

# 2018-02-27\_eclosion\_summaries

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## Eclosion data

```
library(data.table)
library(ggplot2)
library(plyr)
```

### Loading in the data

```
##grabbing data if git cloned
#eclosions<-fread("../Data/2018-01-26_rhagoletis_masterdata_data_slice.csv")
#grabbing from online
eclosions<-fread("https://raw.githubusercontent.com/adnguyen/Circadian_rhythm_runs_seasonal_timing/master/Data/2018-01-26_rhagoletis_masterdata_data_slice.csv")
## Warning in fread("https://raw.githubusercontent.com/adnguyen/Circadian_rhythm_runs_seasonal_timing/master/Data/2018-01-26_rhagoletis_masterdata_data_slice.csv"): Bumped column 41 to
## type character on data row 530, field contains 'change food 2017-10-31
## 21:50'. Coercing previously read values in this column from logical,
## integer or numeric back to character which may not be lossless; e.g., if
## '00' and '000' occurred before they will now be just '0', and there may
## be inconsistencies with treatment of ',', and ',NA,' too (if they occurred
## in this column before the bump). If this matters please rerun and set
## 'colClasses' to 'character' for this column. Please note that column type
## detection uses a sample of 1,000 rows (100 rows at 10 points) so hopefully
## this message should be very rare. If reporting to datatable-help, please
## rerun and include the output from verbose=TRUE.

head(eclosions,10)

##      Ind_ID tape Site_name mass_day10 purge_time_1 purgel collection_date
## 1:      1 blue      OG      6.938      13:38      NA      2017-08-21
## 2:      2 blue  Ferris     11.175     13:39      NA      2017-08-21
## 3:      3 blue  Ferris      6.719     13:39      NA      2017-08-21
## 4:      4 blue  Ferris     10.719     13:40      NA      2017-08-21
## 5:      5 blue      OG      3.848     13:41      NA      2017-08-21
## 6:      6 blue      OG      7.576     13:37      NA      2017-08-21
## 7:      7 blue      OG      6.413     13:35      NA      2017-08-21
## 8:      8 blue      OG      9.365     13:57      NA      2017-08-21
## 9:      9 blue  Ferris      7.978     13:41      NA      2017-08-21
## 10:     10 blue      OG      4.895     13:36      NA      2017-08-21
##      day10 cohort_date cohort_day Host Li-cor_1 resp_time_1
```

```

## 1: 2017-09-04 2017-08-25      2 Apple      6262
## 2: 2017-09-04 2017-08-25      2 Apple      6262      10:13:15
## 3: 2017-09-04 2017-08-25      2 Apple      6262      10:14:47
## 4: 2017-09-04 2017-08-25      2 Apple      6262      10:16:43
## 5: 2017-09-04 2017-08-25      2 Apple      6262      10:18:41
## 6: 2017-09-04 2017-08-25      2 Apple      6262      10:20:19
## 7: 2017-09-04 2017-08-25      2 Apple      6262      10:22:07
## 8: 2017-09-04 2017-08-25      2 Apple      6262      10:23:42
## 9: 2017-09-04 2017-08-25      2 Apple      6262      10:25:39
## 10: 2017-09-04 2017-08-25      2 Apple      6262      10:27:14
##      resp_day11 mass_day14 purge_time_2 resp_time_2 resp_day15 Li_cor2
## 1:      NA      6.187      10:51      10:13:48 0.1432514      6262
## 2: 0.2941100      9.967      10:16:22 0.1702350      6262
## 3: 0.1052925      6.118      10:18:10 0.1076286      6262
## 4: 1.3445380      9.539      10:19:38 1.3873900      6262
## 5: 0.1492267      3.479      10:21:23 0.1182286      6262
## 6: 1.4202160      6.824      10:22:55 1.4689120      6262
## 7: 0.1365561      5.738      10:24:36 0.1601623      6262
## 8: 1.3082910      8.401      10:25:57 1.4328830      6262
## 9: 0.1591373      7.323      10:27:35 0.0809000      6262
## 10: 0.1027624      4.349      10:28:53 0.0642000      6262
##      notes Resp_code treatment uniqueID eclosion_date eclosion_days well_id
## 1:      0      SO      2b1      NA      A1
## 2:      1      GC      2b2      NA
## 3:      1      RT      2b3      2017-10-29      64      A1
## 4:      1      GC      2b4      NA
## 5:      1      RT      2b5      2017-10-20      56      A2
## 6:      1      SO      2b6      NA      A2
## 7:      1      SO      2b7      NA      A3
## 8:      1      RT      2b8      2017-09-26      32      A3
## 9:      1      SO      2b9      NA      A4
## 10:      1      GC      2b10      NA
##      organism Trikinetics_position Trikinetics_monitor
## 1:      NA      NA
## 2:      NA      NA
## 3:      fly      8      1
## 4:      NA      NA
## 5:      fly      15      2
## 6:      NA      NA
## 7:      NA      NA
## 8:      fly      30      2
## 9:      NA      NA
## 10:      NA      NA
##      Trikinetics_entry_LD_time Trikinetic_exit_date
## 1:
## 2:
## 3:      3:34      2107-11-05
## 4:
## 5:      13:03      2017-10-25
## 6:
## 7:
## 8:      16:08      2017-10-05
## 9:
## 10:

```

```

##      Trikinetics_exit_LD_time          notes_2
## 1:
## 2:
## 3:          20:33 changed water 2017-11-03 11:56
## 4:
## 5:          9:58
## 6:
## 7:
## 8:          12:45
## 9:
## 10:
##      Free_run_monitor Free_run_position Free_run_entry_date
## 1:          NA          NA
## 2:          NA          NA
## 3:          4          11          2017-11-05
## 4:          NA          NA
## 5:          NA          NA
## 6:          NA          NA
## 7:          NA          NA
## 8:          NA          NA
## 9:          NA          NA
## 10:         NA          NA
##      Free_run_entry_time Free_run_exit_date Free_run_exit_time
## 1:
## 2:
## 3:          20:34          2017-12-09          20:00
## 4:
## 5:
## 6:
## 7:
## 8:
## 9:
## 10:
##          notes_3 V41
## 1:
## 2:
## 3: changed water 2017-11-28
## 4:
## 5:
## 6:
## 7:
## 8:
## 9:
## 10:

names(eclosions)
## [1] "Ind_ID"          "tape"
## [3] "Site_name"       "mass_day10"
## [5] "purge_time_1"    "purge1"
## [7] "collection_date" "day10"
## [9] "cohort_date"     "cohort_day"
## [11] "Host"            "Li-cor_1"
## [13] "resp_time_1"     "resp_day11"
## [15] "mass_day14"      "purge_time_2"

```

```
## [17] "resp_time_2"          "resp_day15"
## [19] "Li_cor2"              "notes"
## [21] "Resp_code"            "treatment"
## [23] "uniqueID"             "eclosion_date"
## [25] "eclosion_days"         "well_id"
## [27] "organism"              "Trikinetics_position"
## [29] "Trikinetics_monitor"   "Trikinetics_entry_LD_time"
## [31] "Trikinetic_exit_date"  "Trikinetics_exit_LD_time"
## [33] "notes_2"               "Free_run_monitor"
## [35] "Free_run_position"     "Free_run_entry_date"
## [37] "Free_run_entry_time"   "Free_run_exit_date"
## [39] "Free_run_exit_time"    "notes_3"
## [41] "V41"
```

```
dim(eclosions)
```

```
## [1] 1909 41
```

```
#tail(eclosions,10)
```

```
### getting numbers for eclosions without simulated overwintering, so these pupae were left at rearing
sub<-subset(eclosions,eclosion_days>1)
t1<-ddply(sub,. (Host,organism),summarize,counts=length(eclosion_days))
knitr::kable(t1)
```

Host	organism	counts
Apple		1
Apple	fly	192
Apple	wasp	4
Haw	fly	32
Haw	wasp	21

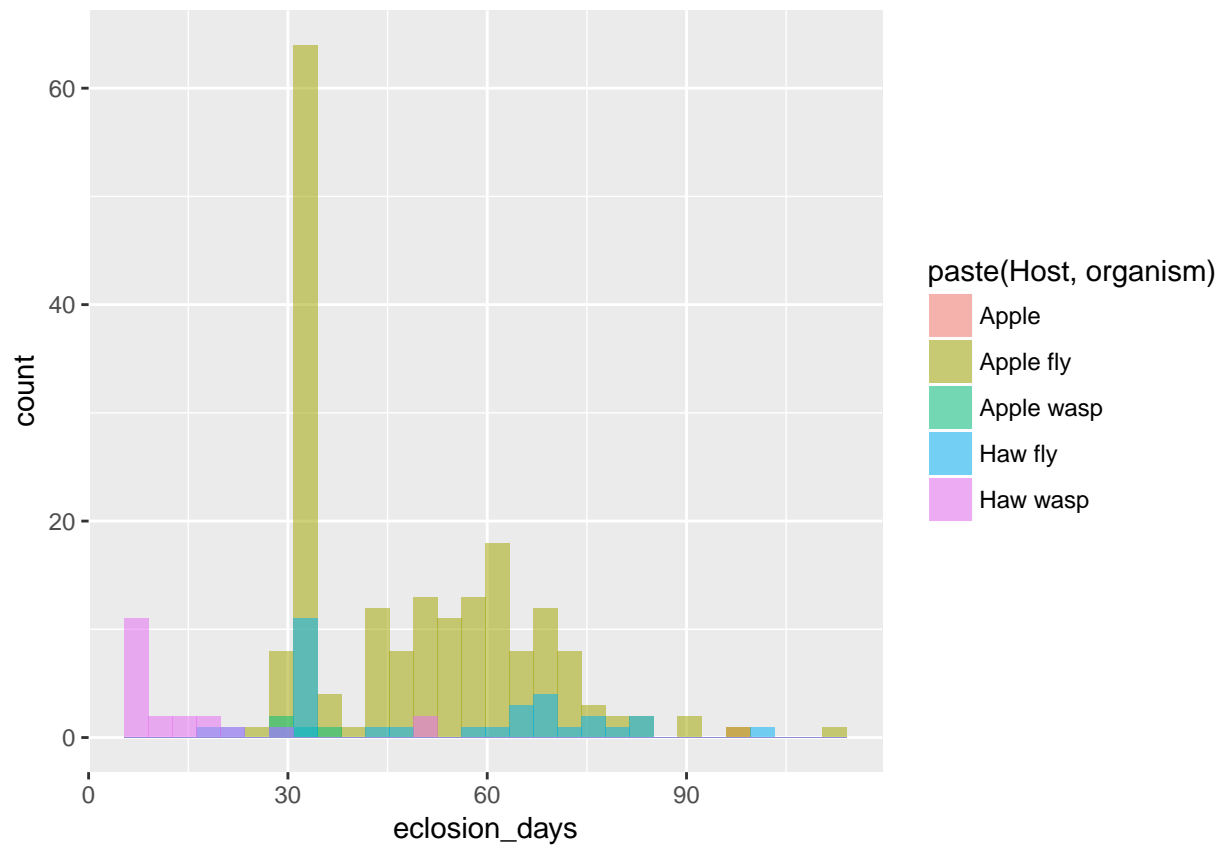
## plotting distributions with Ggplot

```
#histogram
```

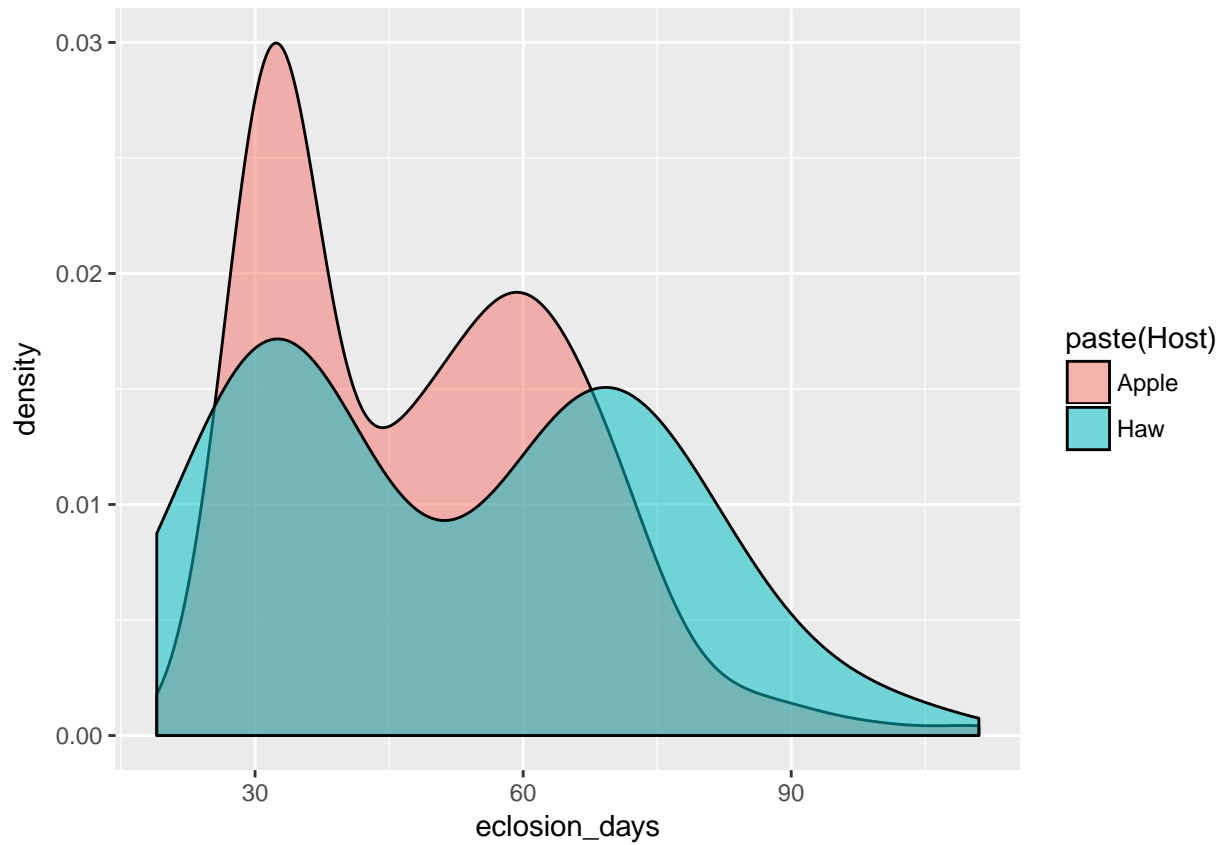
```
ggplot(eclosions,aes(x=eclosion_days,fill=paste(Host,organism)))+geom_histogram(position="identity",alpha=0.5)
```

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

```
## Warning: Removed 1659 rows containing non-finite values (stat_bin).
```



```
#density of flies only
flies<-subset(eclosions,organism=="fly")
ggplot(flies,aes(x=eclosion_days,fill=paste(Host)))+geom_density(position="identity",alpha=.52)
## Warning: Removed 1 rows containing non-finite values (stat_density).
```



## Skipped eclosion data

1. Load in the data from skipped cohorts

- Use this link: [https://raw.githubusercontent.com/adnguyen/Circadian\\_rhythm\\_runs\\_seasonal\\_timing/master/Data/2017-10-22\\_skipped\\_apple\\_cohort\\_eclosions.csv](https://raw.githubusercontent.com/adnguyen/Circadian_rhythm_runs_seasonal_timing/master/Data/2017-10-22_skipped_apple_cohort_eclosions.csv)

2. Plot (using ggplot) a histogram of eclosion\_days

```
eclosions<-fread("https://raw.githubusercontent.com/adnguyen/Circadian_rhythm_runs_seasonal_timing/master/Data/2017-10-22_skipped_apple_cohort_eclosions.csv")
```