

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 3.1.6       v dplyr 1.0.7
## v tidyr 1.1.4        v stringr 1.4.0
## v readr 2.1.0        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")
condition <- c("Light", "Dark", "Light", "Dark")
ns <- c(7, 7, 9, 9)
mean_sleep <- c(0.6520544, 0.4565667, 0.6436465, 0.3419856)
sds <- 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)

sleepdata

## # A tibble: 4 x 6
##   Genotype condition    ns mean_sleep    sds    ses
##   <chr>    <chr>      <dbl>      <dbl> <dbl> <dbl>
## 1 McKO    Light         7      0.652 0.0840 0.0317
## 2 McKO    Dark          7      0.457 0.106 0.0402
## 3 WT      Light         9      0.644 0.0615 0.0205
## 4 WT      Dark          9      0.342 0.0661 0.0220

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,
```

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      expand = expansion(mult = c(0, 0.1))) +  
scale_fill_manual(values = c("grey60", "grey20"))  
  
ggsave("../figures/sleep_plot.png", plot=sleep_plot, height=5, width=8)
```