Sleep/Wake Analysis

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3/25/2022

```r
library(tidyverse)
library(lme4)
```

```r
xl <- read.csv("../data/WT_McKO_combined_sleep.csv")
colnames(xl)[1] <- gsub('^...','',colnames(xl)[1])

t_wt <- xl %>%
    group_by(Transmitter, Genotype, ZT, Day) %>%
    dplyr::summarise(sum_wake = sum(Wake),
                     sum_sws = sum(SWS),
                     sum_ps = sum(PS),
                     sum_art = sum(Artifact))
```

```
## `summarise()` has grouped output by 'Transmitter', 'Genotype', 'ZT'. You can override using the `.gro
```

```r
t_wt$PercentWake <- (t_wt$sum_wake / (t_wt$sum_sws + t_wt$sum_wake + t_wt$sum_ps + t_wt$sum_art))
t_wt$PercentSWS <- (t_wt$sum_sws / (t_wt$sum_sws + t_wt$sum_wake + t_wt$sum_ps + t_wt$sum_art))
t_wt$PercentPS <- (t_wt$sum_ps / (t_wt$sum_sws + t_wt$sum_wake + t_wt$sum_ps + t_wt$sum_art))
t_wt$PercentArt <- ((t_wt$sum_art)/ (t_wt$sum_sws + t_wt$sum_wake + t_wt$sum_ps + t_wt$sum_art))

t_wt <- t_wt %>% dplyr::mutate(phase= ifelse(ZT>11, "dark", "light"))

t_wt$ZT <- as.factor(t_wt$ZT)


SumStatwt <- dplyr::summarise(group_by(t_wt, Genotype, ZT, phase),
n = n(),
mean_Wake = mean(PercentWake),
sd_Wake = sd(PercentWake),
se_Wake = sd_Wake/sqrt(n),
mean_SWS = mean(PercentSWS),
sd_SWS = sd(PercentSWS),
se_SWS = sd_SWS/sqrt(n),
mean_PS = mean(PercentPS),
sd_PS = sd(PercentPS),
se_PS = sd_PS/sqrt(n))
```

```
## `summarise()` has grouped output by 'Genotype', 'ZT'. You can override using the `.groups` argument.
```

```
SumStatwt
```

```
## # A tibble: 48 x 13
## # Groups:   Genotype, ZT [48]
##    Genotype ZT    phase     n mean_Wake sd_Wake se_Wake mean_SWS sd_SWS se_SWS
##    <chr>    <fct> <chr> <int>     <dbl>   <dbl>   <dbl>    <dbl>  <dbl>  <dbl>
##  1 McKO     0     light    40     0.207   0.140  0.0222    0.720  0.141 0.0223
##  2 McKO     1     light    40     0.222   0.173  0.0274    0.709  0.162 0.0257
##  3 McKO     2     light    40     0.158   0.148  0.0234    0.767  0.147 0.0232
##  4 McKO     3     light    40     0.206   0.139  0.0219    0.716  0.128 0.0203
##  5 McKO     4     light    40     0.149   0.147  0.0232    0.774  0.145 0.0230
##  6 McKO     5     light    40     0.209   0.185  0.0292    0.726  0.176 0.0279
##  7 McKO     6     light    40     0.179   0.155  0.0244    0.750  0.149 0.0235
##  8 McKO     7     light    40     0.175   0.160  0.0253    0.748  0.159 0.0251
##  9 McKO     8     light    40     0.197   0.141  0.0224    0.724  0.132 0.0208
## 10 McKO     9     light    40     0.276   0.178  0.0281    0.654  0.171 0.0270
## # ... with 38 more rows, and 3 more variables: mean_PS <dbl>, sd_PS <dbl>,
## #   se_PS <dbl>
```

```
t_wt_days <- t_wt %>%
   group_by(Transmitter, Genotype, ZT, phase) %>%
   dplyr::summarise(mean_wake = mean(PercentWake),
                    mean_sws = mean(PercentSWS),
                    mean_ps = mean(PercentPS))
```

```
## `summarise()` has grouped output by 'Transmitter', 'Genotype', 'ZT'. You can override using the `.gr
```

```
SumStatwt$ZT <- as.numeric(as.character(SumStatwt$ZT))

wake_plot <- ggplot(data=SumStatwt, aes(ZT, mean_Wake, color=Genotype)) +
  geom_line(aes(group=Genotype)) +
  geom_point(stat="identity", position=position_dodge(), size=2)  +
  geom_errorbar(data=SumStatwt,
                aes(x=ZT, ymin=mean_Wake-se_Wake,
                    ymax=mean_Wake+se_Wake, color=Genotype),
                width=.5) +
  scale_y_continuous(labels = scales::percent,
                     name = "Average % Time Spent Awake",
                     limits = c(0.1,0.9)) +
  scale_x_continuous(limits=c(-1,24), breaks = seq(from=0, to=23, by=2)) +
  annotate("rect", xmin=12, xmax=23, ymin=-Inf, ymax=Inf,
           alpha=0.2, fill="black") +
  theme_bw()

#ggsave("../figures/wake_plot.svg", plot=wake_plot, height=4, width=7)

sleep_plot <- ggplot(data=SumStatwt, aes(ZT, mean_Sleep, color=Genotype)) +
  geom_line(aes(group=Genotype)) +
  geom_point(stat="identity", position=position_dodge(), size=2) +
  geom_errorbar(data=SumStatwt,
                aes(x=ZT, ymin=mean_Sleep-se_Sleep,
                    ymax=mean_Sleep+se_Sleep, color=Genotype),
```

```
                          width=.5) +
    scale_y_continuous(labels = scales::percent,
                       name = "Average % Time Spent Asleep",
                       limits = c(0.15,0.9)) +
    scale_x_continuous(limits=c(-1,24), breaks = seq(from=0, to=23, by=2)) +
    annotate("rect", xmin=12, xmax=23, ymin=-Inf, ymax=Inf,
             alpha=0.2, fill="black") +
    theme_bw()

#ggsave("../figures/sleep_plot.svg", plot=sleep_plot, height=4, width=7)

sws_plot <- ggplot(data=SumStatwt, aes(ZT, mean_SWS, color=Genotype)) +
    geom_line(aes(group=Genotype)) +
    geom_point(stat="identity", position=position_dodge(), size=2)  +
    geom_errorbar(data=SumStatwt,
                  aes(x=ZT, ymin=mean_SWS-se_SWS,
                      ymax=mean_SWS+se_SWS, color=Genotype),
                  width=.5) +
    scale_y_continuous(labels = scales::percent,
                       name = "Average % Time Spent in SWS",
                       limits = c(0.1,0.85)) +
    scale_x_continuous(limits=c(-1,24), breaks = seq(from=0, to=23, by=2)) +
    annotate("rect", xmin=12, xmax=23, ymin=-Inf, ymax=Inf,
             alpha=0.2, fill="black") +
    theme_bw()

#ggsave("../figures/sws_plot.svg", plot=sws_plot, height=4, width=7)

ps_plot <- ggplot(data=SumStatwt, aes(ZT, mean_PS, color=Genotype)) +
    geom_line(aes(group=Genotype)) +
    geom_point(stat="identity", position=position_dodge(), size=2)  +
    geom_errorbar(data=SumStatwt,
                  aes(x=ZT, ymin=mean_PS-se_PS,
                      ymax=mean_PS+se_PS, color=Genotype),
                  width=.5) +
    scale_y_continuous(labels = scales::percent,
                       name = "Average % Time Spent in Paradoxical Sleep",
                       limits = c(0.02,0.1)) +
    scale_x_continuous(limits=c(-1,24), breaks = seq(from=0, to=23, by=2)) +
    annotate("rect", xmin=12, xmax=23, ymin=-Inf, ymax=Inf,
             alpha=0.2, fill="black") +
    theme_bw()

#ggsave("../figures/ps_plot.png", plot=ps_plot, height=4, width=7)


SumStatwtp <- dplyr::summarise(group_by(t_wt, Genotype, phase),
n = n(),
mean_Wake = mean(PercentWake),
sd_Wake = sd(PercentWake),
se_Wake = sd_Wake/sqrt(n),
mean_SWS = mean(PercentSWS),
sd_SWS = sd(PercentSWS),
se_SWS = sd_SWS/sqrt(n),
```

```
mean_PS = mean(PercentPS),
sd_PS = sd(PercentPS),
se_PS = sd_PS/sqrt(n))
```

`summarise()` has grouped output by 'Genotype'. You can override using the `.groups` argument.

```
SumStatwtp
```

```
## # A tibble: 4 x 12
## # Groups:   Genotype [2]
##   Genotype phase      n mean_Wake sd_Wake se_Wake mean_SWS sd_SWS  se_SWS mean_PS
##   <chr>    <chr> <int>     <dbl>   <dbl>   <dbl>    <dbl>  <dbl>   <dbl>   <dbl>
## 1 McKO     dark    480     0.521   0.223 0.0102    0.437  0.211 0.00962  0.0395
## 2 McKO     light   480     0.229   0.180 0.00824   0.700  0.173 0.00790  0.0689
## 3 WT       dark    552     0.558   0.279 0.0119    0.395  0.267 0.0114   0.0437
## 4 WT       light   552     0.270   0.201 0.00854   0.653  0.190 0.00808  0.0745
## # ... with 2 more variables: sd_PS <dbl>, se_PS <dbl>
```

```
t_wtp <- t_wt %>%
  group_by(Transmitter, Genotype, phase)%>%
  dplyr::summarise(mean_wake = mean(PercentWake),
                   mean_sws = mean(PercentSWS),
                   mean_ps = mean(PercentPS),
                   mean_art = mean(PercentArt))
```

`summarise()` has grouped output by 'Transmitter', 'Genotype'. You can override using the `.groups` a

```
phase_sumstats <- t_wtp %>% group_by(Genotype, phase) %>%
  summarise(n = n(),
            mean_wake_perc = mean(mean_wake),
            sd_wake_perc = sd(mean_wake),
            mean_sws_perc = mean(mean_sws),
            sd_sws_perc = sd(mean_sws),
            mean_ps_perc = mean(mean_ps),
            sd_ps_perc = sd(mean_ps))
```

`summarise()` has grouped output by 'Genotype'. You can override using the `.groups` argument.

```
phase_sumstats
```

```
## # A tibble: 4 x 9
## # Groups:   Genotype [2]
##   Genotype phase      n mean_wake_perc sd_wake_perc mean_sws_perc sd_sws_perc
##   <chr>    <chr> <int>          <dbl>        <dbl>         <dbl>       <dbl>
## 1 McKO     dark      9          0.546       0.0700         0.414      0.0696
## 2 McKO     light     9          0.224       0.0349         0.704      0.0578
## 3 WT       dark     10          0.560       0.0411         0.392      0.0555
## 4 WT       light    10          0.268       0.0360         0.655      0.0696
## # ... with 2 more variables: mean_ps_perc <dbl>, sd_ps_perc <dbl>
```

```
temp <- t_wt %>%
  group_by(Transmitter, Genotype)%>%
  dplyr::summarise(mean_wake = mean(PercentWake),
                   mean_sws = mean(PercentSWS),
                   mean_ps = mean(PercentPS),
                   mean_Art = mean(PercentArt))
```

`summarise()` has grouped output by 'Transmitter'. You can override using the `.groups` argument.

```
max(temp$mean_Art)
```

[1] 0.006751485

```
temp %>% group_by(Genotype) %>%
  summarise(n = n(),
            wake_perc = mean(mean_wake),
            sd_wake = sd(mean_wake),
            sws_perc = mean(mean_sws),
            sd_sws = sd(mean_sws),
            ps_perc = mean(mean_ps),
            sd_ps = sd(mean_ps))
```

```
## # A tibble: 2 x 8
##   Genotype     n wake_perc sd_wake sws_perc sd_sws ps_perc  sd_ps
##   <chr>    <int>     <dbl>   <dbl>    <dbl>  <dbl>   <dbl>  <dbl>
## 1 McKO         9     0.385  0.0370    0.559 0.0497  0.0544 0.0233
## 2 WT          10     0.414  0.0327    0.524 0.0568  0.0590 0.0291
```

```
#ggplot() +
#  geom_bar(data=SumStatwtp, aes(phase, mean_Wake,fill=Genotype), stat="identity", position=position_do
#  geom_errorbar(data=SumStatwtp, aes(x=phase,ymin=mean_Wake - se_Wake, ymax=mean_Wake + se_Wake, fill=
#  geom_point(data=t_wtp, aes(x=phase, y=mean_wake, fill=Genotype), position=position_dodge(width=0.5))

#ggplot() +
#  geom_bar(data=SumStatwtp, aes(phase, mean_Sleep,fill=Genotype), stat="identity", position=position_d
#  geom_errorbar(data=SumStatwtp, aes(x=phase,ymin=mean_Sleep - se_Sleep, ymax=mean_Sleep + se_Sleep, f
#  geom_point(data=t_wtp, aes(x=phase, y=mean_sleep, fill=Genotype), position=position_dodge(width=0.5)
```

```
t_wt$ZT <- as.factor(t_wt$ZT)

t_wt$phase <- as.factor(t_wt$phase)
t_wt$Genotype <- as.factor(t_wt$Genotype)
t_wt_days$phase <- as.factor(t_wt_days$phase)
t_wt_days$Genotype <- as.factor(t_wt_days$Genotype)
t_wt_days$Transmitter <- as.factor(t_wt_days$Transmitter)

#over entire day
wake_day <- wilcox.test(mean_wake ~ Genotype, data= t_wt_days)
wake_day
```

```
## 
##  Wilcoxon rank sum test with continuity correction
## 
## data:  mean_wake by Genotype
## W = 24278, p-value = 0.2427
## alternative hypothesis: true location shift is not equal to 0
```

```
sws_day <- wilcox.test(mean_sws ~ Genotype, data=t_wt_days)
sws_day
```

```
## 
##  Wilcoxon rank sum test with continuity correction
## 
## data:  mean_sws by Genotype
## W = 27970, p-value = 0.1447
## alternative hypothesis: true location shift is not equal to 0
```

```
ps_day <- wilcox.test(mean_ps ~ Genotype, data=t_wt_days)
ps_day
```

```
## 
##  Wilcoxon rank sum test with continuity correction
## 
## data:  mean_ps by Genotype
## W = 24881, p-value = 0.4598
## alternative hypothesis: true location shift is not equal to 0
```

```
#by phase
lmer_wake <- lmer(mean_wake ~ phase*Genotype+(1|Transmitter), data = t_wt_days)
#plot(lmer_wake, type=c("p","smooth"), col.line=1)
#lattice::qqmath(lmer_wake)
anova(lmer_wake)
```

```
## Analysis of Variance Table
##                 npar  Sum Sq Mean Sq  F value
## phase              1 10.7003 10.7003 432.2658
## Genotype           1  0.0838  0.0838   3.3843
## phase:Genotype     1  0.0253  0.0253   1.0225
```

```
emmeans::emmeans(lmer_wake, pairwise ~ Genotype | phase)$contrasts
```

```
## phase = dark:
##  contrast  estimate     SE   df t.ratio p.value
##  McKO - WT  -0.0145 0.0218 56.7  -0.666  0.5080
## 
## phase = light:
##  contrast  estimate     SE   df t.ratio p.value
##  McKO - WT  -0.0443 0.0218 56.7  -2.038  0.0463
## 
## Degrees-of-freedom method: kenward-roger
```

```
emmeans::emmeans(lmer_wake, pairwise ~ phase | Genotype)$contrasts
```

```
## Genotype = McKO:
##  contrast      estimate      SE  df t.ratio p.value
##  dark - light     0.322 0.0214 435  15.043  <.0001
##
## Genotype = WT:
##  contrast      estimate      SE  df t.ratio p.value
##  dark - light     0.292 0.0203 435  14.387  <.0001
##
## Degrees-of-freedom method: kenward-roger
```

```
lmer_sws <- lmer(mean_sws ~ phase*Genotype+(1|Transmitter), data = t_wt_days)
#plot(lmer_sws, type=c("p","smooth"), col.line=1)
#lattice::qqmath(lmer_sws)
anova(lmer_sws)
```

```
## Analysis of Variance Table
##                npar Sum Sq Mean Sq  F value
## phase           1 8.6962  8.6962 405.4033
## Genotype        1 0.0442  0.0442   2.0607
## phase:Genotype  1 0.0208  0.0208   0.9675
```

```
emmeans::emmeans(lmer_sws, pairwise ~ Genotype | phase)$contrasts
```

```
## phase = dark:
##  contrast estimate      SE   df t.ratio p.value
##  McKO - WT   0.0218 0.0282 29.1   0.774  0.4451
##
## phase = light:
##  contrast estimate      SE   df t.ratio p.value
##  McKO - WT   0.0488 0.0282 29.1   1.733  0.0937
##
## Degrees-of-freedom method: kenward-roger
```

```
emmeans::emmeans(lmer_sws, pairwise ~ phase | Genotype)$contrasts
```

```
## Genotype = McKO:
##  contrast      estimate      SE  df t.ratio p.value
##  dark - light   -0.290 0.0199 435 -14.571  <.0001
##
## Genotype = WT:
##  contrast      estimate      SE  df t.ratio p.value
##  dark - light   -0.263 0.0189 435 -13.930  <.0001
##
## Degrees-of-freedom method: kenward-roger
```

```
lmer_ps <- lmer(mean_ps ~ phase*Genotype+(1|Transmitter), data = t_wt_days)
#plot(lmer_ps, type=c("p","smooth"), col.line=1)
#lattice::qqmath(lmer_ps)
anova(lmer_ps)
```

```
## Analysis of Variance Table
##                  npar    Sum Sq   Mean Sq  F value
## phase               1 0.115184 0.115184 178.5871
## Genotype            1 0.000092 0.000092   0.1430
## phase:Genotype      1 0.000139 0.000139   0.2159
```

```
#emmeans::emmeans(lmer_ps, pairwise ~ Genotype | phase)$contrasts
emmeans::emmeans(lmer_ps, pairwise ~ phase | Genotype)$contrasts
```

```
## Genotype = McKO:
##  contrast      estimate       SE  df t.ratio p.value
##  dark - light   -0.0330 0.00346 435  -9.535  <.0001
##
## Genotype = WT:
##  contrast      estimate       SE  df t.ratio p.value
##  dark - light   -0.0307 0.00328 435  -9.375  <.0001
##
## Degrees-of-freedom method: kenward-roger
```

```
#by ZT
t_wt_days$ZT <- as.factor(t_wt_days$ZT)

lmer_wake_zt <- lmer(mean_wake ~ ZT*Genotype+(1|Transmitter), data = t_wt_days)
#plot(lmer_wake_zt, type=c("p","smooth"), col.line=1)
#lattice::qqmath(lmer_wake_zt)
anova(lmer_wake_zt)
```

```
## Analysis of Variance Table
##             npar  Sum Sq Mean Sq F value
## ZT            23 13.4075 0.58293 32.0622
## Genotype       1  0.0615 0.06153  3.3843
## ZT:Genotype   23  0.9773 0.04249  2.3372
```

```
#emmeans::emmeans(lmer_wake_zt, pairwise ~ ZT | Genotype)
emmeans::emmeans(lmer_wake_zt, pairwise ~  Genotype | ZT)$contrasts
```

```
## ZT = 0:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -1.23e-01 0.0627 403  -1.956  0.0511
##
## ZT = 1:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -7.01e-04 0.0627 403  -0.011  0.9911
##
## ZT = 2:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -6.66e-02 0.0627 403  -1.062  0.2889
##
## ZT = 3:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -4.31e-02 0.0627 403  -0.687  0.4924
##
```

```
## ZT = 4:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -1.01e-01 0.0627 403  -1.612  0.1077
##
## ZT = 5:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  1.00e-02 0.0627 403   0.160  0.8728
##
## ZT = 6:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  2.54e-03 0.0627 403   0.040  0.9677
##
## ZT = 7:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -1.28e-01 0.0627 403  -2.040  0.0420
##
## ZT = 8:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -5.38e-02 0.0627 403  -0.857  0.3917
##
## ZT = 9:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -2.96e-02 0.0627 403  -0.472  0.6372
##
## ZT = 10:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  9.08e-03 0.0627 403   0.145  0.8850
##
## ZT = 11:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -8.19e-03 0.0627 403  -0.131  0.8962
##
## ZT = 12:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  1.18e-01 0.0627 403   1.884  0.0603
##
## ZT = 13:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -8.80e-02 0.0627 403  -1.403  0.1613
##
## ZT = 14:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -2.34e-01 0.0627 403  -3.725  0.0002
##
## ZT = 15:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -1.65e-01 0.0627 403  -2.632  0.0088
##
## ZT = 16:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -5.53e-02 0.0627 403  -0.882  0.3781
##
## ZT = 17:
##  contrast   estimate     SE  df t.ratio p.value
```

```
##  McKO - WT  6.15e-02 0.0627 403    0.981   0.3274
##
## ZT = 18:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  1.71e-01 0.0627 403    2.722   0.0068
##
## ZT = 19:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  9.30e-02 0.0627 403    1.483   0.1389
##
## ZT = 20:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  7.88e-02 0.0627 403    1.256   0.2097
##
## ZT = 21:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -1.05e-02 0.0627 403   -0.168   0.8666
##
## ZT = 22:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  5.45e-05 0.0627 403    0.001   0.9993
##
## ZT = 23:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT -1.44e-01 0.0627 403   -2.289   0.0226
##
## Degrees-of-freedom method: kenward-roger
```

```r
lmer_sws_zt <- lmer(mean_sws ~ ZT*Genotype+(1|Transmitter), data = t_wt_days)
#plot(lmer_sws_zt, type=c("p","smooth"), col.line=1)
#lattice::qqmath(lmer_sws_zt)
anova(lmer_sws_zt)
```

```
## Analysis of Variance Table
##              npar  Sum Sq Mean Sq F value
## ZT             23 11.0658 0.48112 30.8128
## Genotype        1  0.0322 0.03218  2.0607
## ZT:Genotype    23  0.8769 0.03813  2.4418
```

```r
#emmeans::emmeans(lmer_sws_zt, pairwise ~ ZT | Genotype)
emmeans::emmeans(lmer_sws_zt, pairwise ~  Genotype | ZT)$contrasts
```

```
## ZT = 0:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  0.10913 0.0614 301    1.779   0.0763
##
## ZT = 1:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  0.00306 0.0614 301    0.050   0.9602
##
## ZT = 2:
##  contrast   estimate     SE  df t.ratio p.value
##  McKO - WT  0.07281 0.0614 301    1.187   0.2363
```

```
## 
## ZT = 3:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.02681 0.0614 301   0.437  0.6625
## 
## ZT = 4:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.10417 0.0614 301   1.698  0.0906
## 
## ZT = 5:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.01395 0.0614 301   0.227  0.8203
## 
## ZT = 6:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.01475 0.0614 301   0.240  0.8102
## 
## ZT = 7:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.12452 0.0614 301   2.029  0.0433
## 
## ZT = 8:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.06289 0.0614 301   1.025  0.3062
## 
## ZT = 9:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.03490 0.0614 301   0.569  0.5699
## 
## ZT = 10:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.00325 0.0614 301   0.053  0.9578
## 
## ZT = 11:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.01588 0.0614 301   0.259  0.7960
## 
## ZT = 12:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT -0.10121 0.0614 301  -1.650  0.1001
## 
## ZT = 13:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.10178 0.0614 301   1.659  0.0982
## 
## ZT = 14:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.23898 0.0614 301   3.895  0.0001
## 
## ZT = 15:
##  contrast estimate     SE  df t.ratio p.value
##  McKO - WT  0.16625 0.0614 301   2.709  0.0071
## 
## ZT = 16:
```

```
## contrast  estimate     SE  df t.ratio p.value
##  McKO - WT  0.05593 0.0614 301    0.911  0.3628
##
## ZT = 17:
##  contrast  estimate     SE  df t.ratio p.value
##  McKO - WT -0.05698 0.0614 301   -0.929  0.3538
##
## ZT = 18:
##  contrast  estimate     SE  df t.ratio p.value
##  McKO - WT -0.15191 0.0614 301   -2.476  0.0138
##
## ZT = 19:
##  contrast  estimate     SE  df t.ratio p.value
##  McKO - WT -0.08947 0.0614 301   -1.458  0.1459
##
## ZT = 20:
##  contrast  estimate     SE  df t.ratio p.value
##  McKO - WT -0.06989 0.0614 301   -1.139  0.2556
##
## ZT = 21:
##  contrast  estimate     SE  df t.ratio p.value
##  McKO - WT  0.02042 0.0614 301    0.333  0.7395
##
## ZT = 22:
##  contrast  estimate     SE  df t.ratio p.value
##  McKO - WT  0.01968 0.0614 301    0.321  0.7487
##
## ZT = 23:
##  contrast  estimate     SE  df t.ratio p.value
##  McKO - WT  0.12827 0.0614 301    2.091  0.0374
##
## Degrees-of-freedom method: kenward-roger
```

```r
lmer_ps_zt <- lmer(mean_ps ~ ZT*Genotype+(1|Transmitter), data = t_wt_days)
#plot(lmer_ps_zt, type=c("p","smooth"), col.line=1)
#lattice::qqmath(lmer_ps_zt)
anova(lmer_ps_zt)
```

```
## Analysis of Variance Table
##              npar    Sum Sq   Mean Sq F value
## ZT             23 0.133665 0.0058115  9.1017
## Genotype        1 0.000091 0.0000913  0.1430
## ZT:Genotype    23 0.012563 0.0005462  0.8555
```

```r
#emmeans::emmeans(lmer_ps_zt, pairwise ~ ZT | Genotype)
emmeans::emmeans(lmer_ps_zt, pairwise ~  Genotype | ZT)$contrasts
```

```
## ZT = 0:
##  contrast  estimate     SE   df t.ratio p.value
##  McKO - WT 0.014341 0.0167 57.5   0.860  0.3932
##
## ZT = 1:
##  contrast  estimate     SE   df t.ratio p.value
```

```
##  McKO - WT -0.001925 0.0167 57.5  -0.115  0.9085
##
## ZT = 2:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.004487 0.0167 57.5  -0.269  0.7888
##
## ZT = 3:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT  0.016226 0.0167 57.5   0.973  0.3345
##
## ZT = 4:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.001553 0.0167 57.5  -0.093  0.9261
##
## ZT = 5:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.023187 0.0167 57.5  -1.391  0.1696
##
## ZT = 6:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.016316 0.0167 57.5  -0.979  0.3318
##
## ZT = 7:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT  0.005188 0.0167 57.5   0.311  0.7568
##
## ZT = 8:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.007859 0.0167 57.5  -0.471  0.6391
##
## ZT = 9:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.003685 0.0167 57.5  -0.221  0.8258
##
## ZT = 10:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.011978 0.0167 57.5  -0.719  0.4753
##
## ZT = 11:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.006817 0.0167 57.5  -0.409  0.6841
##
## ZT = 12:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.017422 0.0167 57.5  -1.045  0.3003
##
## ZT = 13:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.010501 0.0167 57.5  -0.630  0.5312
##
## ZT = 14:
##  contrast   estimate    SE   df t.ratio p.value
##  McKO - WT -0.003280 0.0167 57.5  -0.197  0.8447
##
```

```
## ZT = 15:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT   0.000754 0.0167 57.5   0.045  0.9641
##
## ZT = 16:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT   0.001628 0.0167 57.5   0.098  0.9225
##
## ZT = 17:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT  -0.003584 0.0167 57.5  -0.215  0.8305
##
## ZT = 18:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT  -0.018485 0.0167 57.5  -1.109  0.2721
##
## ZT = 19:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT  -0.003875 0.0167 57.5  -0.232  0.8170
##
## ZT = 20:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT  -0.007489 0.0167 57.5  -0.449  0.6549
##
## ZT = 21:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT  -0.008013 0.0167 57.5  -0.481  0.6326
##
## ZT = 22:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT  -0.017233 0.0167 57.5  -1.034  0.3056
##
## ZT = 23:
##  contrast    estimate     SE    df t.ratio p.value
##  McKO - WT   0.018886 0.0167 57.5   1.133  0.2620
##
## Degrees-of-freedom method: kenward-roger
```