McKO sleep data

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```
library(tidyverse)
## -- Attaching packages ------ tidyverse 1.3.1 --
## v ggplot2 3.3.5 v purrr
                                0.3.4
## v tibble 3.1.5 v dplyr 1.0.7
## v tidyr 1.1.4 v stringr 1.4.0
## v readr
           2.0.2
                   v forcats 0.5.1
## -- Conflicts ----- tidyverse conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                   masks stats::lag()
library(ggpubr)
#making the dataframe
#from Nik's analysis
Genotype <- c("McKO", "McKO", "WT", "WT")</pre>
condition <- c("Light", "Dark", "Light", "Dark")</pre>
ns \leftarrow c(7, 7, 9, 9)
mean_sleep <- c(0.6520544, 0.4565667, 0.6436465, 0.3419856)
sds \leftarrow c(0.0840014, 0.1064821, 0.0614947, 0.0661068)
ses < c(0.0317495, 0.0402464, 0.0204982, 0.0220356)
sleepdata <- tibble(Genotype, condition, ns, mean_sleep, sds, ses)</pre>
sleepdata
## # A tibble: 4 x 6
    Genotype condition ns mean_sleep
                                          sds
##
     <chr>
             <chr> <dbl>
                                 <dbl> <dbl> <dbl>
## 1 McKO
             Light
                         7
                                  0.652 0.0840 0.0317
                          7
## 2 McKO
             Dark
                                 0.457 0.106 0.0402
## 3 WT
                         9
                                  0.644 0.0615 0.0205
             Light
## 4 WT
                                  0.342 0.0661 0.0220
             Dark
sleep_plot <- sleepdata %>% ggplot(aes(x=condition, y=mean_sleep, fill=Genotype)) +
 geom_bar(stat="identity", position="dodge") +
 geom_errorbar(stat="identity",
```

```
aes(ymin=mean_sleep-ses, ymax=mean_sleep+ses),
                position=position_dodge(0.9),
                width=0.2) +
  labs(x="Light Condition",
       y="Time Spent Sleeping") +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1),
                     expand = expansion(mult = c(0, 0.1))) +
  scale_fill_manual(values = c("grey60", "grey20"))
ggsave("../figures/sleep_plot.png", plot=sleep_plot, height=3, width=5)
sleepdata_dark_only <- sleepdata %>%
  filter(condition == "Dark") %>%
  mutate(Genotype = fct_relevel(Genotype, c("WT", "McKO")))
sleep_plot_dark_only <- sleepdata_dark_only %>% ggplot(aes(x=Genotype, y=mean_sleep)) +
  geom_bar(stat="identity", position="dodge") +
  geom_errorbar(stat="identity",
                aes(ymin=mean_sleep-ses, ymax=mean_sleep+ses),
                position=position dodge(0.9),
                width=0.2) +
  labs(x="",
       y="Time Spent Sleeping") +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1),
                     expand = expansion(mult = c(0, 0.1))) +
  scale_fill_manual(values = c("grey60", "grey20"))
ggsave("../figures/sleep_plot_dark_only.png", plot=sleep_plot_dark_only, height=2, width=2.5)
```