

Sleep/Wake Analysis

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3/25/2022

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

```
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 `.groups` argument.

```
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 `.groups` argument.

```
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` argument.

```
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),
            median_wake = median(mean_wake),
```

```

    sws_perc = mean(mean_sws),
    sd_sws = sd(mean_sws),
    median_sws = median(mean_sws),
    ps_perc = mean(mean_ps),
    sd_ps = sd(mean_ps),
    median_ps = median(mean_ps))

## # A tibble: 2 x 11
##   Genotype      n wake_perc sd_wake median_wake sws_perc sd_sws median_sws
##   <chr>      <int>   <dbl>   <dbl>      <dbl>   <dbl> <dbl>      <dbl>
## 1 McKO         9     0.385  0.0370      0.372   0.559 0.0497      0.579
## 2 WT          10     0.414  0.0327      0.408   0.524 0.0568      0.534
## # ... with 3 more variables: ps_perc <dbl>, sd_ps <dbl>, median_ps <dbl>

#ggplot() +
#  geom_bar(data=SumStatwtp, aes(phase, mean_Wake, fill=Genotype), stat="identity", position=position_dodge(width=0.5))
#  geom_errorbar(data=SumStatwtp, aes(x=phase, ymin=mean_Wake - se_Wake, ymax=mean_Wake + se_Wake, fill=Genotype), position=position_dodge(width=0.5))
#  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_dodge(width=0.5))
#  geom_errorbar(data=SumStatwtp, aes(x=phase, ymin=mean_Sleep - se_Sleep, ymax=mean_Sleep + se_Sleep, fill=Genotype), position=position_dodge(width=0.5))
#  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

wake_Zstat <- qnorm(wake_day$p.value/2)
abs(wake_Zstat)/sqrt(9.5)

## [1] 0.3790348

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
sws_Zstat <- qnorm(sws_day$p.value/2)
abs(sws_Zstat)/sqrt(9.5)

## [1] 0.4732451

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
ps_Zstat <- qnorm(ps_day$p.value/2)
abs(ps_Zstat)/sqrt(9.5)

## [1] 0.2397976

#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

emmmeans::emmmeans(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

emmmeans::emmmeans(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
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

#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:

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## 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

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##
## 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
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
#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
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## 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
##

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## 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

```