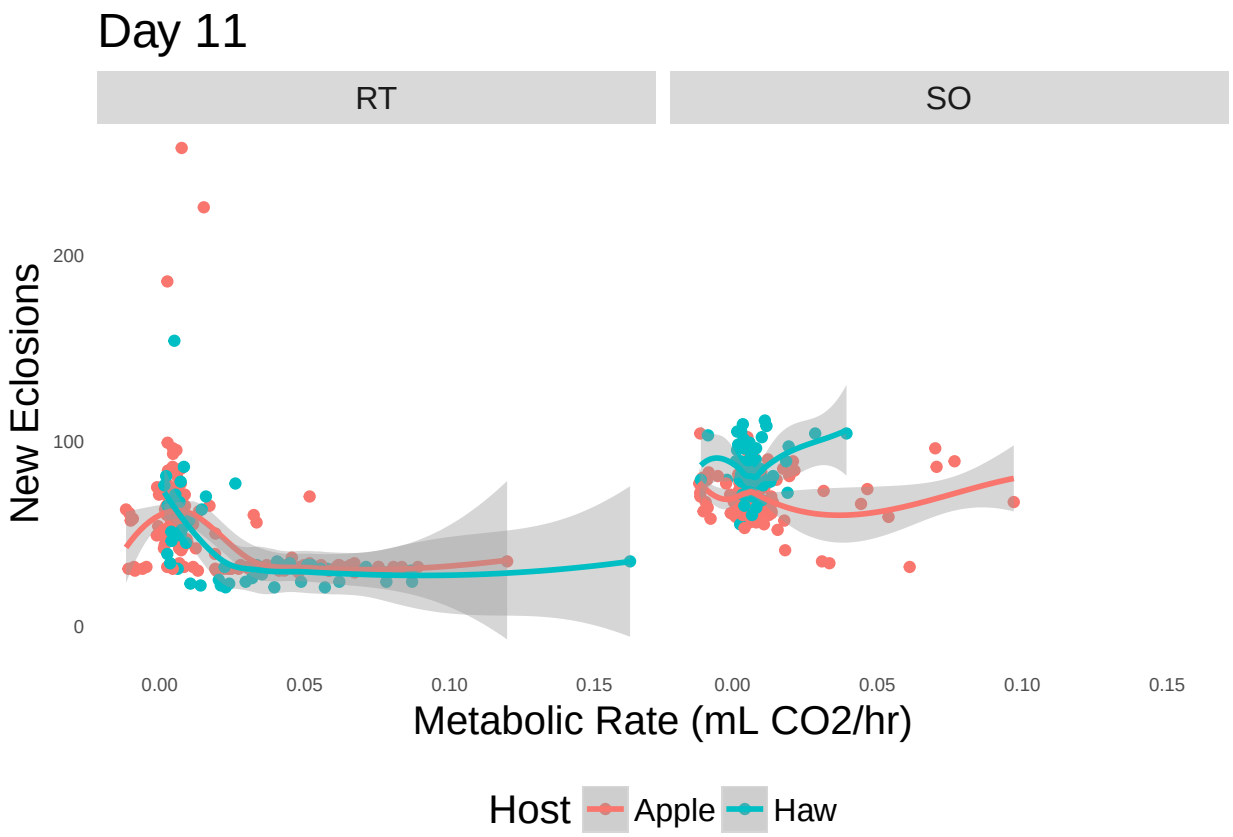
Explore relationship between eclosion days and MR

scatter plots

```
ggplot(data5.treatsub,aes(x=MR11.cor, y=neweclosions, colour=Host))+geom_point()+stat_smooth(method="lo
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Warning: Removed 609 rows containing non-finite values (stat_smooth).
```

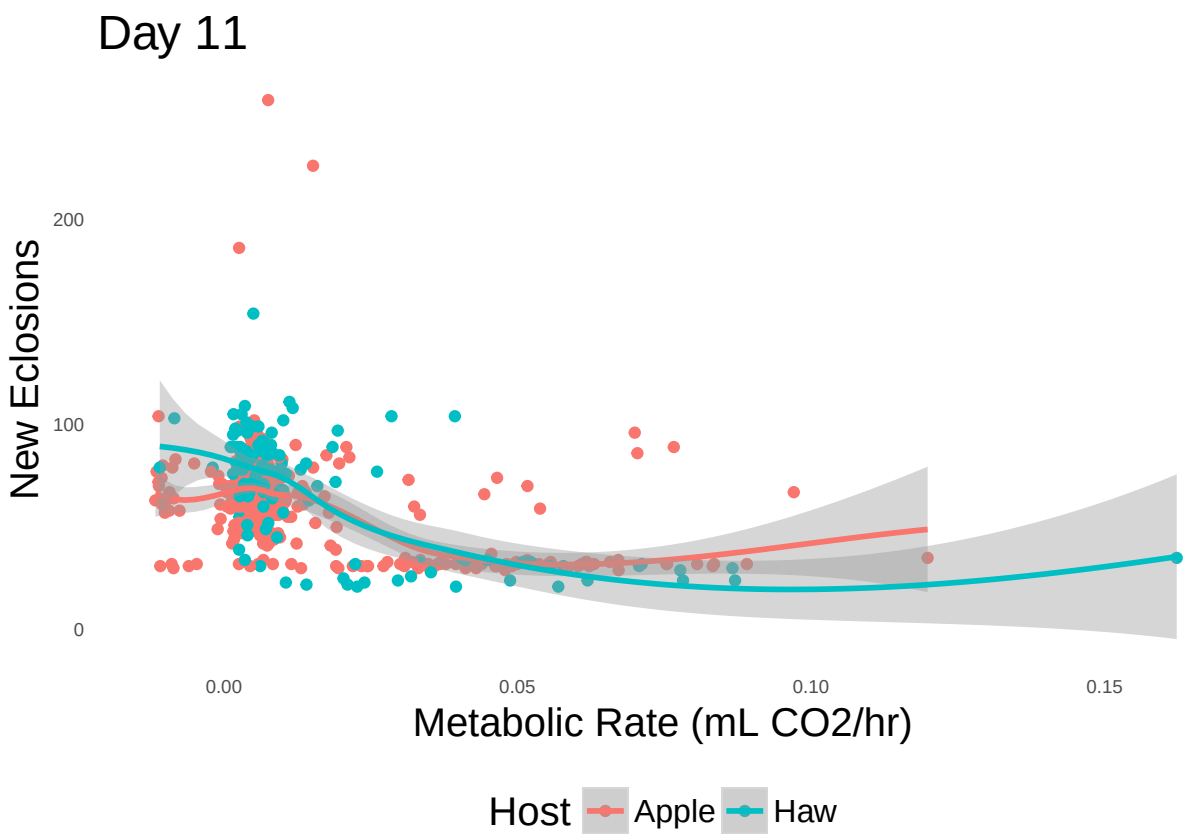
```
## Warning: Removed 609 rows containing missing values (geom_point).
```




```
#plotting mr11 on the x axis and new eclosions on the y axis; color points by host, fit curve to data
ggplot(data5.treatsub,aes(x=MR11.cor, y=neweclosions, colour=Host))+geom_point()+stat_smooth(method="lo
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Warning: Removed 609 rows containing non-finite values (stat_smooth).

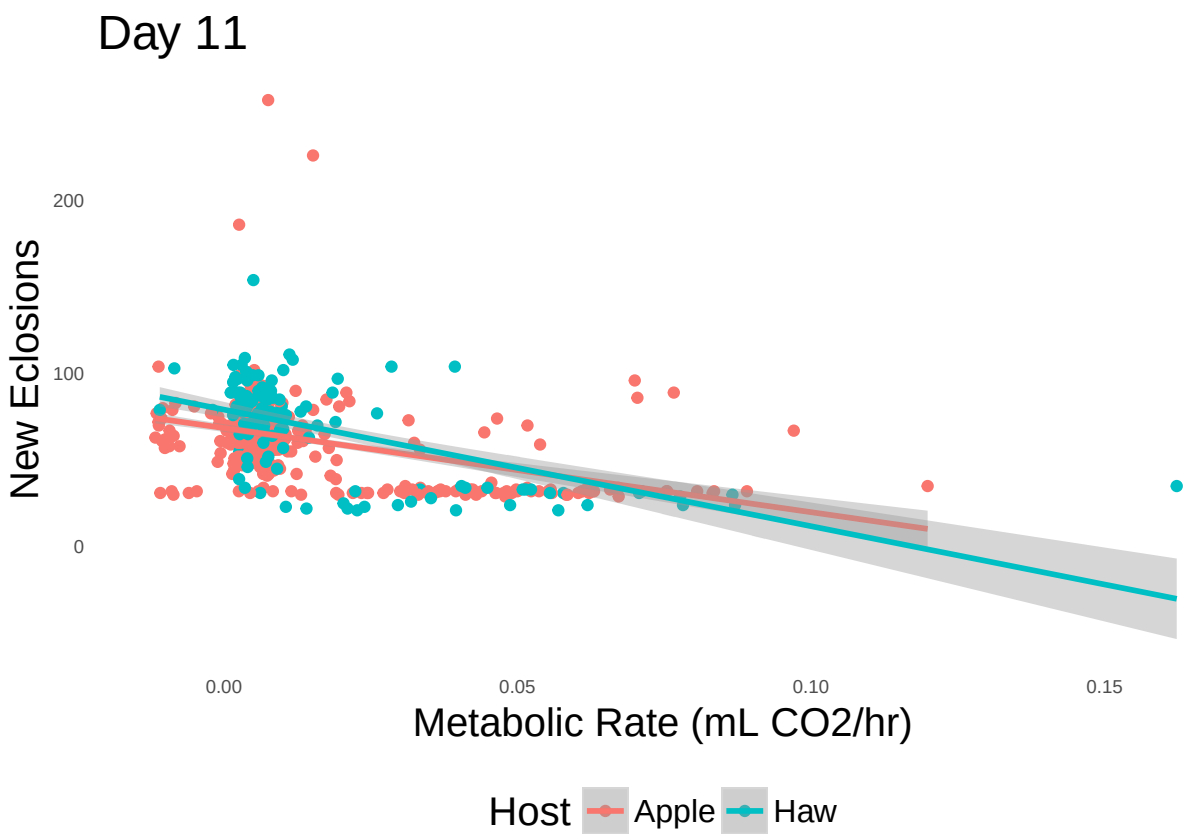
## Warning: Removed 609 rows containing missing values (geom_point).
```




```
#same - fit linear curve to data
ggplot(data5.treatsub,aes(x=MR11.cor, y=neweclosions, colour=Host))+geom_point()+stat_smooth(method="lm
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

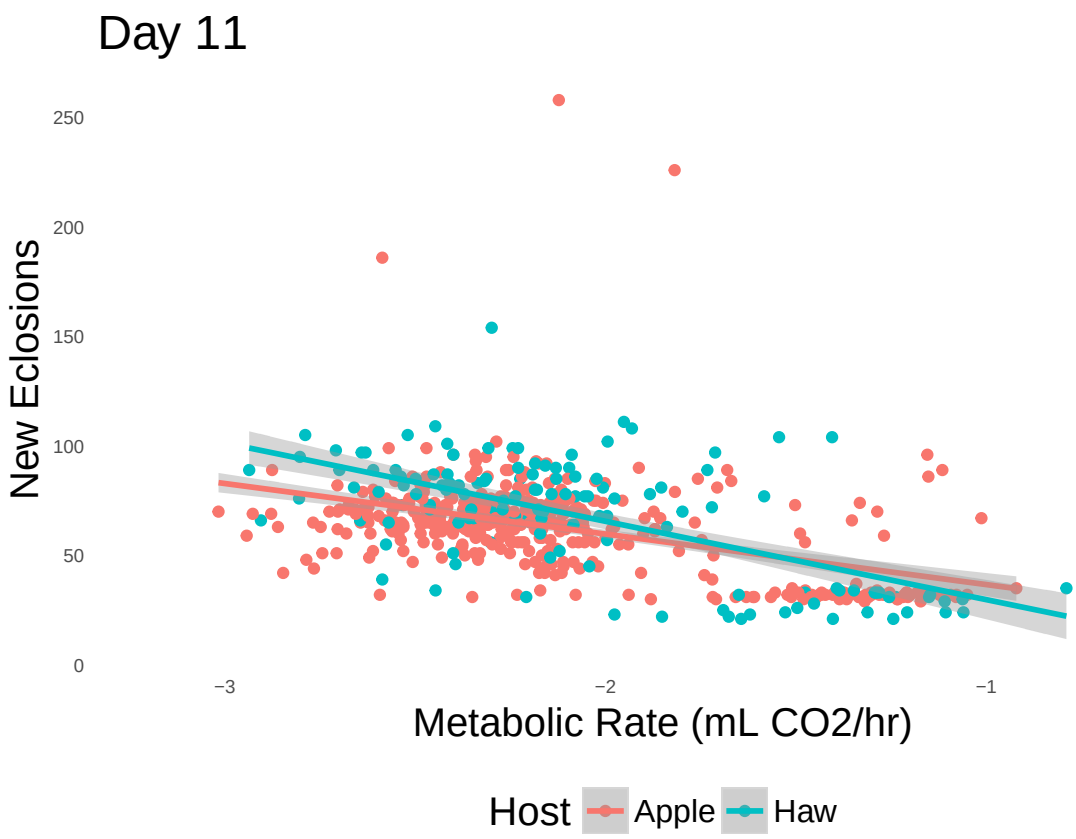
```
## Warning: Removed 609 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 609 rows containing missing values (geom_point).
```




```
#could log transform mr to make it more linear
ggplot(data5.treatsub,aes(x=log10(MR11.cor), y=neweclosions, colour=Host))+geom_point()+stat_smooth(meth
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(si
```

```
## Warning in FUN(X[[i]], ...): NaNs produced
## Warning in FUN(X[[i]], ...): NaNs produced
## Warning: Removed 644 rows containing non-finite values (stat_smooth).
## Warning: Removed 644 rows containing missing values (geom_point).
```



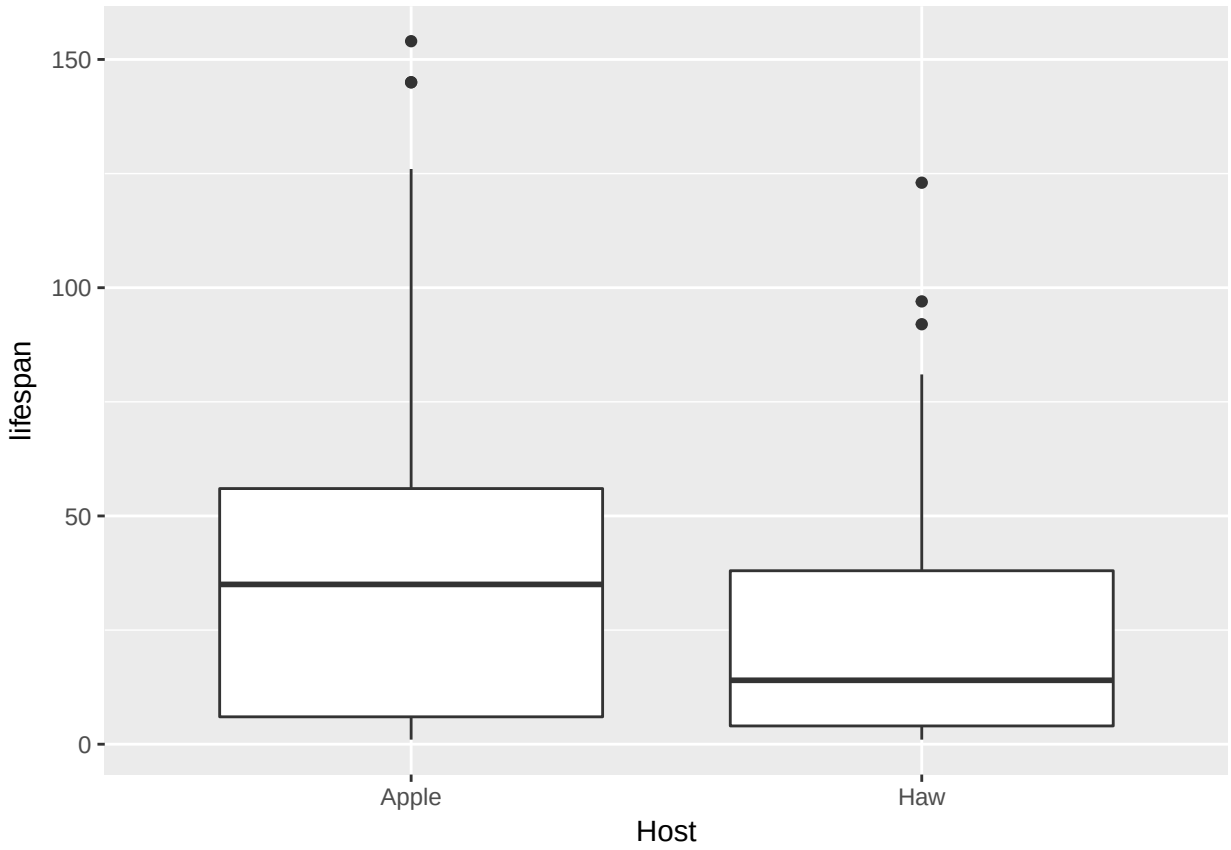
Calculating lifespan

```
data5.treatsub$lifespan<-difftime(as.Date(data5.treatsub$Adult_death_date, na.rm=TRUE), as.Date(data5.t
```

Figures of lifespan between hosts

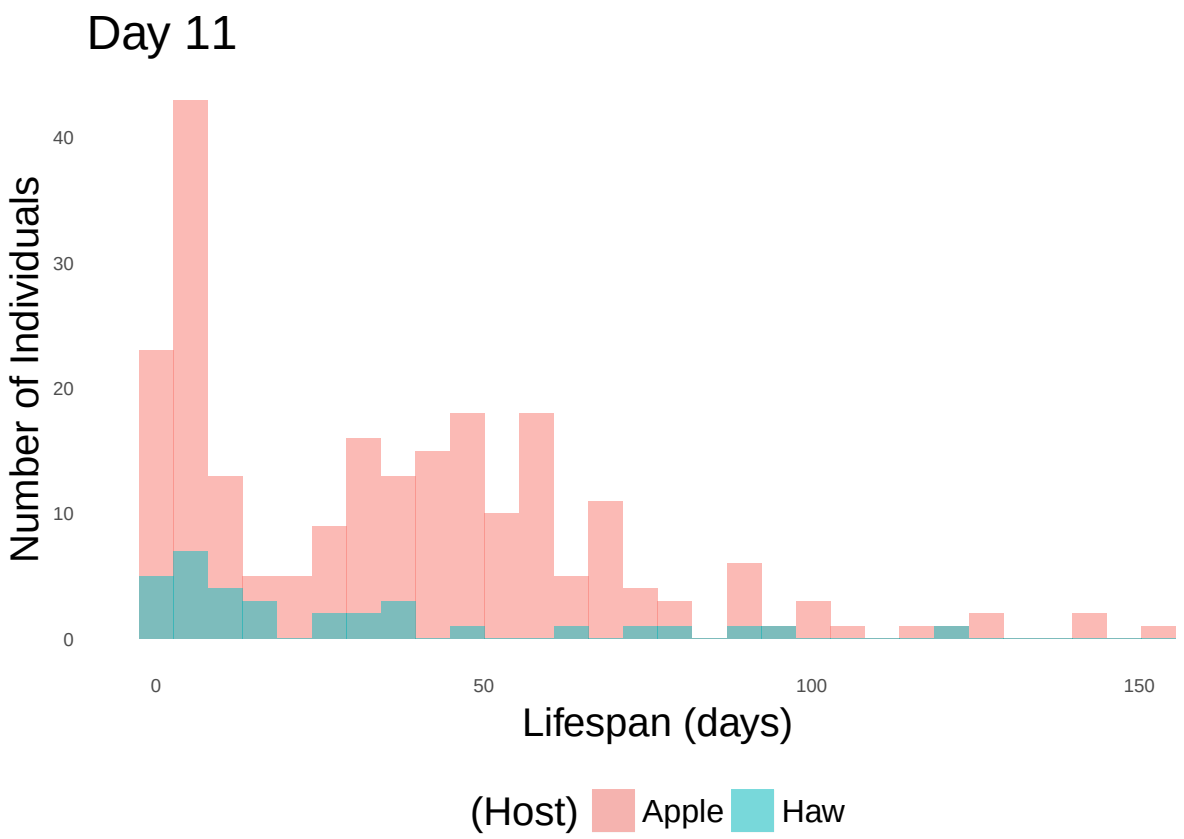
```
ggplot(data5.treatsub, aes(x=Host, y=lifespan))+geom_boxplot()
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## Warning: Removed 927 rows containing non-finite values (stat_boxplot).
```




```
ggplot(data5.treatsub, aes(x=lifespan, fill=(Host)))+geom_histogram(position = "identity", alpha=.5) +la
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(si
```

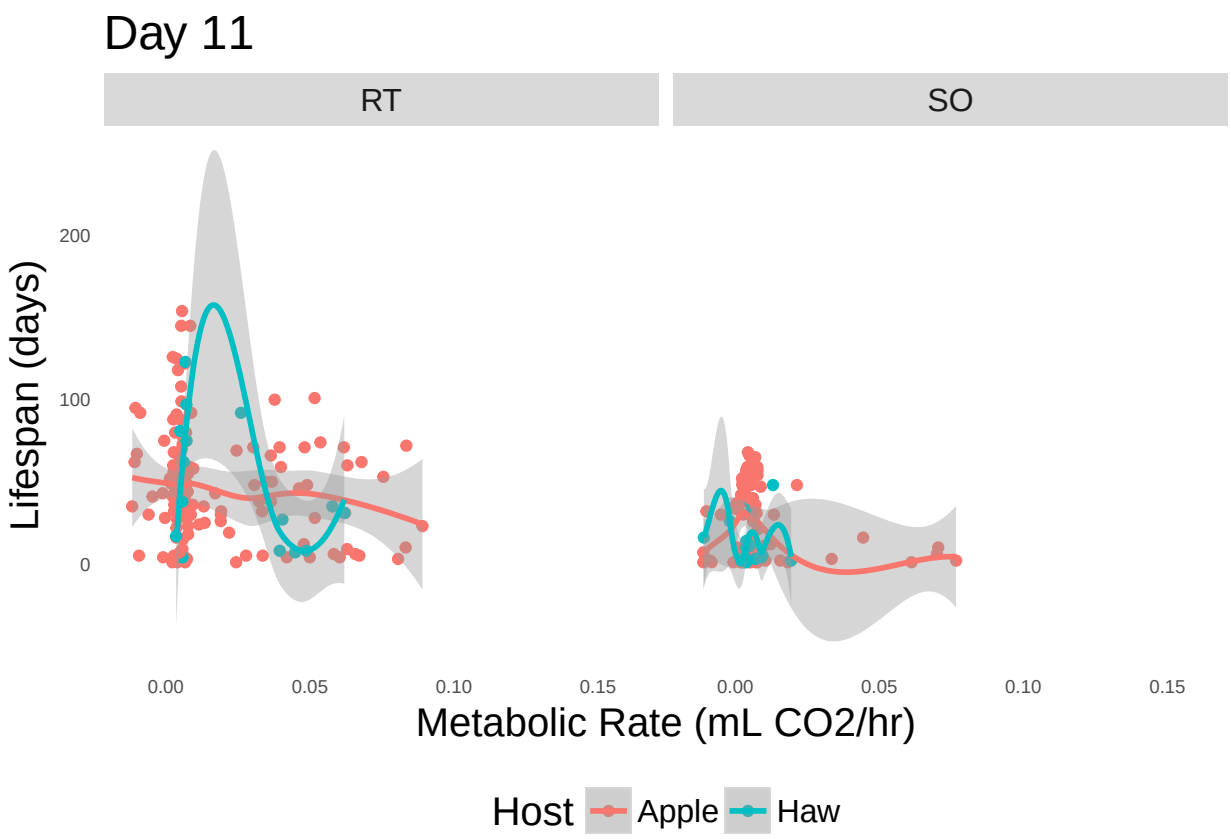
```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## Warning: Removed 927 rows containing non-finite values (stat_bin).
```



Figures Associating MR with lifespan

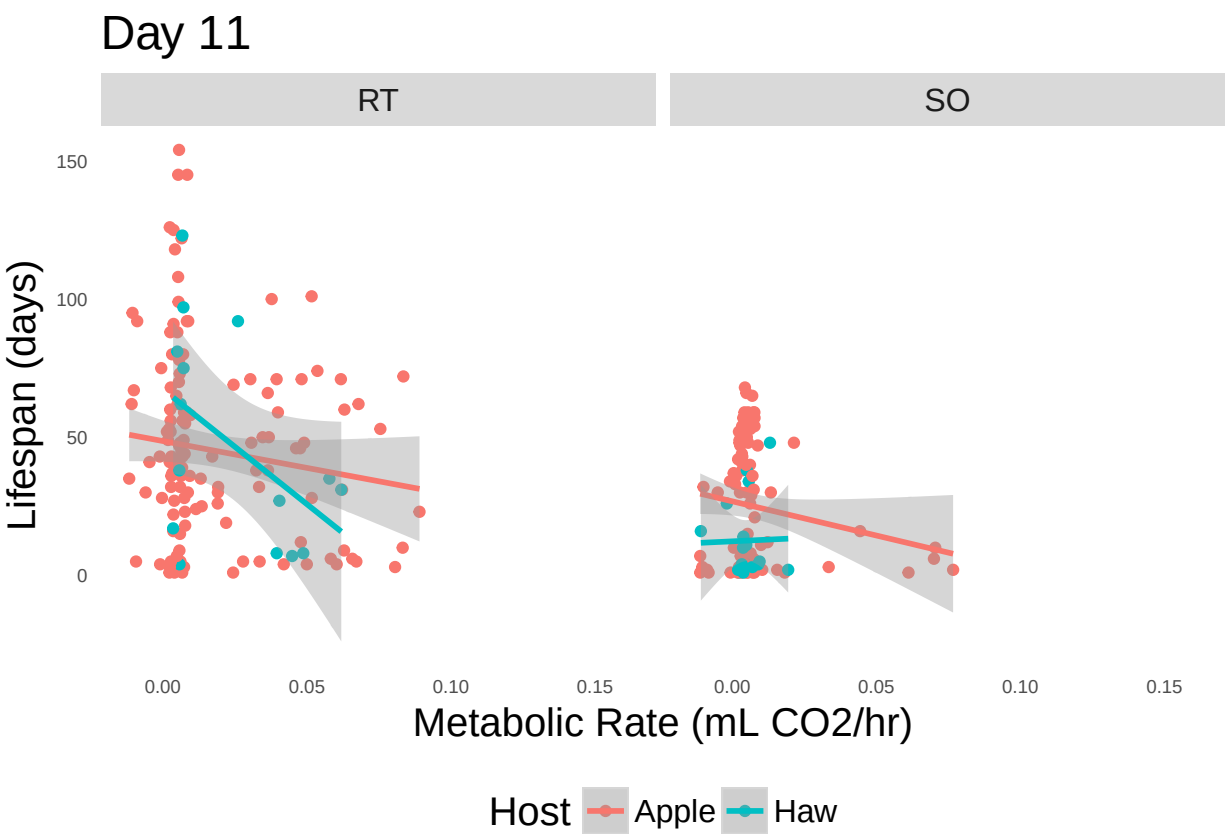
```
#Loess
ggplot(data5.treatsub,aes(x= MR11.cor, y=lifespan, colour=Host))+geom_point()+stat_smooth(method="loess
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## Warning: Removed 928 rows containing non-finite values (stat_smooth).
## Warning: Removed 928 rows containing missing values (geom_point).
```




```
#Linear
ggplot(data5.treatsub,aes(x=MR11.cor, y=lifespan, colour=Host))+geom_point()+stat_smooth(method="lm") +
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## Warning: Removed 928 rows containing non-finite values (stat_smooth).
## Warning: Removed 928 rows containing missing values (geom_point).
```



Day 15 Cohort

Repeat above, but with day 15, starting with time sequence

```
#glimpse(data$purge_time_2)
#hm(data$purge_time_2)
data$day15purge <- lubridate::hour(hm(data$purge_time_2))+lubridate::minute(hm(data$purge_time_2))/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
```

```
#Getting start and end (min and max) of purges and sample size for each host, cohort day, and tape
param <- data%>%
  group_by(cohort_day, tape)%>%
  summarise(max=max(day15purge, na.rm=TRUE), min=min(day10purge, na.rm=TRUE), n=length(cohort_day))

#goal: for this section, we want a sequence of times for day 15 purge
data2.15 <- data%>%
  group_by(cohort_day, tape)%>%
  mutate(.,day15purge.trans=seq(from = min(day15purge, na.rm=TRUE), to = max(day15purge, na.rm=TRUE), l
#glimpse(data2.15)
```

Calculating start and end time for total amount of hours of CO2 production

```
#glimpse(data$resp_time_2)
#hms(data$resp_time_2)
data2.15$day15resp <- lubridate::hour(hms(data$resp_time_2))+lubridate::minute(hms(data$resp_time_2))/6
```

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

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

```
#Obtaining total time in hours
data2.15$total_time_day15 <- (24 - data2.15$day15purge.trans) + data2.15$day15resp
```

Metabolic Rate Calculation

```
#getting denominator for mass-specific mr
data2.15$total_time_day15 * data$mass_day14
```

```
##    [1] 151.89085 244.99206 150.46594 234.57320  85.59947 167.88136
##    [7] 141.24237 206.76750 180.33549 107.08496 145.60199  87.54758
##   [13] 219.72889 188.20758 109.40677 166.33217 159.74371 148.21321
##   [19] 139.29352 132.69243 264.27349 145.03540 200.82687 195.30696
##   [25] 137.22043 205.96616 217.92167 169.64426 135.43424 185.96447
##   [31]        NA 189.15792 235.00100 217.26289 107.62898 177.09695
##   [37] 242.53165 217.52194 183.53694  90.97667 220.16532 155.78098
##   [43] 168.99835        NA 253.48203 220.72387 118.98165 138.53605
##   [49]        NA 222.12480 145.28668 208.30287        NA 152.61490
##   [55] 132.65624 118.17762 164.74597 142.90597 125.99792 239.47423
##   [61] 191.25882 137.47027 203.71383 149.26840  86.66776 205.22603
##   [67]  97.64181 170.79156 195.36288 154.11864 181.02458 219.17927
##   [73] 255.98020 170.75549 171.73724 185.57046  94.75507 113.18864
##   [79] 199.16352 217.87870 176.58789 231.42917 217.81565 147.70479
##   [85] 178.31970 151.90227 172.69412 235.22770        NA        NA
##   [91] 173.43143        NA 161.67000  91.22169 160.17619  88.70424
##   [97] 104.30327 154.93066 100.55314 135.34997 158.52950 142.55519
##  [103] 175.23779 139.58000 169.75765 141.66045 140.31098 131.80457
##  [109] 189.45019 141.89187 128.67182        NA 149.68498 167.49996
##  [115] 135.92331 173.37573 123.86904  91.83773 158.17120 115.64842
##  [121] 156.25751 142.34213 166.27355 136.34649 220.06983 167.20783
##  [127] 132.09796        NA 122.61788 146.20692 147.20671 145.89665
##  [133] 164.58226 115.15517 137.13308 188.94774 120.96411 206.39749
##  [139] 133.42545 123.53940 138.02871  93.64513 140.24610  76.19920
##  [145] 145.25555 132.18991 166.64653 204.62503 138.78969 129.51853
##  [151]        NA        NA 104.29522 153.22821 132.91935 125.37235
##  [157]  94.20718 187.64379 154.92192 109.38803 139.56381  95.03147
##  [163]  96.64490 193.94313 130.03819 171.59728 201.32973  75.63907
##  [169] 157.46692 118.95714 120.10717 170.30659 118.87453 188.22498
##  [175] 188.65869 129.95582  93.55194 117.67849 133.91280 105.32226
##  [181] 187.08785 113.11787 149.29462 103.57299 175.68833 138.54515
##  [187] 100.13237 158.88923 102.29142 161.39253 135.52780 125.88503
##  [193] 145.33989 125.99277 194.01531 120.26475 113.70353 133.49780
```

```
##  [199] 213.14419 156.11278 127.26062 151.08781 111.35458 145.92023
##  [205]  77.42203 167.94754 159.35110 118.51955 181.54629        NA
##  [211]        NA 210.92280        NA 239.07768 223.58864 248.24841
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##  [223] 156.70936 185.37084 188.98484 167.57158 293.79324 169.37080
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##  [259]        NA 181.98857 221.75317 157.50294 253.53012 325.74404
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##  [271] 156.07641 177.37436  62.72913 106.17287 114.52053 249.50545
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##  [295] 143.53541 208.47114 150.71091 232.84130 287.52325 169.39526
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##  [307]        NA 213.37724 187.11563 244.50529 155.81848 161.84259
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##  [319] 167.63052 140.58888 243.49872 100.45010        NA        NA
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##  [331]  79.80375 176.82501 224.76932 242.91789 165.13514 228.38918
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```

```
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```

```
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```

```
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## [1393]  88.81461 119.27532 114.94706        NA        NA        NA
## [1399]  85.11790 208.96956        NA 137.09795 100.60509        NA
## [1405]  94.15180 110.77646 112.77084  76.34200        NA 130.87021
## [1411]  85.11067 176.66107 160.55216  46.49058 122.77251 157.58435
## [1417] 114.85455 180.72516  47.55750  49.82075 222.28067 156.72825
## [1423] 192.32518 137.86516 118.75153 154.49490 171.13653 127.39541
## [1429]  41.67827 156.30701        NA        NA 102.52178 139.47623
## [1435]        NA        NA 119.66567 236.07220 121.74142 189.48305
## [1441] 162.62837        NA 116.84083 125.88978        NA 244.67069
## [1447]        NA 139.92927 113.31414  95.29627  48.50283 140.51240
## [1453] 146.43951  78.81370 218.29109 123.35742 185.91030        NA
## [1459] 112.36917  46.53600  58.05370        NA        NA 126.67133
## [1465]        NA        NA  21.98117  58.07681  97.73594  86.29161
## [1471] 104.33818  39.45489 104.97681 155.53929 128.79015 136.88200
## [1477] 160.23670 121.34268  90.06578 130.07233 106.71204        NA
## [1483] 104.33652        NA        NA 139.33920 141.37884        NA
## [1489] 170.06010 116.97167 160.57186        NA 169.83861 118.96600
```

```
## [1495] 125.37667 119.82736  86.32223 192.16016 133.57331  41.94566
## [1501] 105.04054 116.81096        NA        NA 209.23848 166.76409
## [1507]  90.18104  98.32764 177.78933  76.49713 189.06318 232.21556
## [1513] 198.26908 157.65782 181.37117 172.30585  59.78497 177.88338
## [1519] 183.95332 167.10854 230.02523        NA 215.54974 201.50898
## [1525] 112.80392 274.20991 226.16207 158.05350 103.14852 100.17539
## [1531] 159.97480 119.93497 165.56494 160.68316 164.00951 190.76995
## [1537] 183.05694        NA        NA 149.10296 214.80001 144.76424
## [1543] 178.52991 200.31255 175.95890 183.33887 178.24855 245.58114
## [1549] 147.72093 263.30008 117.47655 118.72364 245.91689 137.95587
## [1555] 230.63749 177.45229 196.65643 101.93301 236.50376 248.94311
## [1561] 242.58495  98.23182 245.84062 169.47697 172.44119 114.44906
## [1567] 166.00263 147.84572 192.37546 220.97363  77.67518 186.77626
## [1573]        NA        NA  79.43571  92.24309  75.48601 125.34606
## [1579] 161.20744  68.31486 218.24924 203.77884  78.94708  81.34468
## [1585]  96.84808 153.67885 170.69681 121.80736 144.49813 156.06282
## [1591]  73.20968 177.53706 197.98525  94.15520 140.17270 166.06029
## [1597] 129.86142 140.57108 117.42571 143.67859        NA        NA
## [1603] 148.85326 103.02119 152.28510 143.84563 136.54512 202.20190
## [1609] 124.28306  51.67115 191.41012 124.85152 132.82674 195.58169
## [1615] 192.28484  77.13881 171.38010 172.64505 178.81140 133.37580
## [1621] 185.69787        NA 121.39132 196.66217 126.38441 166.38630
## [1627]  67.91207        NA        NA        NA 160.26970 161.05106
## [1633] 224.63528 174.32319  97.34354 108.46619 193.05100  76.36842
## [1639] 226.22979 185.55198  94.76189 174.31425 190.58042 159.07028
## [1645] 231.45871 166.33221 126.24730 183.84861 217.99322  99.20873
## [1651] 252.68084  96.85710  81.13505 152.40973        NA        NA
## [1657] 123.73153 239.64653 154.33846  85.85031 265.68861 163.54675
## [1663] 250.33914        NA 179.42565 114.18896 182.68615 190.13307
## [1669] 190.54843 262.25482 119.48470 146.59442 169.41549 215.11515
## [1675] 129.80599 233.69133        NA 246.40602  95.98497 155.47802
## [1681] 196.01322        NA        NA 134.50125 219.59214 152.04994
## [1687] 180.25875 195.58610 156.19833 161.23809 197.13476        NA
## [1693]  75.56701  72.35841 116.12870 194.59992 128.69037 163.67792
## [1699] 141.03004 225.71903 188.40986  63.21329  76.09883 155.49287
## [1705]  82.06272        NA        NA 196.38645 142.28533 150.06583
## [1711]  91.09380 135.44795 114.54000  85.28640 185.15258 144.66357
## [1717] 105.45520 128.83733 142.08705  96.83333 144.21960 168.10950
## [1723] 120.18155 199.70853 190.39113 147.54600 217.05440  73.70763
## [1729]        NA        NA        NA 248.79800 182.77229 232.41392
## [1735] 244.36720 213.50815 221.64391 169.24760 166.72520 140.56383
## [1741] 242.17462 172.30871  77.61304 165.98987 177.25161 148.76411
## [1747] 164.73786 234.53318 253.50825  48.96582 183.86504  76.23554
## [1753] 129.85366  55.26739  53.70520 213.67313 166.38941 214.57532
## [1759] 179.90624 132.03194 112.45647        NA        NA 219.78250
## [1765] 138.01833 156.32913 156.26399 155.67097 217.61147  73.94129
## [1771]  72.29062  66.85996 145.28368 145.90492 217.95305 199.61770
## [1777] 215.61712 167.38887 245.40952  81.27106 240.01241 149.43238
## [1783] 233.98965 187.03385  63.66374  94.71431 161.29734 236.19405
## [1789] 248.68916 177.33225 233.25807 261.99605  95.61695        NA
## [1795]        NA 253.88243 190.76824 168.04693 182.70481  77.43916
## [1801] 116.19455 192.02371 161.06931 201.83333 232.88043 233.91636
## [1807] 233.74640 210.00292 130.27605 208.92148 243.84071 218.50840
## [1813]        NA        NA 153.58400 179.45459 219.89365 248.00314
```

```
## [1819] 214.50364 189.38241 153.78191 175.82525  93.24695 169.50176
## [1825] 257.13091  88.76400 182.33058 177.13056 262.24014 207.97490
## [1831]        NA        NA 178.46812 177.07151 246.56321  93.49180
## [1837] 100.34719 231.49734  74.55641 263.23700 151.34114 101.99627
## [1843] 187.35244  95.40382 225.77281 196.91302 137.03403 166.55808
## [1849] 251.21986 150.64306        NA        NA 147.06193 145.58719
## [1855] 198.11833  87.37408 185.54678 217.81529 228.37900 172.61262
## [1861] 233.31954 211.46488 216.23507 184.86772 156.03840 226.67209
## [1867] 230.76247 185.24200 183.39856        NA        NA 199.68795
## [1873] 164.27075 164.32162 200.03163        NA        NA 226.41480
## [1879] 157.70811 235.94518 155.81043        NA        NA 260.40647
## [1885] 190.04787 164.00737 274.88237 282.88944 209.70457        NA
## [1891]        NA 275.67330 222.38083 166.19319 211.14833 149.70539
## [1897]        NA        NA 296.31403 301.30817 171.42998 241.50760
## [1903]        NA        NA        NA        NA        NA        NA
## [1909]        NA
```

```
#Metabolic Rate
data2.15$MR15<- data$resp_day15/(data2.15$total_time_day15)

#Mass specfic metabolic rate
data2.15$msMR15<- data$resp_day15/(data2.15$total_time_day15 * data$mass_day14)
```

Controlling for Blanks

```
data3.15 <- data2.15%>%
  group_by(cohort_day, tape)%>%
  filter(Site_name=="Blank")%>%
  summarise(mean.blank2=mean(MR15,na.rm=TRUE))

#check columns
#glimpse(data3.15)
data3.15$mean.blank2
```

```
##  [1] 0.0005641578 0.0004986472 0.0004491015 0.0013998016 0.0007086216
##  [6] 0.0004586952 0.0008301721 0.0010078476 0.0006573110 0.0004078814
## [11] 0.0006396536 0.0010072904 0.0009850978 0.0006266569 0.0013045121
## [16] 0.0005749230 0.0006262029 0.0003713112 0.0005021056 0.0006112672
## [21] 0.0004834431 0.0004612535 0.0004729824 0.0005167701 0.0005268374
## [26] 0.0002867896 0.0004687064 0.0003718163 0.0050939720 0.0012094708
## [31] 0.0037153831 0.0004513217 0.0005082236 0.0007341679 0.0004501632
## [36] 0.0002760230 0.0012459416 0.0017019482
```

```
#merge data3 and data2 by cohort day and tape
data4.15 <- inner_join(data2.15, data3.15, by=c("cohort_day", "tape"))
data4.15$mean.blank2
```

```
##    [1] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##    [6] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##   [11] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##   [16] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##   [21] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##   [26] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##   [31] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
```

```
##   [36] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##   [41] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0005641578
##   [46] 0.0005641578 0.0005641578 0.0005641578 0.0005641578 0.0004986472
##   [51] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
##   [56] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
##   [61] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
##   [66] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
##   [71] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
##   [76] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
##   [81] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
##   [86] 0.0004986472 0.0004986472 0.0004986472 0.0004986472 0.0004986472
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##   [96] 0.0004491015 0.0004491015 0.0004491015 0.0004491015 0.0004491015
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## [1781] 0.0006396536 0.0006396536 0.0006396536 0.0006396536 0.0006396536
## [1786] 0.0006396536 0.0006396536 0.0006396536 0.0006396536 0.0006396536
## [1791] 0.0006396536 0.0006396536 0.0006396536 0.0006396536 0.0006396536
## [1796] 0.0006266569 0.0006266569 0.0006266569 0.0006266569 0.0006266569
## [1801] 0.0006266569 0.0006266569 0.0006266569 0.0006266569 0.0006266569
## [1806] 0.0006266569 0.0006266569 0.0006266569 0.0006266569 0.0006266569
## [1811] 0.0006266569 0.0006266569 0.0006266569 0.0006266569 0.0009850978
## [1816] 0.0009850978 0.0009850978 0.0009850978 0.0009850978 0.0009850978
## [1821] 0.0009850978 0.0009850978 0.0009850978 0.0009850978 0.0009850978
## [1826] 0.0009850978 0.0009850978 0.0009850978 0.0009850978 0.0009850978
## [1831] 0.0009850978 0.0009850978 0.0005749230 0.0005749230 0.0005749230
## [1836] 0.0005749230 0.0005749230 0.0005749230 0.0005749230 0.0005749230
## [1841] 0.0005749230 0.0005749230 0.0005749230 0.0005749230 0.0005749230
## [1846] 0.0005749230 0.0005749230 0.0005749230 0.0005749230 0.0005749230
## [1851] 0.0005749230 0.0005749230 0.0013045121 0.0013045121 0.0013045121
## [1856] 0.0013045121 0.0013045121 0.0013045121 0.0013045121 0.0013045121
## [1861] 0.0013045121 0.0013045121 0.0013045121 0.0013045121 0.0013045121
## [1866] 0.0013045121 0.0013045121 0.0013045121 0.0013045121 0.0013045121
## [1871] 0.0013045121 0.0003713112 0.0003713112 0.0003713112 0.0003713112
## [1876] 0.0003713112 0.0003713112 0.0006262029 0.0006262029 0.0006262029
## [1881] 0.0006262029 0.0006262029 0.0006262029 0.0005021056 0.0005021056
## [1886] 0.0005021056 0.0005021056 0.0005021056 0.0005021056 0.0005021056
## [1891] 0.0005021056 0.0004834431 0.0004834431 0.0004834431 0.0004834431
## [1896] 0.0004834431 0.0004834431 0.0004834431 0.0005167701 0.0005167701
## [1901] 0.0005167701 0.0005167701 0.0005167701 0.0005167701 0.0002867896
## [1906] 0.0002867896 0.0002867896 0.0002867896 0.0002867896
```

```
#do some corrections
data5.15 <- data4.15%>%
```

```
  mutate(MR15.cor = MR15 - mean.blank2, msMR15.cor = msMR15 - mean.blank2)
#glimpse(data5.15)

#Filter out negatives
data5.15.neg <- data5.15%>%
  filter(MR15.cor<0)
```

Calculate Eclosions Dates

```
#Focus only on RT and SO treatments
data5.15.treatsub<-data5%>%
  filter(treatment!="GC"&treatment!="")

data5.15$neweclosions <- difftime(as.Date(data5.15$eclosion_date), as.Date(data5.15$Eclosion_reference_

data5.15.treatsub$neweclosions<-difftime(as.Date(data5.15.treatsub$eclosion_date), as.Date(data5.15.trea
```

Test differences in eclosion timing between host and experiment for Day 15 (ANOVA)

```
#Two Way ANOVA
mod1<- aov(neweclosions ~ Host*treatment, data=data5.15.treatsub)
summary(mod1)
```

```
##                 Df Sum Sq Mean Sq F value   Pr(>F)
## Host             1   3685    3685   9.705  0.00193 **
## treatment        1  82798   82798 218.056  < 2e-16 ***
## Host:treatment   1   9903    9903  26.080 4.45e-07 ***
## Residuals      579 219851     380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 606 observations deleted due to missingness
```

```
#narrow down to SO & RT
data5.15SO<-data5.15.treatsub%>%
  filter(treatment=="SO")

data5.15RT<-data5.15.treatsub%>%
  filter(treatment=="RT")

#One Way ANOVA for RT & SO
mod2RT15<-aov(neweclosions~Host, data=data5.15)
summary(mod2RT15)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Host          1   3685    3685    6.85 0.0091 **
## Residuals   581 312552     538
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 1326 observations deleted due to missingness
```

```
mod2SO15<-aov(neweclosions~Host, data=data5.15)
summary(mod2SO15)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Host          1   3685    3685    6.85 0.0091 **
## Residuals   581 312552     538
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 1326 observations deleted due to missingness
```

```
#how balanced is it?
data5.SO%>%
  group_by(Host)%>%
  summarise(n=length(Host))
```

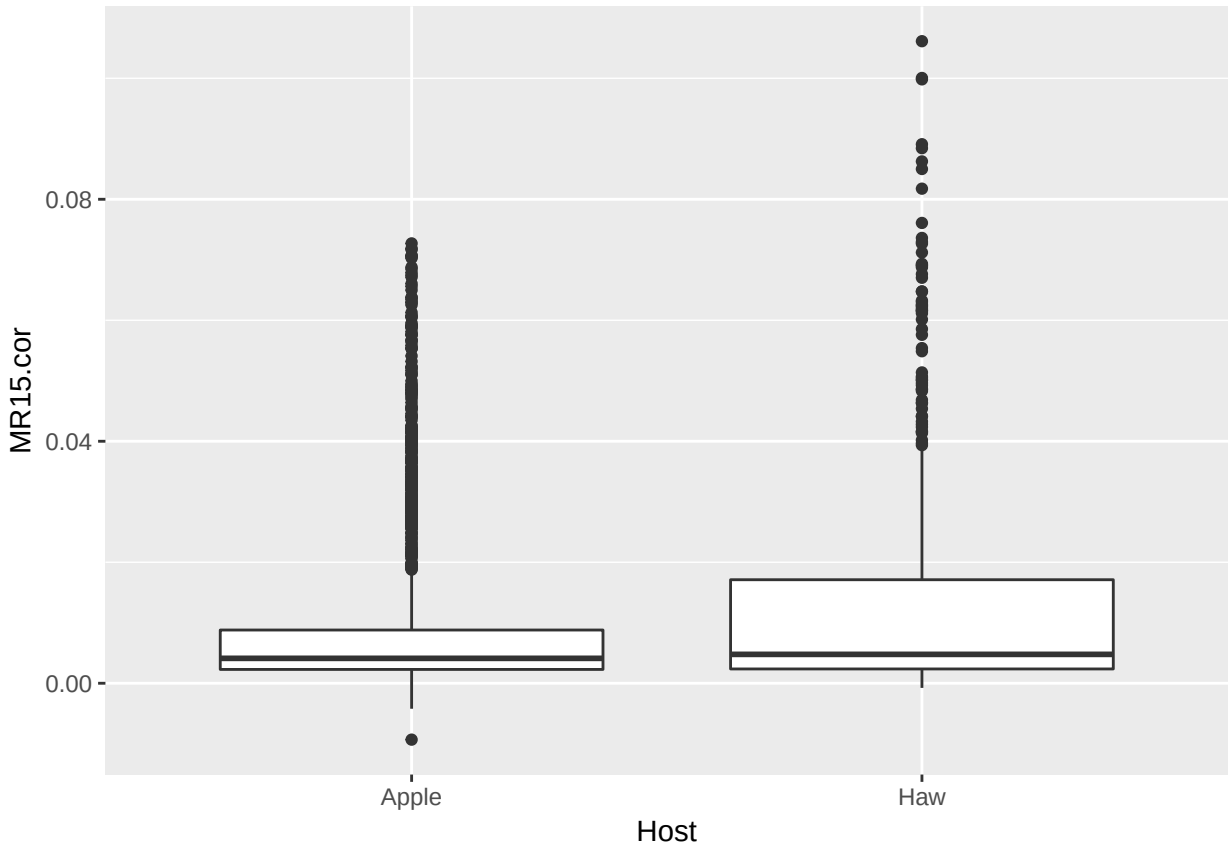
```
## # A tibble: 2 x 2
##   Host      n
##   <chr> <int>
## 1 Apple   428
## 2 Haw     163
```

This ANOVA test reflects the same results from the ANOVA done on Day 11.

Figures looking at MR between hosts

```
ggplot(data5.15, aes(x=Host, y=MR15.cor))+geom_boxplot()
```

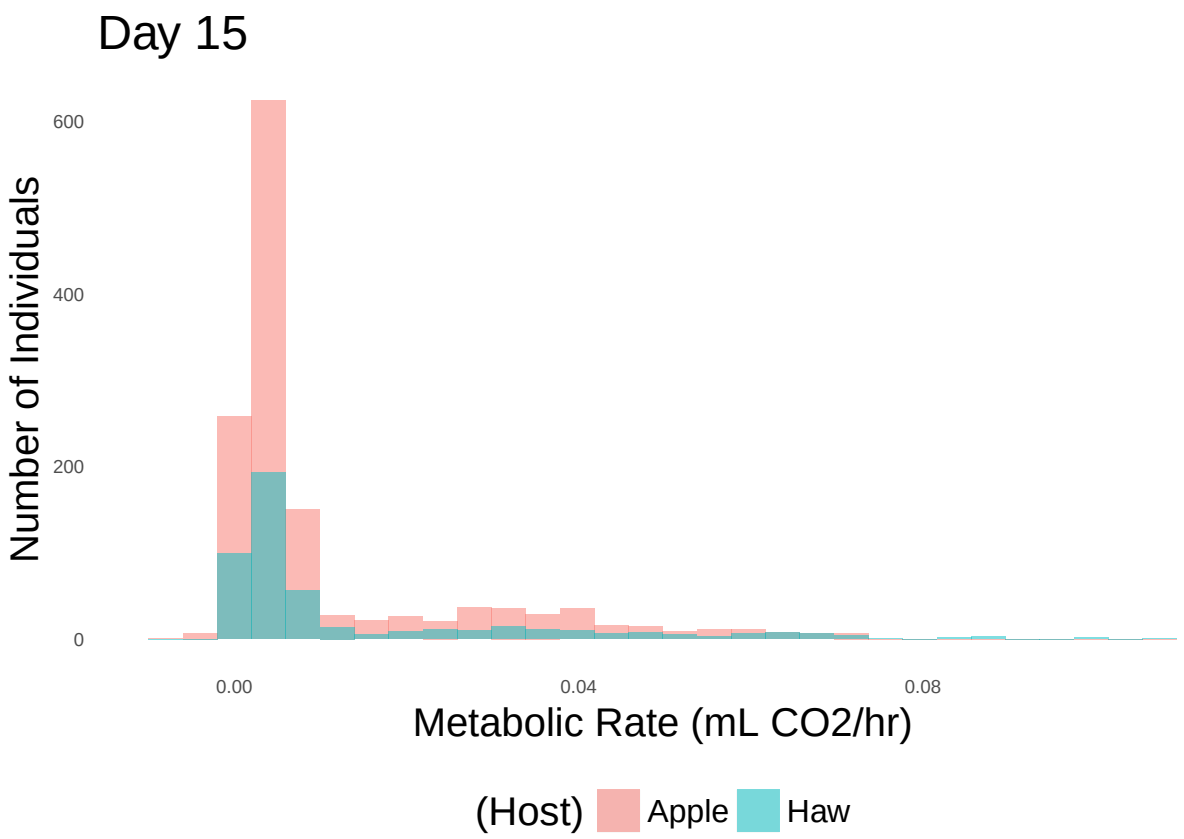
```
## Warning: Removed 63 rows containing non-finite values (stat_boxplot).
```




```
ggplot(data5.15, aes(x=MR15.cor, fill=(Host)))+geom_histogram(position = "identity", alpha=.5) +labs(x =
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

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

```
## Warning: Removed 63 rows containing non-finite values (stat_bin).
```



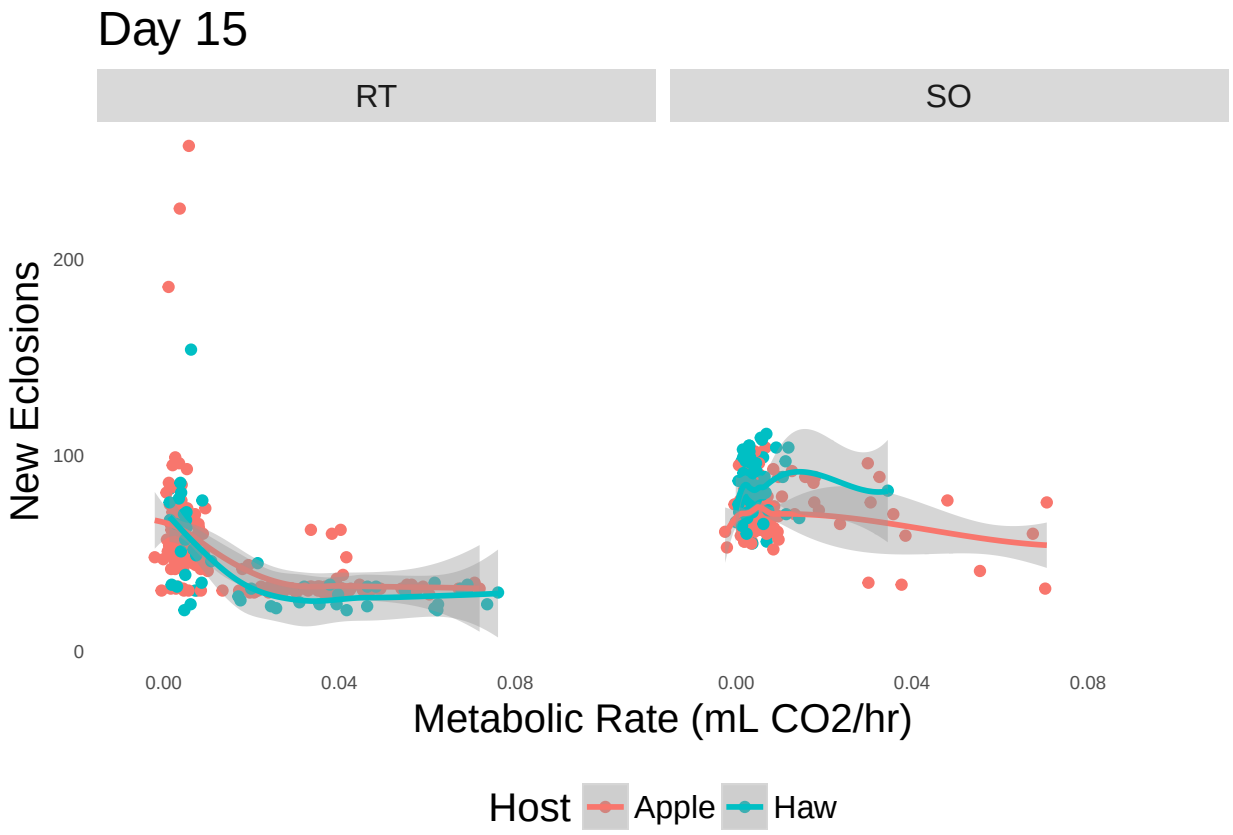
Explore relationship between eclosion days and MR

scatter plots

```
#Filter out GC and blank treatments
data5.15.treatsub<-data5.15%>%
  filter(treatment!="GC"&treatment!="")

ggplot(data5.15.treatsub, aes(x=MR15.cor, y=neweclosions, colour=Host))+geom_point()+stat_smooth(method=
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## Warning: Removed 607 rows containing non-finite values (stat_smooth).
## Warning: Removed 607 rows containing missing values (geom_point).
```

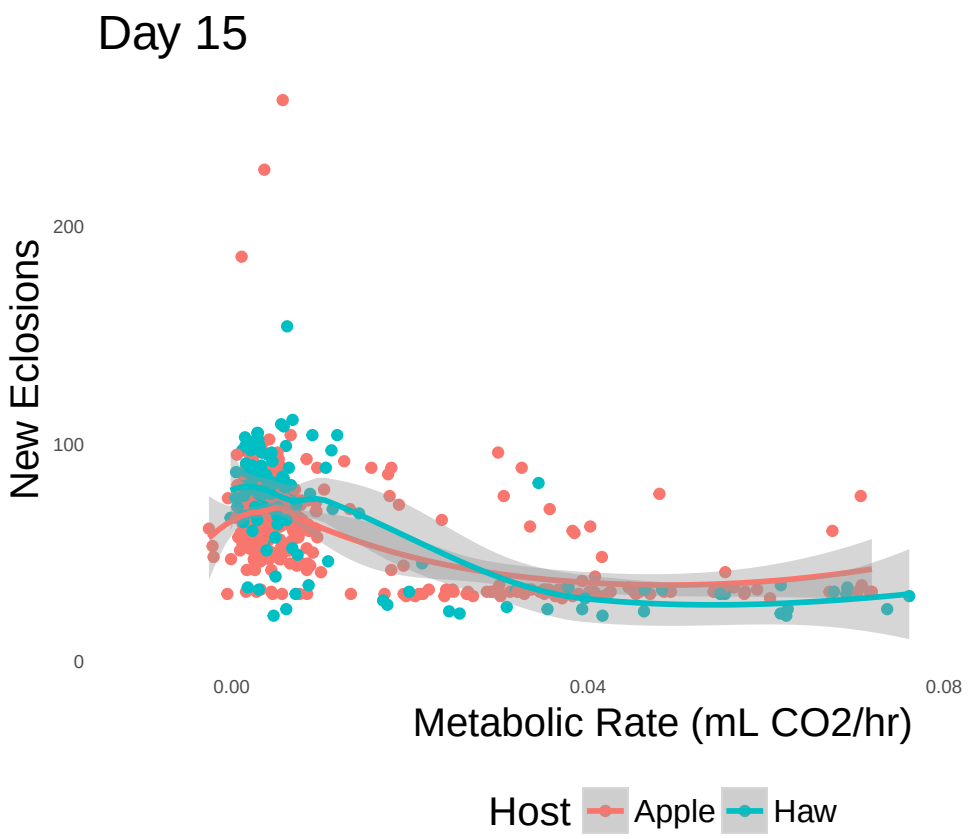



```
#plotting mr15 on the x axis and new eclosions on the y axis; color points by host, fit curve to data
ggplot(data5.15.treatsub,aes(x=MR15.cor, y=neweclosions, colour=Host))+geom_point()+stat_smooth(method=
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
```

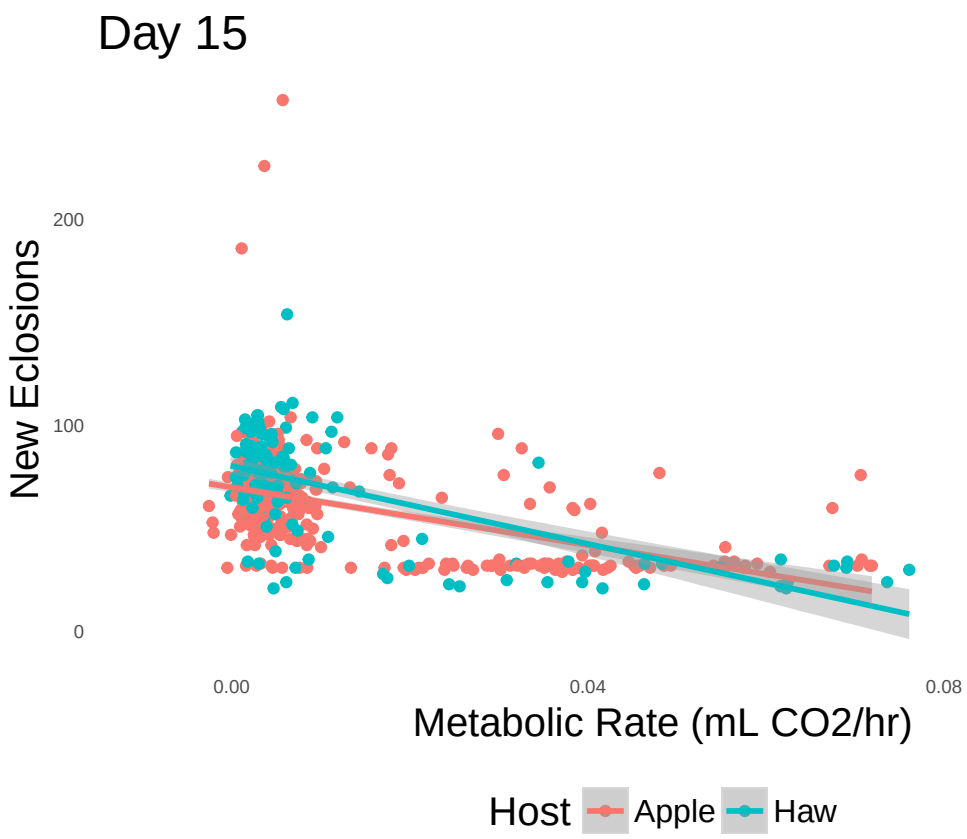
```
## Warning: Removed 607 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 607 rows containing missing values (geom_point).
```



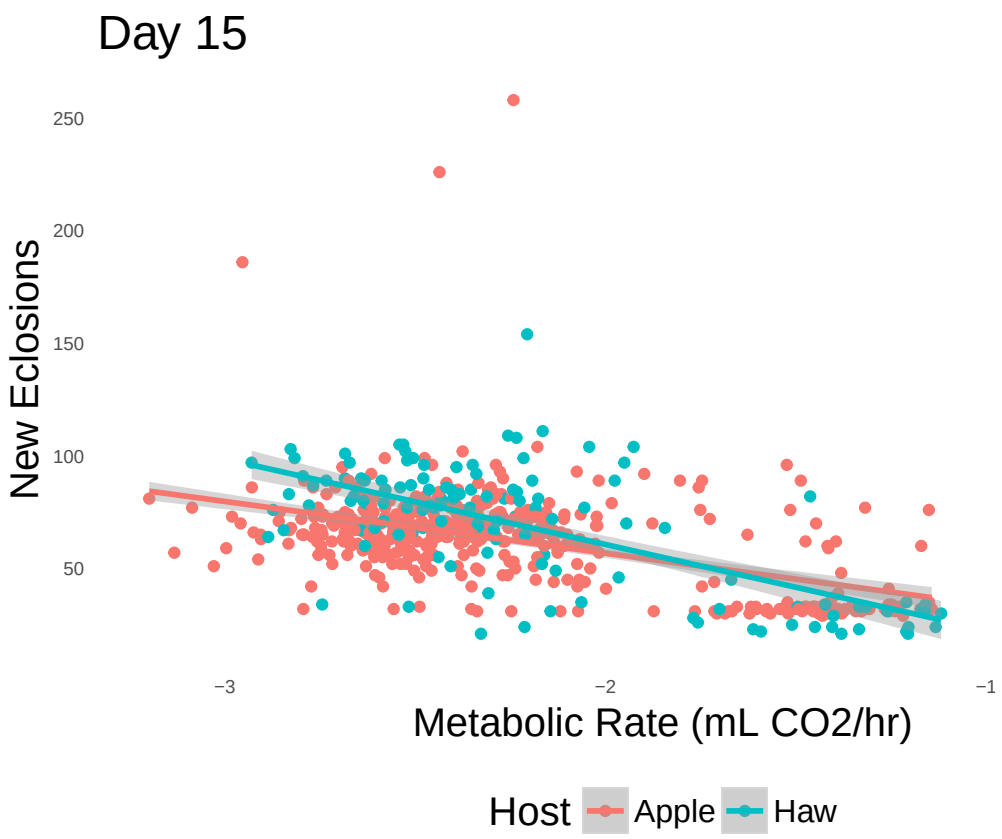

```
#same - fit linear curve to data
ggplot(data5.15.treatsub,aes(x=MR15.cor, y=neweclosions, colour=Host))+geom_point()+stat_smooth(method=
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## Warning: Removed 607 rows containing non-finite values (stat_smooth).
## Warning: Removed 607 rows containing missing values (geom_point).
```




```
#could log transform mr to make it more linear
ggplot(data5.15.treatsub,aes(x=log10(MR15.cor), y=neweclosions, colour=Host))+geom_point()+stat_smooth(
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## Warning in FUN(X[[i]], ...): NaNs produced
## Warning in FUN(X[[i]], ...): NaNs produced
## Warning: Removed 619 rows containing non-finite values (stat_smooth).
## Warning: Removed 619 rows containing missing values (geom_point).
```

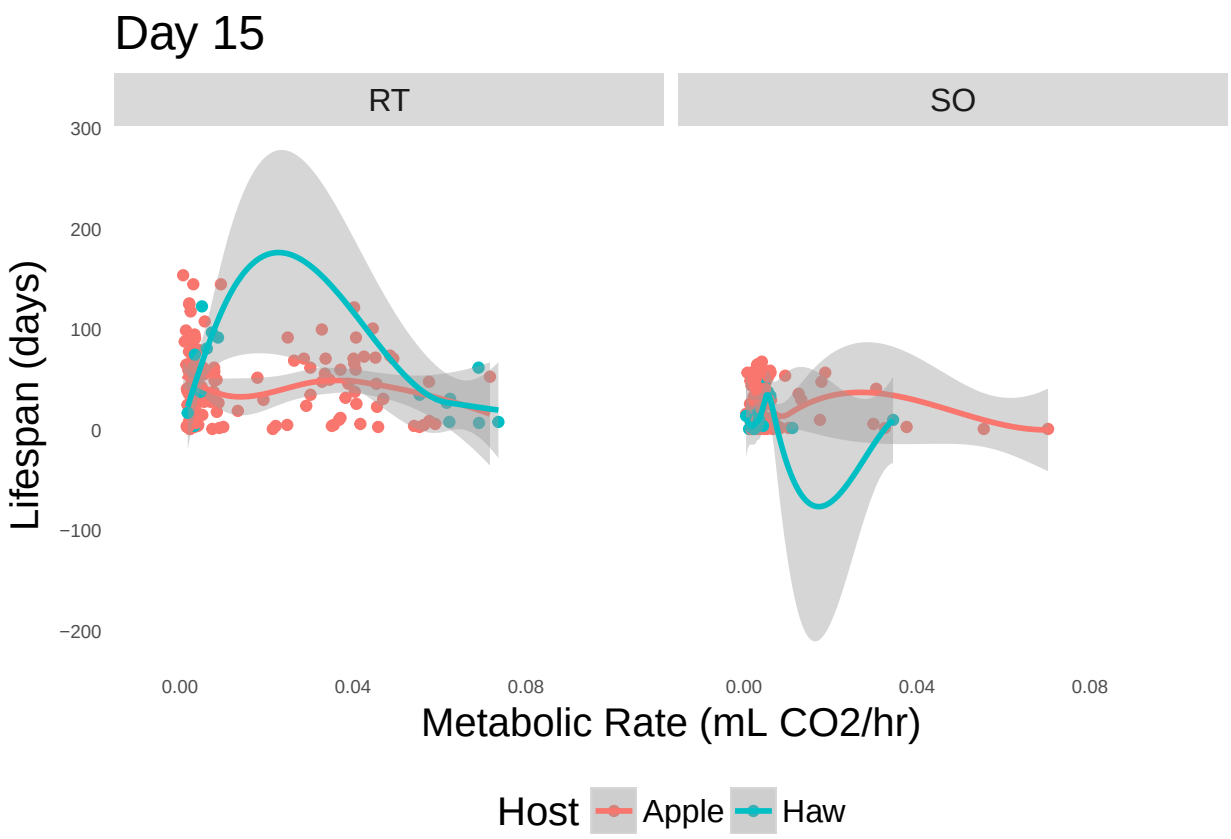


Figures associating MR with lifespan

```
#mr15 w lifespan
data5.15.treatsub$lifespan<-difftime(as.Date(data5.15.treatsub$Adult_death_date, na.rm=TRUE), as.Date(da

ggplot(data5.15.treatsub,aes(x= MR15.cor, y=lifespan, colour=Host))+geom_point()+stat_smooth(method="lo
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(si
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
## Warning: Removed 928 rows containing non-finite values (stat_smooth).
## Warning: Removed 928 rows containing missing values (geom_point).
```

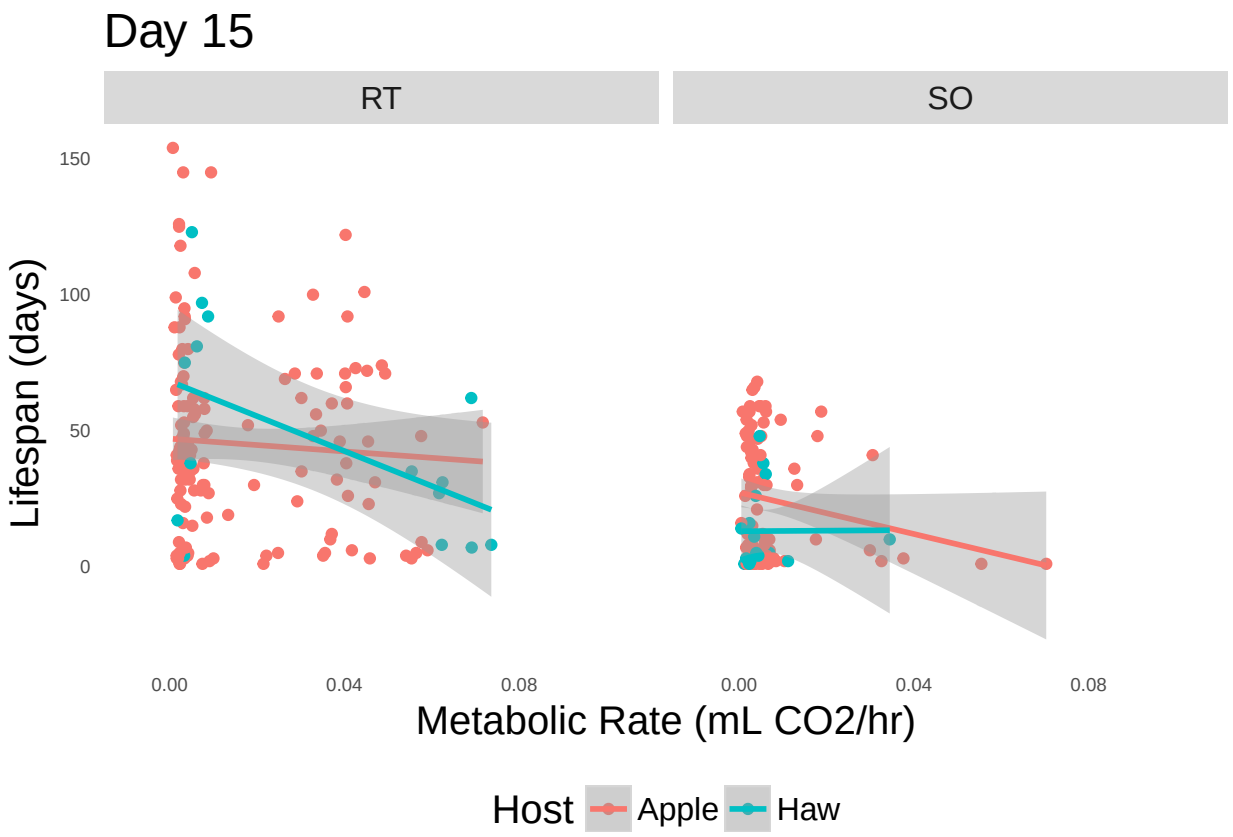



```
ggplot(data5.15.treatsub,aes(x=MR15.cor, y=lifespan, colour=Host))+geom_point()+stat_smooth(method="lm"
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```

```
## Don't know how to automatically pick scale for object of type difftime. Defaulting to continuous.
```

```
## Warning: Removed 928 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 928 rows containing missing values (geom_point).
```



Double Checking Eclosion for Pupal Deaths

```
#Assign names to each column and column bind in order to simplify and find data easily
host <- data[,11]
cd <- data[,10]
wid <- data[,29]
unid<-data[,26]
edate <- data[,27]
dcheck<-cbind(host, cd, wid, unid, edate)
```

Merging pupal death data sheet lifespans

Data available on github

```
pupdeaths<- fread("https://raw.githubusercontent.com/adnguyen/Circadian_rhythm_runs_seasonal_timing/mas

#Filter out non-eclosers
data5.na <- data5.15%>%
  mutate(neweclosions=as.numeric(neweclosions))%>%
  #glimpse()
  filter(is.na(neweclosions))

#Filter out individuals with adult lifespans
data5.ls <- data5.15.treatsub%>%
  filter(!is.na(lifespan))
```

```r
#Merge the two sets of data (lifespan and non-eclosers) by "Host", "cohort_day", "well_id", and "unique
mergedat1 <- inner_join(pupdeaths, data5.na, by = c("Host", "cohort_day", "well_id", "uniqueID"))

#column bind the merged data with the lifespan data to check same column dim
cbind(names(data5.ls), names(mergedat1)[-56])
```

```
## Warning in cbind(names(data5.ls), names(mergedat1)[-56]): number of rows of
## result is not a multiple of vector length (arg 2)
```

```
##       [,1]                        [,2]
##  [1,] "Ind_ID"                    "Host"
##  [2,] "tape"                      "cohort_day"
##  [3,] "Site_name"                 "well_id"
##  [4,] "mass_day10"                "uniqueID"
##  [5,] "purge_time_1"              "lifespan"
##  [6,] "purge1"                    "Ind_ID"
##  [7,] "collection_date"           "tape"
##  [8,] "day10"                     "Site_name"
##  [9,] "cohort_date"               "mass_day10"
## [10,] "cohort_day"                "purge_time_1"
## [11,] "Host"                      "purge1"
## [12,] "Li-cor_1"                  "collection_date"
## [13,] "resp_time_1"               "day10"
## [14,] "resp_day11"                "cohort_date"
## [15,] "mass_day14"                "Li-cor_1"
## [16,] "purge_time_2"              "resp_time_1"
## [17,] "resp_time_2"               "resp_day11"
## [18,] "resp_day15"                "mass_day14"
## [19,] "Li_cor2"                   "purge_time_2"
## [20,] "treatment_day15"           "resp_time_2"
## [21,] "exit_fridge_date"          "resp_day15"
## [22,] "Eclosion_reference_date"   "Li_cor2"
## [23,] "notes"                     "treatment_day15"
## [24,] "Resp_code"                 "exit_fridge_date"
## [25,] "treatment"                 "Eclosion_reference_date"
## [26,] "uniqueID"                  "notes"
## [27,] "eclosion_date"             "Resp_code"
## [28,] "eclosion_days"             "treatment"
## [29,] "well_id"                   "eclosion_date"
## [30,] "organism"                  "eclosion_days"
## [31,] "Trikinetics_position"      "organism"
## [32,] "Trik_monitor"              "Trikinetics_position"
## [33,] "Trikinetics_entry_LD_time" "Trik_monitor"
## [34,] "Trikinetic_exit_date"      "Trikinetics_entry_LD_time"
## [35,] "Trikinetics_exit_LD_time"  "Trikinetic_exit_date"
## [36,] "notes_2"                   "Trikinetics_exit_LD_time"
## [37,] "Free_run_trik_monitor"     "notes_2"
## [38,] "Free_run_trik_position"    "Free_run_trik_monitor"
## [39,] "Free_run_entry_date"       "Free_run_trik_position"
## [40,] "Free_run_entry_time"       "Free_run_entry_date"
## [41,] "Free_run_exit_date"        "Free_run_entry_time"
## [42,] "Free_run_exit_time"        "Free_run_exit_date"
## [43,] "notes_3"                   "Free_run_exit_time"
## [44,] "Adult_death_date"          "notes_3"
```

```
## [45,] "day10purge"                "Adult_death_date"
## [46,] "day15purge"                "day10purge"
## [47,] "day15purge.trans"          "day15purge"
## [48,] "day15resp"                 "day15purge.trans"
## [49,] "total_time_day15"          "day15resp"
## [50,] "MR15"                      "total_time_day15"
## [51,] "msMR15"                    "MR15"
## [52,] "mean.blank2"               "msMR15"
## [53,] "MR15.cor"                  "mean.blank2"
## [54,] "msMR15.cor"                "MR15.cor"
## [55,] "neweclosions"              "msMR15.cor"
## [56,] "lifespan"                  "Host"
```

```
#once the column dimensions are the same, merge the two sets of data
mergedata<- merge(data5.ls, mergedat1)

#Finally, row bind the data with the desired conditions
finalmerge<- rbind(data5.ls[,c("Host", "cohort_day", "well_id", "uniqueID", "lifespan", "MR15.cor","msM

#glimpse(finalmerge)
```

Negative binomial regression reanalyzed with pupal death data

```
#Filtering done to separate the two treatments
RT15.n <- finalmerge%>%
    filter(treatment=="RT")

SO15.n <- finalmerge%>%
    filter(treatment=="SO")

#RT summary (no stat significance)
RT15.n$lifespan <- as.numeric(RT15.n$lifespan)
mod3.n<- glm.nb(lifespan~MR15.cor*Host, data=RT15.n)
summary(mod3.n)
```

```
##
## Call:
## glm.nb(formula = lifespan ~ MR15.cor * Host, data = RT15.n, init.theta = 0.4064870624,
##     link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.9351  -1.3934  -0.1234   0.3376   1.2813
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         3.5189     0.1575  22.345   <2e-16 ***
## MR15.cor            3.6204     7.0097   0.516    0.606
## HostHaw            -0.1046     0.4437  -0.236    0.814
## MR15.cor:HostHaw   -7.0638    13.6632  -0.517    0.605
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for Negative Binomial(0.4065) family taken to be 1)
##
##     Null deviance: 231.07  on 195  degrees of freedom
## Residual deviance: 230.28  on 192  degrees of freedom
## AIC: 1705
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.4065
##           Std. Err.:  0.0419
##
##  2 x log-likelihood:  -1694.9600
```

```
#summary : HostHaw (in reference to apple) - as lifespan increases, the MR decreases by the estimate (l
#Coefficient describes relationship, i.e. for mod4SO, higher mass=higher life span according to this mo
  #mod4 shows interaction b/w host and mr
mod4.nRT<-glm.nb(lifespan~MR15.cor*Host + mass_day14, data=RT15.n)
summary(mod4.nRT)
```

```
##
## Call:
## glm.nb(formula = lifespan ~ MR15.cor * Host + mass_day14, data = RT15.n,
##     init.theta = 0.4249870689, link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.0723  -1.3914  -0.2088   0.3326   1.4933
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         2.1633     0.3769   5.740 9.49e-09 ***
## MR15.cor            1.4843     7.0176   0.212 0.832488
## HostHaw            -0.4048     0.4368  -0.927 0.353964
## mass_day14          0.2047     0.0553   3.702 0.000214 ***
## MR15.cor:HostHaw   -3.2856    13.4285  -0.245 0.806711
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.425) family taken to be 1)
##
##     Null deviance: 239.80  on 195  degrees of freedom
## Residual deviance: 230.27  on 191  degrees of freedom
## AIC: 1698.5
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.4250
##           Std. Err.:  0.0442
##
##  2 x log-likelihood:  -1686.4600
```

```
SO15.n$lifespan <- as.numeric(SO15.n$lifespan)
mod4.nSO<-glm.nb(lifespan~MR15.cor*Host + mass_day14, data=SO15.n)
```

```r
summary(mod4.nSO)
```

```
##
## Call:
## glm.nb(formula = lifespan ~ MR15.cor * Host + mass_day14, data = SO15.n,
##     init.theta = 0.8729265479, link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.2740  -1.2062  -0.2847   0.5513   1.6254
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        2.55542    0.42475   6.016 1.78e-09 ***
## MR15.cor         -30.63664   11.28046  -2.716  0.00661 **
## HostHaw           -1.13706    0.37668  -3.019  0.00254 **
## mass_day14         0.11472    0.05573   2.058  0.03956 *
## MR15.cor:HostHaw  33.18788   37.14903   0.893  0.37166
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.8729) family taken to be 1)
##
##     Null deviance: 139.26  on 111  degrees of freedom
## Residual deviance: 126.36  on 107  degrees of freedom
##   (1 observation deleted due to missingness)
## AIC: 923.59
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.873
##           Std. Err.:  0.112
##
##  2 x log-likelihood:  -911.594
```

```r
figmod4.nSO<-glm.nb(lifespan~MR15.cor*Host, data=SO15.n)
summary(figmod4.nSO)
```

```
##
## Call:
## glm.nb(formula = lifespan ~ MR15.cor * Host, data = SO15.n, init.theta = 0.8485587795,
##     link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3936  -1.2487  -0.4853   0.5522   1.5282
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         3.3912     0.1375  24.659  < 2e-16 ***
## MR15.cor          -32.9921    11.4113  -2.891  0.00384 **
## HostHaw            -0.8280     0.3668  -2.257  0.02400 *
## MR15.cor:HostHaw   34.0782    37.5036   0.909  0.36353
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.8486) family taken to be 1)
##
##     Null deviance: 135.74  on 111  degrees of freedom
## Residual deviance: 126.80  on 108  degrees of freedom
##   (1 observation deleted due to missingness)
## AIC: 925.26
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.849
##           Std. Err.:  0.108
##
##  2 x log-likelihood:  -915.265
```

```
figmod4.nRT<-glm.nb(lifespan~MR15.cor*Host, data=RT15.n)
summary(figmod4.nRT)
```

```
##
## Call:
## glm.nb(formula = lifespan ~ MR15.cor * Host, data = RT15.n, init.theta = 0.4064870624,
##     link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.9351  -1.3934  -0.1234   0.3376   1.2813
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)        3.5189     0.1575  22.345   <2e-16 ***
## MR15.cor           3.6204     7.0097   0.516    0.606
## HostHaw           -0.1046     0.4437  -0.236    0.814
## MR15.cor:HostHaw  -7.0638    13.6632  -0.517    0.605
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.4065) family taken to be 1)
##
##     Null deviance: 231.07  on 195  degrees of freedom
## Residual deviance: 230.28  on 192  degrees of freedom
## AIC: 1705
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.4065
##           Std. Err.:  0.0419
##
##  2 x log-likelihood:  -1694.9600
```

```
  #mod4.1 shows interaction b/w host and msmr
mod4.1.nSO<-glm.nb(lifespan~msMR15.cor*Host, data=SO15.n)
```

```r
summary(mod4.1.nSO)
```

```
##
## Call:
## glm.nb(formula = lifespan ~ msMR15.cor * Host, data = SO15.n,
##     init.theta = 0.848594471, link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3703  -1.2461  -0.3624   0.6299   1.5013
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)           3.2505     0.1172  27.734  < 2e-16 ***
## msMR15.cor         -182.2773    62.8655  -2.899  0.00374 **
## HostHaw              -0.6846     0.2971  -2.304  0.02123 *
## msMR15.cor:HostHaw  224.5755   356.0600   0.631  0.52822
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.8486) family taken to be 1)
##
##     Null deviance: 135.75  on 111  degrees of freedom
## Residual deviance: 126.85  on 108  degrees of freedom
##   (1 observation deleted due to missingness)
## AIC: 925.31
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.849
##           Std. Err.:  0.108
##
##  2 x log-likelihood:  -915.308
```

```r
mod4.1.nRT<-glm.nb(lifespan~msMR15.cor*Host, data=RT15.n)
summary(mod4.1.nRT)
```

```
##
## Call:
## glm.nb(formula = lifespan ~ msMR15.cor * Host, data = RT15.n,
##     init.theta = 0.4071281808, link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.9507  -1.3966  -0.1284   0.3380   1.2736
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          3.53929    0.13867  25.524   <2e-16 ***
## msMR15.cor          21.20632   44.94809   0.472    0.637
## HostHaw             -0.08528    0.39366  -0.217    0.828
## msMR15.cor:HostHaw -67.07964   78.15514  -0.858    0.391
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.4071) family taken to be 1)
##
##     Null deviance: 231.38  on 195  degrees of freedom
## Residual deviance: 230.28  on 192  degrees of freedom
## AIC: 1704.7
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.4071
##           Std. Err.:  0.0420
##
##  2 x log-likelihood:  -1694.6580
```

```
#Likelihood ratio tests of Negative Binomial Models
m1.nRT <- update(mod4.nRT, . ~ . - prog)
anova(mod4.nRT, m1.nRT)
```

```
## Likelihood ratio tests of Negative Binomial Models
##
## Response: lifespan
##                                          Model     theta Resid. df
## 1                 MR15.cor * Host + mass_day14 0.4249871       191
## 2 MR15.cor + Host + mass_day14 + MR15.cor:Host 0.4249871       191
##      2 x log-lik.   Test    df      LR stat. Pr(Chi)
## 1        -1686.46
## 2        -1686.46 1 vs 2     0 -3.760033e-08       1
```

```
#Checking model assumption -- is negative binomial regression (NBR) a good model for this data?
##Values close to 0 (estimates the dispersion parameter) strongly suggest the NBR model is more appropri
mod5.n <- glm(lifespan ~ Host*MR15.cor, family = "poisson", data = SO15.n)
pchisq(2 * (logLik(mod4.nRT) - logLik(mod5.n)), df = 1, lower.tail = FALSE)
```

```
## 'log Lik.' 6.470061e-238 (df=6)
```

```
mod5.n <- glm(lifespan ~ Host*MR15.cor, family = "poisson", data = SO15.n)
pchisq(2 * (logLik(mod4.nSO) - logLik(mod5.n)), df = 1, lower.tail = FALSE)
```

```
## 'log Lik.' 0 (df=6)
```

```
#output below indicates that Hawthorn is 0.432 times less likely to live than apple
#confidence interval
(est <- cbind(Estimate = coef(mod4.nRT), confint(mod4.nRT)))
```

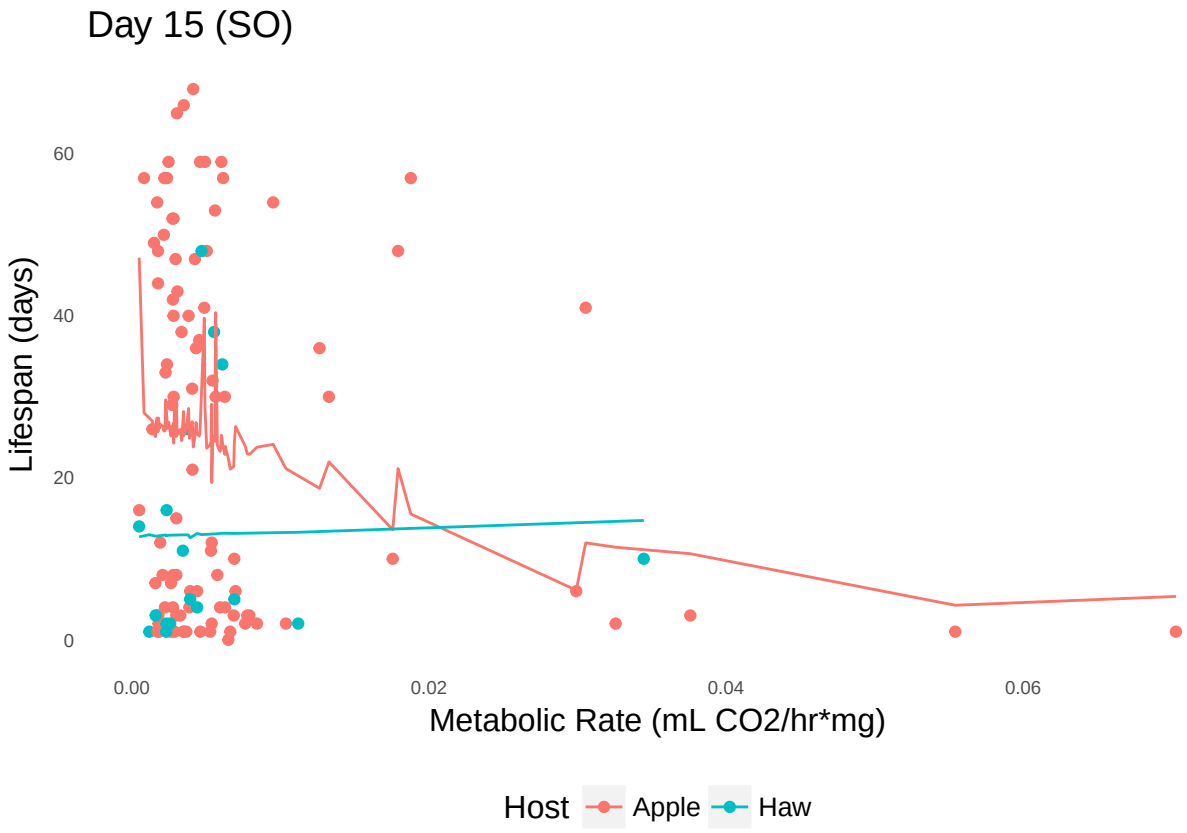
```
## Waiting for profiling to be done...
```

```
##                    Estimate       2.5 %     97.5 %
## (Intercept)       2.1633428   1.2237554  3.1119932
## MR15.cor          1.4842992 -11.7040163 15.8181228
## HostHaw          -0.4048505  -1.2336952  0.5650535
## mass_day14        0.2047244   0.0676875  0.3465155
## MR15.cor:HostHaw -3.2855872 -29.3106300 25.7786008
```

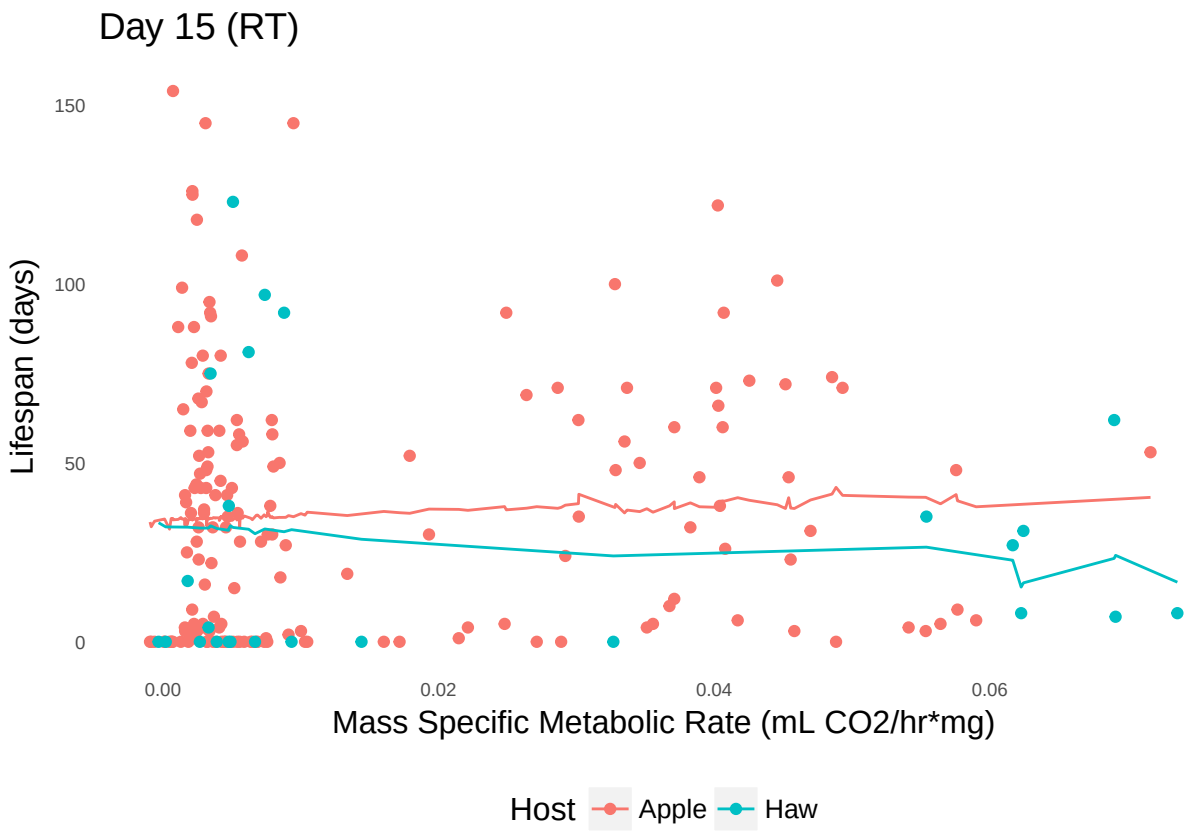
```
#incident rate ratio - lifespan ratio
exp(est)
```

```
##                     Estimate        2.5 %       97.5 %
## (Intercept)      8.70017236 3.399932e+00 2.246578e+01
## MR15.cor         4.41187261 8.260576e-06 7.408384e+06
## HostHaw          0.66707656 2.912145e-01 1.759542e+00
## mass_day14       1.22718686 1.070031e+00 1.414131e+00
## MR15.cor:HostHaw 0.03741861 1.864469e-13 1.568571e+11
```

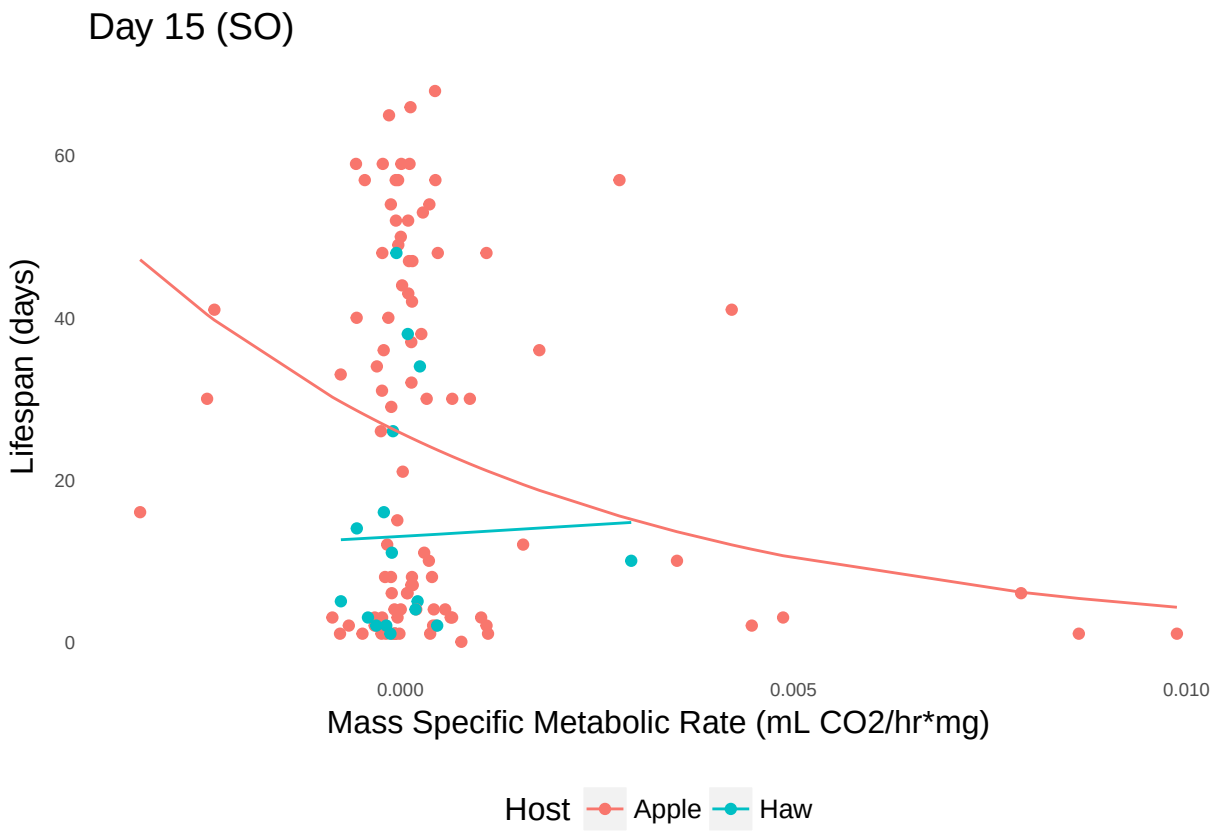
```
#Filter out all the NAs in order to have same dimensions for predvalues
filSO15.ms<- SO15.n%>%
  filter(msMR15.cor!= "NA"&lifespan !="NA")

filRT15.ms<- RT15.n%>%
  filter(msMR15.cor!= "NA"&lifespan !="NA")

#Calculate the predicted values for msMR15
filSO15.ms$predvalues <- predict(mod4.1.nSO, type = "response")

filRT15.ms$predvalues <- predict(mod4.1.nRT, type = "response")

#Filter out all the NAs in order to have same dimensions for predvalues
filSO15.ms<- SO15.n%>%
  filter(msMR15.cor!= "NA"&lifespan !="NA")

filRT15.ms<- RT15.n%>%
  filter(msMR15.cor!= "NA"&lifespan !="NA")

#Calculate the predicted values
filSO15.ms$predvalues <- predict(mod4.1.nSO, type = "response")

filRT15.ms$predvalues <- predict(mod4.1.nRT, type = "response")

#overlay of real data(points)  with predicted values(line) for MR
ggplot(filSO15.ms,aes(x=MR15.cor, y=lifespan, colour=Host))+geom_point()+geom_line(data=filSO15.ms, aes
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```



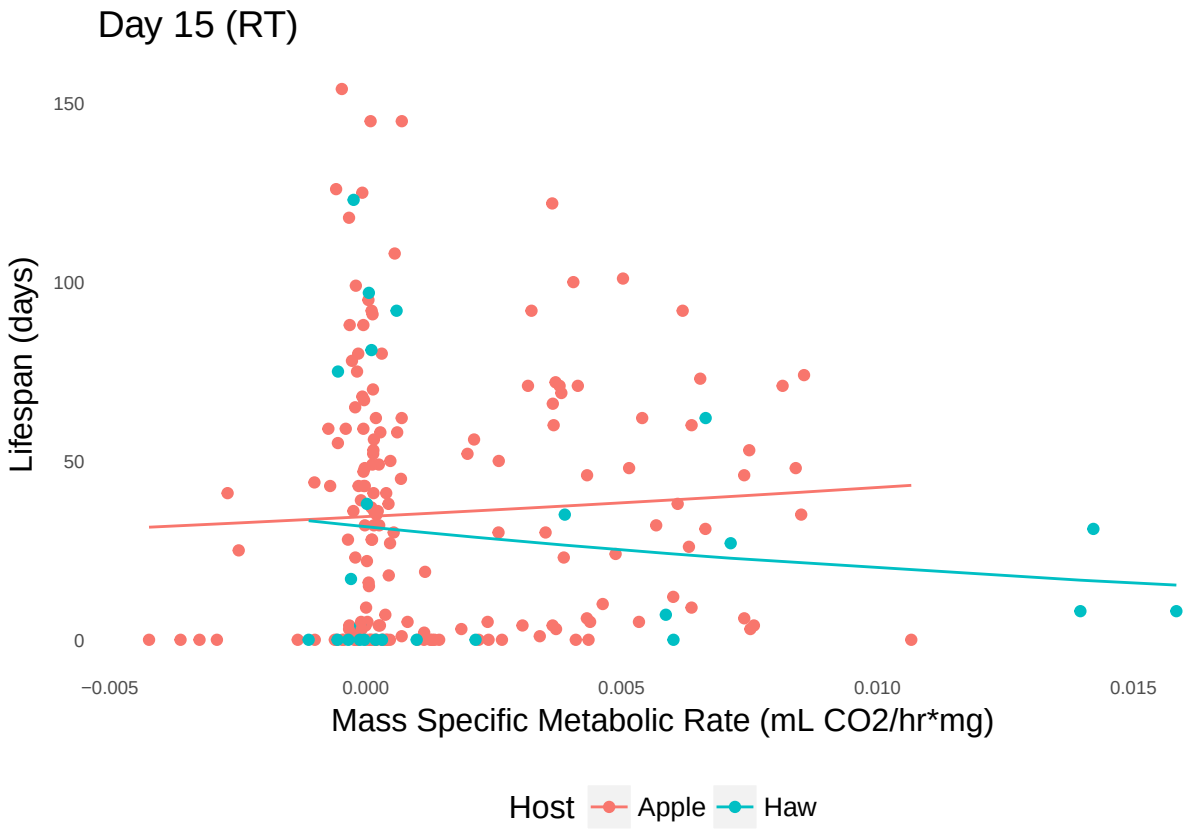

```
ggplot(filRT15.ms,aes(x=MR15.cor, y=lifespan, colour=Host))+geom_point()+geom_line(data=filRT15.ms, aes
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```




```
#overlay of real data(points)  with predicted values(line) for msMR
ggplot(filSO15.ms,aes(x=msMR15.cor, y=lifespan, colour=Host))+geom_point()+geom_line(data=filSO15.ms, a
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```




```
ggplot(filRT15.ms,aes(x=msMR15.cor, y=lifespan, colour=Host))+geom_point()+geom_line(data=filRT15.ms, a
        axis.ticks.x=element_blank(),legend.position="bottom",
        axis.ticks.y=element_blank(),panel.background = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),axis.text=element_text(s
```



Samples were split into two treatments, RT (favorable conditions) and SO (simulated overwintering). The dependent variable was lifespan, while the independent variables were metabolic rate in relation to host and mass. For this model, a negative coefficient of the log value would indicate a shorter lifespan since it produces a log-linear model in which a positive coefficient would indicate a (larger x and y value).

Based on the RT treatment, only mass showed significance which suggests an individual with a larger mass would have a longer lifespan (positive coefficient). Analysis of the SO treatment showed significance in host type, metabolic rate, and mass, in which a lower metabolic rate would suggest longer lifespan (neg. coefficient), and larger mass would suggest longer lifespan(pos. coefficient). Hawthorn individuals also had an overall lower lifespan compared to apple.

Negative binomial regression was shown to be a good model by comparing its log likelihood to a poisson distribution. Values close to 0 (which estimates the dispersion parameter) strongly suggests the NBR model is more appropriate than the Poisson model for both treatments.

Kaplan-Meier Survival Estimate

```
#install.packages(c("survival", "survminer"))
#install.packages(c("ggpubr", "magrittr"))
#Assign censored data and create new column
finalmerge$status[finalmerge$lifespan >= 0] <- 1
```

```
## Warning: Unknown or uninitialised column: 'status'.
```

```
#filter out unwanted treatments
fmerge <- finalmerge %>%
      filter(treatment != "")
```

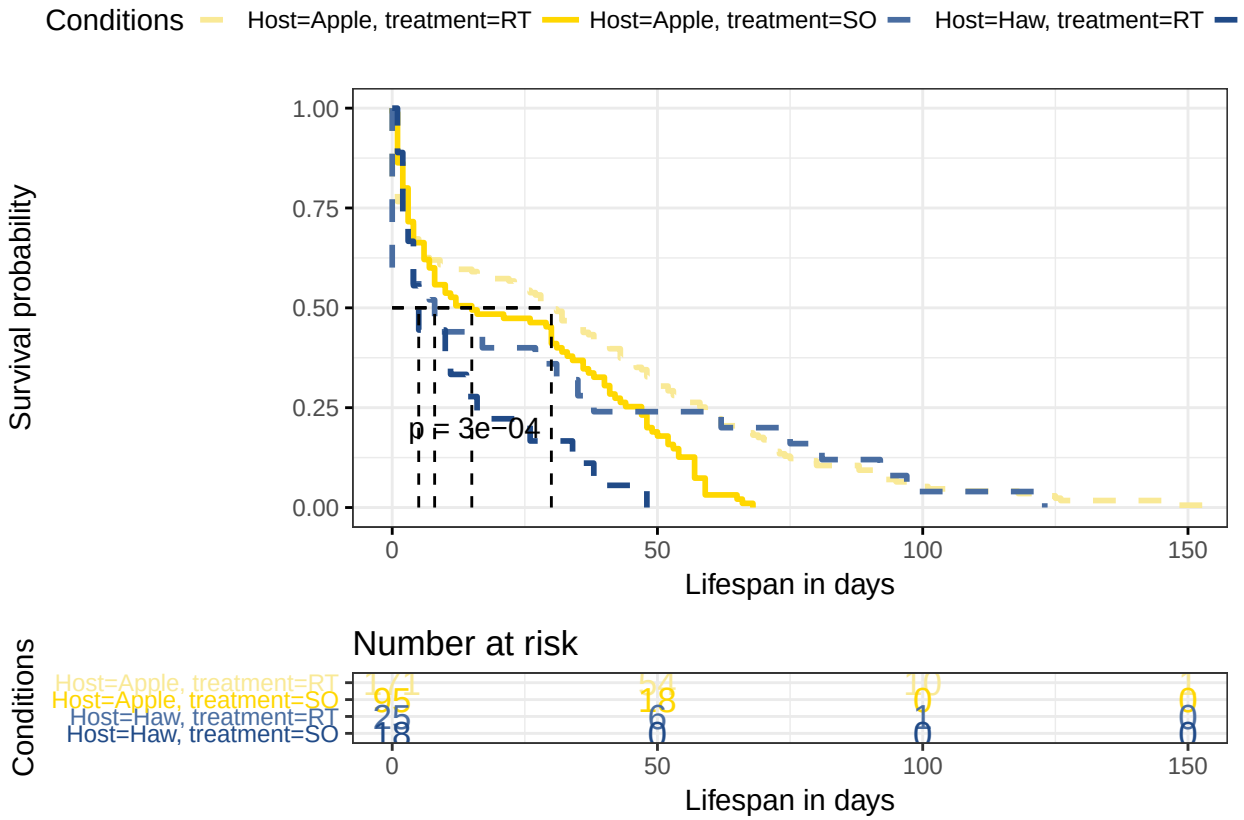
```r
#Filter out unwanted treatments
finalmerge <- finalmerge %>%
  filter(treatment != "")

#compute kaplan-Meier survival estimate-so compute the survival probability by host & treatment:
  #fit1 computes survival probability by Host + Treatment

fit1 <- survfit(Surv(lifespan, status) ~ Host + treatment, data = finalmerge)
print(fit1)
```

```
## Call: survfit(formula = Surv(lifespan, status) ~ Host + treatment,
##     data = finalmerge)
##
##                             n events median 0.95LCL 0.95UCL
## Host=Apple, treatment=RT 171    171     30      22      39
## Host=Apple, treatment=SO  95     95     15       8      33
## Host=Haw, treatment=RT    25     25      8       0      38
## Host=Haw, treatment=SO    18     18      5       3      26
```

```r
# Access to the sort summary table
summary(fit1)$table
```

```
##                           records n.max n.start events   *rmean *se(rmean)
## Host=Apple, treatment=RT      171   171     171    171 33.91520   2.439589
## Host=Apple, treatment=SO       95    95      95     95 24.31579   2.271454
## Host=Haw, treatment=RT         25    25      25     25 27.04000   6.846483
## Host=Haw, treatment=SO         18    18      18     18 12.55556   3.296296
##                           median 0.95LCL 0.95UCL
## Host=Apple, treatment=RT      30      22      39
## Host=Apple, treatment=SO      15       8      33
## Host=Haw, treatment=RT         8       0      38
## Host=Haw, treatment=SO         5       3      26
```

```r
# Visualize curves (Change color, linetype by strata, risk.table color by strata)
ggsurvplot(fit1,
          pval = TRUE, conf.int = FALSE,
          risk.table = TRUE, # Add risk table
          risk.table.col = "strata", # Change risk table color by groups
          linetype = c("dashed","solid", "dashed", "dashed","solid"), # Change line type
          surv.median.line = "hv", # Specify median survival
          ggtheme = theme_bw(), # Change ggplot2 theme
          palette = c("#F9E996","#FFD700","#496DA1","#204A87"),
          xlab = "Lifespan in days",
          legend.title = "Conditions",
          pval.size=4)
```



The Kaplan-Meier Survival Estimate predicts the probability of survival from a specific time, so for this data, the estimates predict the probability of host survival at each time point in their lifespan. According to the figure, Hawthorn flies have an overall lower probability of survival over apple flies, which agrees with the previous analyses. This estimate is best used for categorical values, so MR and mass (which were all unique to the individul) were not good estimators and not used.

Cox Regression

```
#Split up treatments into: SO & RT
fmergeSO <- fmerge%>%
  filter(treatment == "SO")

fmergeRT <- fmerge%>%
  filter(treatment == "RT")

#Merge the data for censoring (all labeled as status 1 for dead)
covariates <- c("host", "treatment", "MR15.cor","mass_day14")
#For RT
univ_formulasRT <- sapply(covariates,
                          function(x) as.formula(paste('Surv(lifespan, status)~', fmergeRT)))
#For SO
univ_formulasSO <- sapply(covariates,
                          function(x) as.formula(paste('Surv(lifespan, status)~', fmergeSO)))

univ_modelsRT <- lapply(univ_formulasRT, function(x){coxph(x, data = fmergeRT)})
univ_modelsSO <- lapply(univ_formulasSO, function(x){coxph(x, data = fmergeSO)})
```

```r
#Multivariate case
#Testing interaction between Host, Treatment, and MR -- Shows interaction b/w treatment & Host
res.cox <- coxph(Surv(lifespan, status) ~ Host*treatment*MR15.cor + mass_day14, data =  fmerge)
summary(res.cox)
```

```
## Call:
## coxph(formula = Surv(lifespan, status) ~ Host * treatment * MR15.cor +
##     mass_day14, data = fmerge)
##
##   n= 308, number of events= 308
##    (1 observation deleted due to missingness)
##
##                                  coef  exp(coef)   se(coef)      z
## HostHaw                      2.178e-01  1.243e+00  2.887e-01  0.754
## treatmentSO                  3.257e-01  1.385e+00  1.698e-01  1.918
## MR15.cor                    -1.494e+00  2.244e-01  4.562e+00 -0.328
## mass_day14                  -1.362e-01  8.727e-01  3.457e-02 -3.940
## HostHaw:treatmentSO          6.938e-01  2.001e+00  4.437e-01  1.564
## HostHaw:MR15.cor             5.393e+00  2.198e+02  8.805e+00  0.612
## treatmentSO:MR15.cor         1.858e+01  1.170e+08  1.163e+01  1.597
## HostHaw:treatmentSO:MR15.cor -2.660e+01  2.804e-12  3.695e+01 -0.720
##                             Pr(>|z|)
## HostHaw                       0.4506
## treatmentSO                   0.0551 .
## MR15.cor                      0.7432
## mass_day14                  8.15e-05 ***
## HostHaw:treatmentSO           0.1179
## HostHaw:MR15.cor              0.5402
## treatmentSO:MR15.cor          0.1102
## HostHaw:treatmentSO:MR15.cor  0.4716
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                             exp(coef) exp(-coef) lower .95 upper .95
## HostHaw                     1.243e+00  8.043e-01 7.060e-01 2.190e+00
## treatmentSO                 1.385e+00  7.220e-01 9.929e-01 1.932e+00
## MR15.cor                    2.244e-01  4.457e+00 2.935e-05 1.715e+03
## mass_day14                  8.727e-01  1.146e+00 8.155e-01 9.338e-01
## HostHaw:treatmentSO         2.001e+00  4.997e-01 8.388e-01 4.775e+00
## HostHaw:MR15.cor            2.198e+02  4.550e-03 7.032e-06 6.870e+09
## treatmentSO:MR15.cor        1.170e+08  8.550e-09 1.469e-02 9.314e+17
## HostHaw:treatmentSO:MR15.cor 2.804e-12  3.566e+11 9.964e-44 7.892e+19
##
## Concordance= 0.611  (se = 0.021 )
## Rsquare= 0.107   (max possible= 1 )
## Likelihood ratio test= 34.75  on 8 df,   p=3e-05
## Wald test            = 36.24  on 8 df,   p=2e-05
## Score (logrank) test = 37.24  on 8 df,   p=1e-05
```

```r
#Coefficient describes relationship: for Cox Regression, coefficient describes relationship to likeliho
#Test interaction between Host, RT, and MR
res.coxRT <- coxph(Surv(lifespan, status) ~ Host*MR15.cor + mass_day14, data =  fmergeRT)
summary(res.coxRT)
```

```
## Call:
```

```
## coxph(formula = Surv(lifespan, status) ~ Host * MR15.cor + mass_day14,
##     data = fmergeRT)
##
##   n= 196, number of events= 196
##
##                       coef exp(coef) se(coef)      z Pr(>|z|)
## HostHaw           0.26512   1.30358  0.29147  0.910 0.363049
## MR15.cor         -0.50118   0.60582  4.57571 -0.110 0.912782
## mass_day14       -0.15524   0.85621  0.04451 -3.488 0.000488 ***
## HostHaw:MR15.cor  2.90449  18.25589  8.85836  0.328 0.743002
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                  exp(coef) exp(-coef) lower .95 upper .95
## HostHaw             1.3036    0.76712 7.363e-01 2.308e+00
## MR15.cor            0.6058    1.65067 7.718e-05 4.755e+03
## mass_day14          0.8562    1.16794 7.847e-01 9.343e-01
## HostHaw:MR15.cor   18.2559    0.05478 5.262e-07 6.334e+08
##
## Concordance= 0.624  (se = 0.028 )
## Rsquare= 0.068   (max possible= 1 )
## Likelihood ratio test= 13.77  on 4 df,   p=0.008
## Wald test            = 13.57  on 4 df,   p=0.009
## Score (logrank) test = 13.62  on 4 df,   p=0.009
```

```
#Test interaction between Host, SO, and MR
res.coxSO <- coxph(Surv(lifespan, status) ~ Host*MR15.cor + mass_day14, data =  fmergeSO)
summary(res.coxSO)
```

```
## Call:
## coxph(formula = Surv(lifespan, status) ~ Host * MR15.cor + mass_day14,
##     data = fmergeSO)
##
##   n= 112, number of events= 112
##    (1 observation deleted due to missingness)
##
##                         coef  exp(coef)   se(coef)      z Pr(>|z|)
## HostHaw           1.175e+00  3.238e+00  3.826e-01  3.071  0.00213 **
## MR15.cor          3.096e+01  2.780e+13  1.176e+01  2.632  0.00849 **
## mass_day14       -1.032e-01  9.019e-01  5.506e-02 -1.874  0.06088 .
## HostHaw:MR15.cor -3.888e+01  1.305e-17  3.748e+01 -1.037  0.29962
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                  exp(coef) exp(-coef) lower .95 upper .95
## HostHaw          3.238e+00  3.088e-01 1.530e+00 6.853e+00
## MR15.cor         2.780e+13  3.597e-14 2.707e+03 2.855e+23
## mass_day14       9.019e-01  1.109e+00 8.097e-01 1.005e+00
## HostHaw:MR15.cor 1.305e-17  7.663e+16 1.627e-49 1.047e+15
##
## Concordance= 0.593  (se = 0.035 )
## Rsquare= 0.122   (max possible= 0.999 )
## Likelihood ratio test= 14.57  on 4 df,   p=0.006
## Wald test            = 16.07  on 4 df,   p=0.003
## Score (logrank) test = 16.72  on 4 df,   p=0.002
```

Samples were split into two treatments, RT (favorable conditions) and SO (simulated overwintering). The dependent variable was lifespan, while the independent variables were metabolic rate in relation to host and mass. For this model, the coefficient relates x variables (metabolic rate, host, and mass) to likelihood of death (hazard rate). The dependent variable is lifespan again.

The RT treatment only showed significance for mass (negative coefficient), in which a lower mass suggests a higher likelihood of death (i.e. longer lifespan).

The SO treatment showed significance for metabolic rate, host, and mass. The positive coefficient for the hawthorn flies and metabolic rate indicate higher likelihood of death if the individual is a host to hawthorn and/or the individual has a high metabolic rate. This agrees with the NBR model. However, the negative coefficient for mass indicates a higher likelihood of death with smaller masses which agrees with the NBR model.

Conclusions

Evolutionarily speaking, linking lower metabolic rate to longer lifespan makes sense since an organism who reserves its energy would take longer to develop, thus longer to die. For example early eclosers tend to have higher metabolic rate vs. late eclosers, so if a group of insects undergo diapause at the same time, those with higher metabolic rates risk eclosing too early in the season, before optimal conditions are available. Late eclosers have a higher energy reserve because they don't need as much energy with lower metabolic rates. This allows them to eclose at suitable seasonal time, lengthening their lifespan/hazard rate.

From this data, the cohorts placed in favorable conditions showed no significance when relating metabolic rate and lifespan. This is most likely because these cohorts had no survival need to undergo diapause which would have separated out the individuals with high and low metabolic rates. Those placed in simulated overwintering conditions would be affected by their metabolic rates – individuals with high metabolic rates would be more likely to eclose earlier and die earlier. Individuals with low metabolic rates would spend more time in diapause and eclose later, extending their lifespan.

According to the evolution theory described in Olshansky & Rattan (2009), higher metabolic rates are liked to species with "high extrinsic mortality" (e.g. targeted prey) since they must quickly develop and reproduce in order to pass down their genes. Lower metabolic rates were linked to individuals with lower extrinsic mortalities and could take their time to gradually develop into larger sizes and live longer. For this theory to hold true, lifespan would need to be considered as a function of metabolic rate.

However, the evolution theory does not consider seasonal timing in this case. It may be possible that both early and late eclosers miss the optimal season for mating by eclosing before or after resource availability. Therefore, individuals who have metabolic rates that are too high or too low would not be able to pass down their genes. However, if we assume these individuals are still able to live, but not reproduce, their lifespans would not be an ideal indicator for fitness.

Session Info

```
sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS High Sierra 10.13.5
##
## 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    gridExtra_2.3     survminer_0.4.2
##  [4] ggpubr_0.1.6      magrittr_1.5      survival_2.42-3
##  [7] BBmisc_1.11       MASS_7.3-49       DiagrammeR_1.0.0
## [10] curl_3.2          lubridate_1.7.4   ggplot2_2.2.1
## [13] data.table_1.11.4 dplyr_0.7.5
##
## loaded via a namespace (and not attached):
##  [1] viridis_0.5.1      tidyr_0.8.1        jsonlite_1.5
##  [4] viridisLite_0.3.0  splines_3.5.0      assertthat_0.2.0
##  [7] yaml_2.1.19        pillar_1.2.3       backports_1.1.2
## [10] lattice_0.20-35    glue_1.2.0         downloader_0.4
## [13] digest_0.6.15      RColorBrewer_1.1-2 checkmate_1.8.5
## [16] colorspace_1.3-2   cmprsk_2.2-7       htmltools_0.3.6
## [19] Matrix_1.2-14      plyr_1.8.4         psych_1.8.4
## [22] XML_3.98-1.11      pkgconfig_2.0.1    broom_0.4.4
## [25] purrr_0.2.5        xtable_1.8-2       scales_0.5.0
## [28] brew_1.0-6         km.ci_0.5-2        KMsurv_0.1-5
## [31] tibble_1.4.2       influenceR_0.1.0   lazyeval_0.2.1
## [34] cli_1.0.0          mnormt_1.5-5       rgexf_0.15.3
## [37] crayon_1.3.4       evaluate_0.10.1    nlme_3.1-137
## [40] foreign_0.8-70     Rook_1.1-1         tools_3.5.0
## [43] hms_0.4.2          stringr_1.3.1      munsell_0.4.3
## [46] compiler_3.5.0     rlang_0.2.0        grid_3.5.0
## [49] rstudioapi_0.7     htmlwidgets_1.2    visNetwork_2.0.3
## [52] igraph_1.2.1       labeling_0.3       rmarkdown_1.9
## [55] gtable_0.2.0       reshape2_1.4.3     R6_2.2.2
## [58] zoo_1.8-1          knitr_1.20         survMisc_0.5.4
## [61] utf8_1.1.4         bindr_0.1.1        rprojroot_1.3-2
## [64] readr_1.1.1        stringi_1.2.2      parallel_3.5.0
## [67] Rcpp_0.12.17       tidyselect_0.2.4
```