

Sleep_score_CTB

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

```
#1 hour bins (by ZT)
xl <- read.csv("../data/McKO_WT_combined.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$PercentSleep <- ((t_wt$sum_sws + t_wt$sum_ps) / (t_wt$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_Sleep = mean(PercentSleep),
  sd_Sleep = sd(PercentSleep),
  se_Sleep = sd_Sleep/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

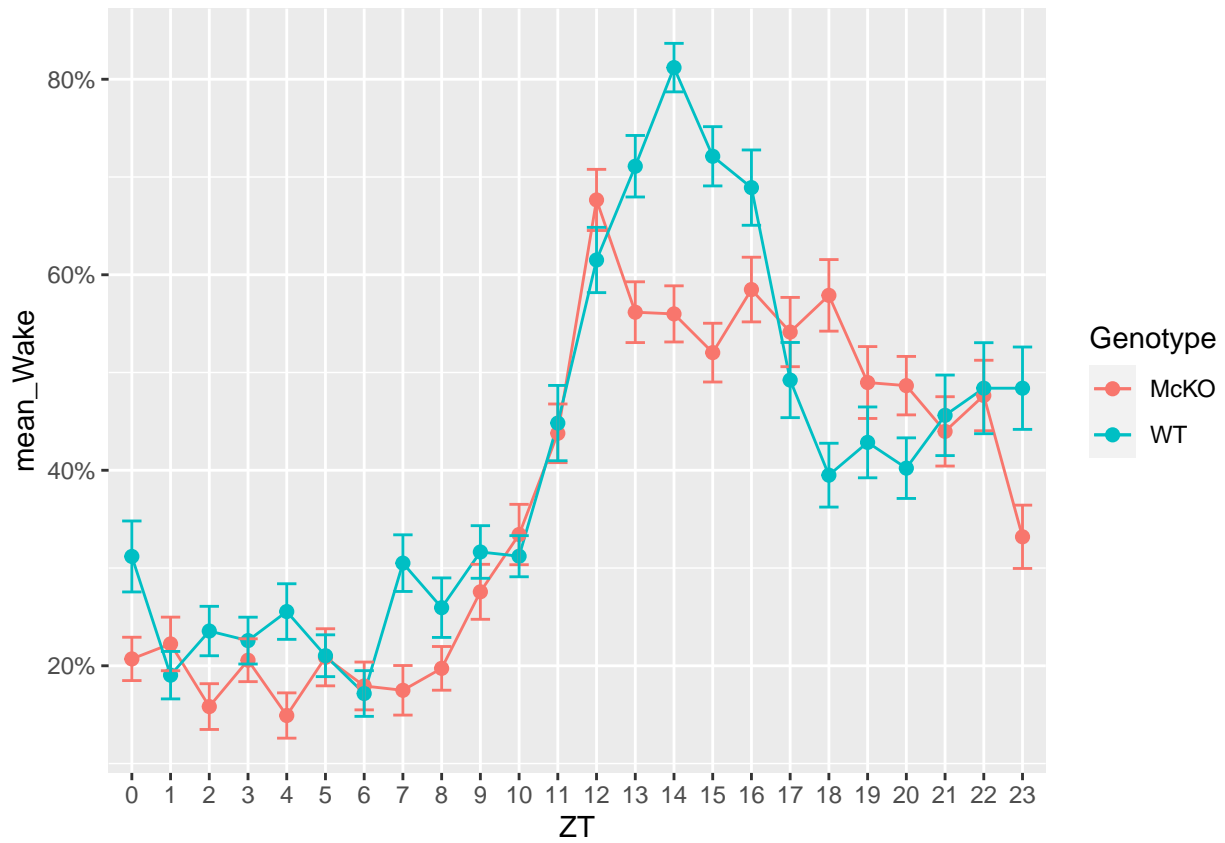
```
## # A tibble: 48 x 16
## # Groups:   Genotype, ZT [48]
##   Genotype ZT phase n mean_Wake sd_Wake se_Wake mean_Sleep sd_Sleep
##   <chr> <fct> <chr> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 McKO 0 light 40 0.207 0.140 0.0222 0.791 0.141
## 2 McKO 1 light 40 0.222 0.173 0.0274 0.776 0.174
## 3 McKO 2 light 40 0.158 0.148 0.0234 0.841 0.148
## 4 McKO 3 light 40 0.206 0.139 0.0219 0.792 0.141
## 5 McKO 4 light 40 0.149 0.147 0.0232 0.850 0.147
## 6 McKO 5 light 40 0.209 0.185 0.0292 0.789 0.185
## 7 McKO 6 light 40 0.179 0.155 0.0244 0.819 0.156
## 8 McKO 7 light 40 0.175 0.160 0.0253 0.824 0.161
## 9 McKO 8 light 40 0.197 0.141 0.0224 0.801 0.143
## 10 McKO 9 light 40 0.276 0.178 0.0281 0.722 0.178
## # ... with 38 more rows, and 7 more variables: se_Sleep <dbl>, mean_SWS <dbl>,
## # sd_SWS <dbl>, se_SWS <dbl>, 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),
                  mean_sleep = mean(PercentSleep))
```

```
## `summarise()` has grouped output by 'Transmitter', 'Genotype', 'ZT'. You can override using the `.groups` argument.
ggplot(data=SumStatwt, aes(ZT, mean_Wake, color=Genotype)) + geom_line(aes(group=Genotype)) + geom_point(aes(group=Genotype))
```

```
## Warning: Ignoring unknown aesthetics: fill
```

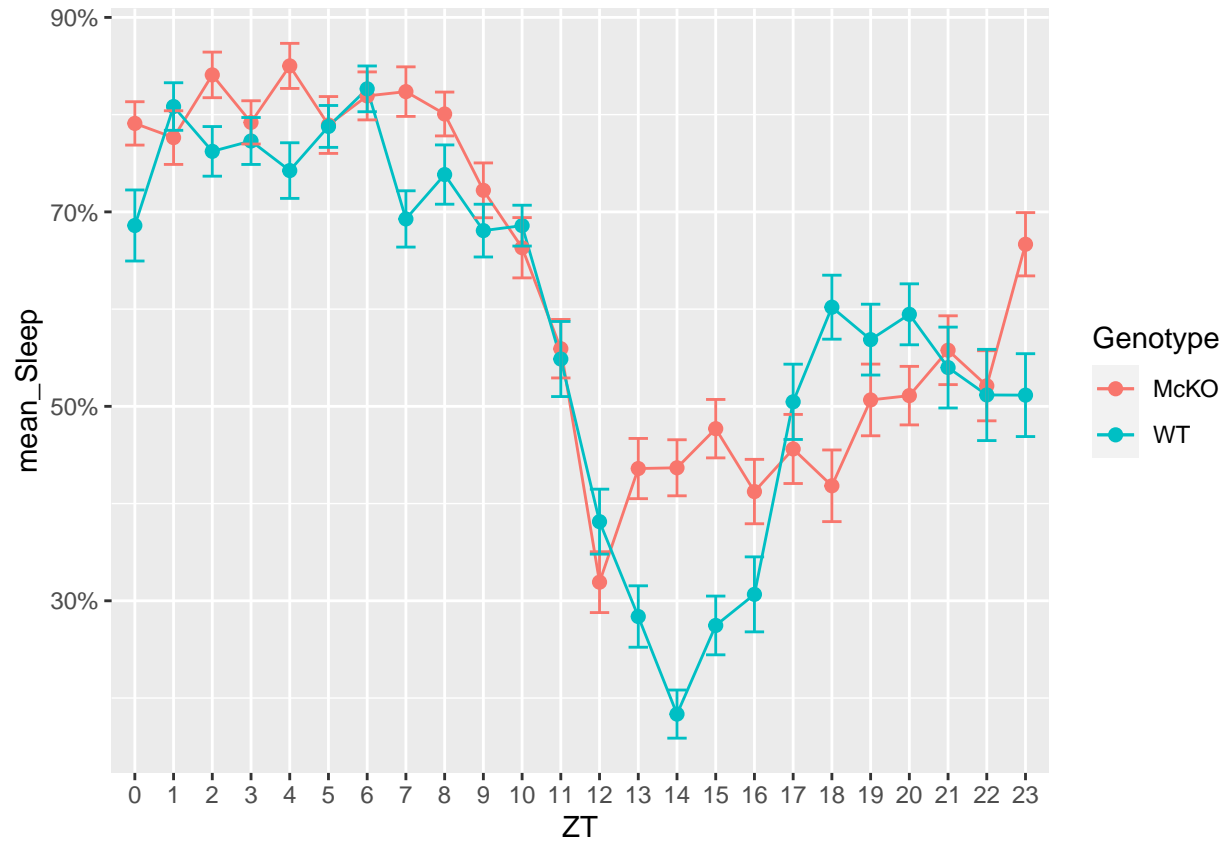
```
## Warning: Width not defined. Set with `position_dodge(width = ?)`
```



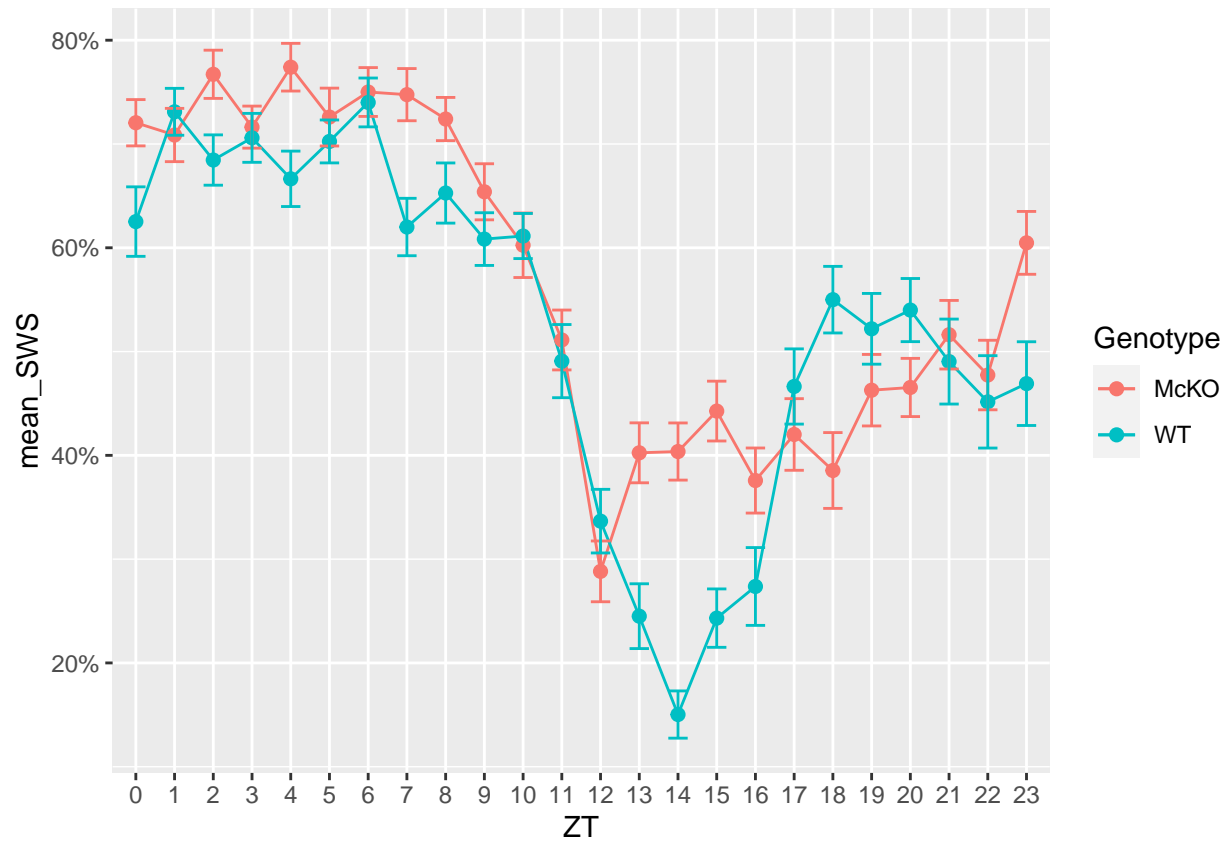
```
ggplot(data=SumStatwt, aes(ZT, mean_Sleep, color=Genotype)) + geom_line(aes(group=Genotype)) + geom_point(aes(group=Genotype))
```

```
## Warning: Ignoring unknown aesthetics: fill
```

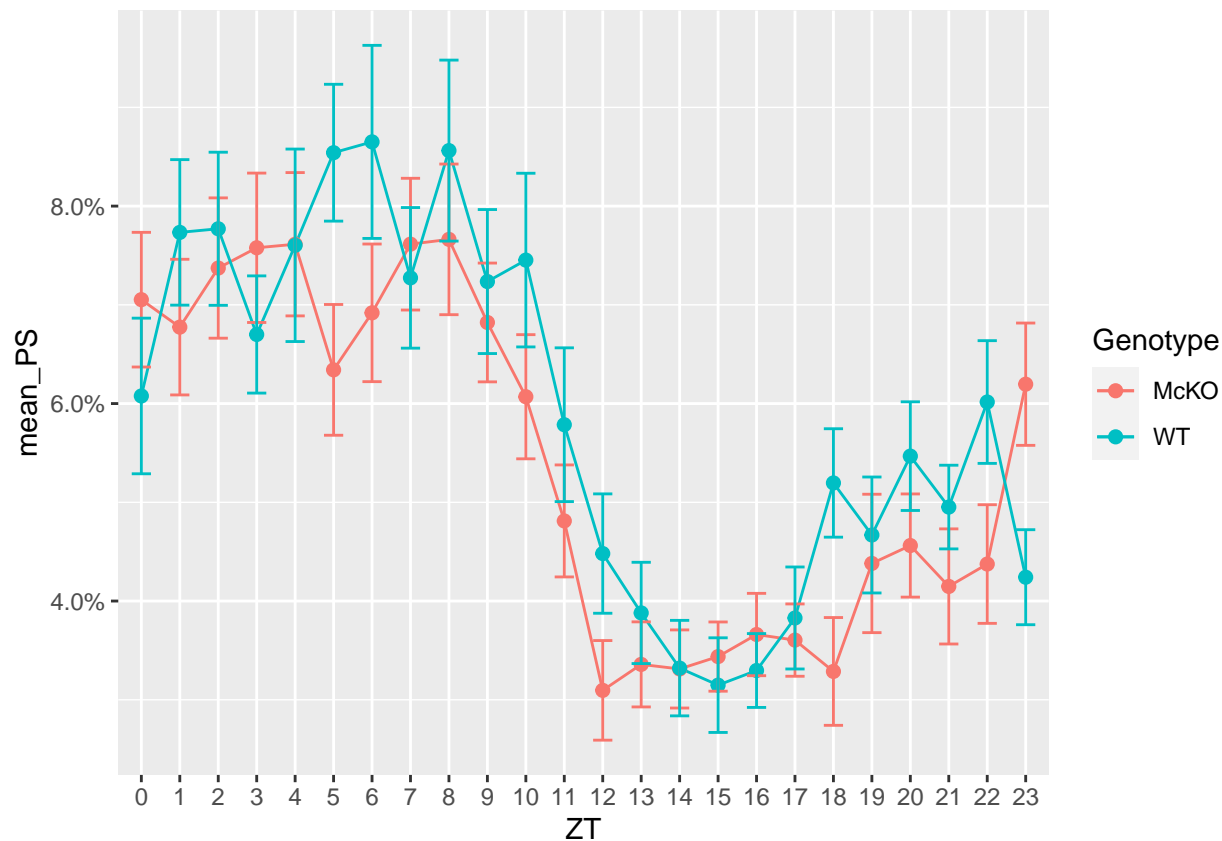
```
## Warning: Width not defined. Set with `position_dodge(width = ?)`
```



```
ggplot(data=SumStatwt, aes(ZT, mean_SWS, color=Genotype)) + geom_line(aes(group=Genotype)) + geom_point
## Warning: Width not defined. Set with `position_dodge(width = ?)`
```



```
ggplot(data=SumStatwt, aes(ZT, mean_PS, color=Genotype)) + geom_line(aes(group=Genotype)) + geom_point(
## Warning: Width not defined. Set with `position_dodge(width = ?)`
```



```
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_Sleep = mean(PercentSleep),
  sd_Sleep = sd(PercentSleep),
  se_Sleep = sd_Sleep/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 15
## # Groups:   Genotype [2]
##   Genotype phase      n mean_Wake sd_Wake se_Wake mean_Sleep sd_Sleep se_Sleep
##   <chr>      <chr> <int>   <dbl>  <dbl>  <dbl>     <dbl>  <dbl>  <dbl>
## 1 McKO      dark   480    0.521  0.223  0.0102    0.477   0.224  0.0102
## 2 McKO      light  480    0.229  0.180  0.00824    0.769   0.181  0.00828
## 3 WT        dark   552    0.558  0.279  0.0119    0.439   0.280  0.0119
## 4 WT        light  552    0.270  0.201  0.00854    0.728   0.202  0.00858
```

```
## # ... with 6 more variables: mean_SWS <dbl>, sd_SWS <dbl>, se_SWS <dbl>,
## #   mean_PS <dbl>, 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_sleep = mean(PercentSleep))
```

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

```
#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$phase <- as.factor(t_wt$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)
```

```
#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
```

```
sleep_day <- wilcox.test(mean_sleep ~ Genotype, data=t_wt_days)
sleep_day
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: mean_sleep by Genotype
## W = 27620, p-value = 0.2265
## 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

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)

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

## Analysis of Variance Table
##              npar  Sum Sq Mean Sq  F value
## phase              1 10.8130  10.8130  432.6017
## Genotype            1  0.0937   0.0937   3.7486
## phase:Genotype      1  0.0243   0.0243   0.9719

emmmeans::emmmeans(lmer_sleep, pairwise ~ Genotype | phase)$contrasts

## phase = dark:
## contrast estimate      SE  df t.ratio p.value
## McKO - WT   0.0161 0.0217 57.9   0.741  0.4614
##
## phase = light:
## contrast estimate      SE  df t.ratio p.value
## McKO - WT   0.0453 0.0217 57.9   2.088  0.0412
##

```



```
## Degrees-of-freedom method: kenward-roger
#emmeans::emmeans(lmer_sleep, pairwise ~ phase | Genotype)

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)

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

## phase = dark:
## contrast estimate      SE   df t.ratio p.value
## McKO - WT -0.00572 0.0124 18.3  -0.460  0.6508
##
## phase = light:
## contrast estimate      SE   df t.ratio p.value
## McKO - WT -0.00350 0.0124 18.3  -0.282  0.7811
##
## 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_sleep_zt <- lmer(mean_sleep ~ ZT*Genotype+(1|Transmitter), data = t_wt_days)
#plot(lmer_sleep_zt, type=c("p","smooth"), col.line=1)
#lattice::qqmath(lmer_sleep_zt)
anova(lmer_sleep_zt)

## Analysis of Variance Table
##              npar  Sum Sq Mean Sq F value
## ZT              23 13.5438  0.58886 32.0848
## Genotype         1  0.0688  0.06880  3.7486
## ZT:Genotype      23  0.9905  0.04306  2.3464

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

## ZT = 0:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.12347 0.063 403   1.961  0.0506
##
## ZT = 1:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.00114 0.063 403   0.018  0.9856
##
## ZT = 2:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.06832 0.063 403   1.085  0.2786
##
## ZT = 3:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.04304 0.063 403   0.683  0.4947
##
## ZT = 4:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.10262 0.063 403   1.630  0.1039
##
## ZT = 5:
## contrast estimate      SE df t.ratio p.value
## McKO - WT -0.00923 0.063 403  -0.147  0.8835
##
## ZT = 6:
## contrast estimate      SE df t.ratio p.value
## McKO - WT -0.00157 0.063 403  -0.025  0.9801
##
## ZT = 7:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.12970 0.063 403   2.060  0.0401
##
## ZT = 8:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.05503 0.063 403   0.874  0.3826
##
## ZT = 9:
## contrast estimate      SE df t.ratio p.value
## McKO - WT  0.03121 0.063 403   0.496  0.6204
```

```

##
## ZT = 10:
## contrast estimate SE df t.ratio p.value
## McKO - WT -0.00873 0.063 403 -0.139 0.8899
##
## ZT = 11:
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.00906 0.063 403 0.144 0.8857
##
## ZT = 12:
## contrast estimate SE df t.ratio p.value
## McKO - WT -0.11864 0.063 403 -1.884 0.0603
##
## ZT = 13:
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.09128 0.063 403 1.450 0.1479
##
## ZT = 14:
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.23570 0.063 403 3.743 0.0002
##
## ZT = 15:
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.16700 0.063 403 2.652 0.0083
##
## ZT = 16:
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.05756 0.063 403 0.914 0.3612
##
## ZT = 17:
## contrast estimate SE df t.ratio p.value
## McKO - WT -0.06056 0.063 403 -0.962 0.3367
##
## ZT = 18:
## contrast estimate SE df t.ratio p.value
## McKO - WT -0.17039 0.063 403 -2.706 0.0071
##
## ZT = 19:
## contrast estimate SE df t.ratio p.value
## McKO - WT -0.09334 0.063 403 -1.482 0.1390
##
## ZT = 20:
## contrast estimate SE df t.ratio p.value
## McKO - WT -0.07738 0.063 403 -1.229 0.2199
##
## ZT = 21:
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.01241 0.063 403 0.197 0.8439
##
## ZT = 22:
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.00244 0.063 403 0.039 0.9691
##
## ZT = 23:

```

```
## contrast estimate SE df t.ratio p.value
## McKO - WT 0.14716 0.063 403 2.337 0.0199
##
## 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:
## 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
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
## 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
```