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## Visualizing Multi-dimensional Relationships

## New functions covered:
# select()
# rename()
# geom_errorbar()
# scale_fill_brewer()
# facet_wrap()
# geom_line()
# theme()
# scale_color_discrete()

## Load tidyverse as usual (which includes ggplot2)
library(tidyverse)
library(viridis)

maait <- read_csv("maait.csv")
####

## Quick look
glimpse(maait)

## See the first few rows
maait

## Last few rows
tail(maait)

## Focus on a subset of variables
dat <- maait %>%
    select(ID, VisitNum, group, sxsgeneral, IgE) %>%
    rename(visit = VisitNum,
        treatment = group,
        symptoms = sxsgeneral)

## Double check first few rows
dat

## Make a bar plot showing the number of observations at each visit
dat %>%
    ggplot(aes(x = visit)) +
    geom_bar()

# Make a bar plot showing the mean level of IgE for each treatment group
dat %>%
    ggplot(aes(x = treatment,
            y = IgE)) +
    geom_bar(stat = "summary", fun = "mean")

# Add error bars (+/- 1 SE) to the bar plot
dat %>%
    ggplot(aes(x = treatment, y = IgE)) +
    geom_bar(aes(fill = treatment),
            stat = "summary", fun = "mean") +
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  geom_errorbar(stat = "summary", fun.data = "mean_se")

# Change the color scheme of the bar plot
dat %>%
  ggplot(aes(x = treatment, y = IgE)) +
  geom_bar(aes(fill = treatment),
      stat = "summary", fun = "mean") +
  geom_errorbar(stat = "summary", fun.data = "mean_se",
        width = 0.3) +
  scale_fill_brewer("Treatment Group",
          type = "qual",
          palette = "Set2")

# Show average symptoms by visit
dat %>%
  ggplot(aes(x = visit, y = symptoms)) +
  geom_bar(stat = "summary", fun = "mean")

## Facet by treatment group
dat %>%
  ggplot(aes(x = visit, y = symptoms)) +
  geom_bar(stat = "summary", fun = "mean") +
  facet_wrap(vars(treatment))

# Make the y axis scale more fine-grained by 0.5 steps
dat %>%
  ggplot(aes(x = visit, y = symptoms)) +
  geom_bar(stat = "summary", fun = "mean") +
  facet_wrap(vars(treatment)) +
  labs(y = "IgE Levels (ng/mL)") +
  scale_y_continuous(breaks = seq(0, 5, 0.5))


## Make a scatterplot of visits and symptoms
dat %>%
  ggplot(aes(x = visit, y = symptoms)) +
  geom_point()

## Jitter the points a little to show individual points
dat %>%
  ggplot(aes(x = visit, y = symptoms)) +
  geom_jitter(width = 0.1, height = 0.1)

## Add lines connecting dots
dat %>%
  ggplot(aes(x = visit, y = symptoms)) +
  geom_point() +
  geom_line()

## Group points by ID and connect with lines (spaghetti plot)
dat %>%
  ggplot(aes(x = visit, y = symptoms)) +
  geom_point() +
  geom_line(aes(group = ID))
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## Color each line grouping by ID
dat %>%
    ggplot(aes(x = visit, y = symptoms)) +
    geom_point() +
    geom_line(aes(group = ID, color = ID))

## Color each line AND point by ID
dat %>%
    ggplot(aes(x = visit, y = symptoms)) +
    geom_point(aes(color = ID)) +
    geom_line(aes(group = ID, color = ID))

## Remove the legend
dat %>%
    ggplot(aes(x = visit, y = symptoms)) +
    geom_point(aes(color = ID)) +
    geom_line(aes(group = ID, color = ID)) +
    theme(legend.position = "none")

## Color lines by treatment variable and fixed color for points
dat %>%
    ggplot(aes(x = visit, y = symptoms)) +
    geom_line(aes(group = ID, color = treatment)) +
    geom_point(size = 2, color = "magenta")

# Make a scatter plot of the mean of symptoms by visit and by treatment group
dat %>%
    ggplot(aes(x = visit, y = symptoms)) +
    geom_point(aes(color = treatment),
            stat = "summary",
            fun = "mean",
            size = 4) +
    geom_line(aes(color = treatment),
            stat = "summary",
            fun = "mean")

## Add the points back (jittered) in to show the variation in the data and
## modify the legend title
dat %>%
    ggplot(aes(x = visit, y = symptoms)) +
    geom_jitter(aes(color = treatment), alpha = 1/2,
            width = 0.1) +
    geom_point(aes(color = treatment),
            stat = "summary",
            fun = "mean",
            size = 4) +
    geom_line(aes(color = treatment),
            stat = "summary",
            fun = "mean") +
    scale_color_discrete("Treatment Group")

## Add the points and lines back in to show the variation in the data and modify
## the legend title
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```r
dat %>%
   ggplot(aes(x = visit, y = symptoms)) +
   geom_point(aes(color = treatment), alpha = 1/2) +
   geom_line(aes(group = ID, color = treatment), alpha = 1/2) +
   geom_point(aes(color = treatment),
         stat = "summary",
         fun = "mean",
         size = 5) +
   geom_line(aes(color = treatment),
         stat = "summary",
         fun = "mean",
         size = 2) +
   scale_color_discrete("Treatment Group")

# Make jittered scatterplot with linear regression lines showing the trends for
# each treatment group
dat %>%
   ggplot(aes(x = visit, y = symptoms)) +
   geom_jitter(aes(color = treatment),
         width = 0.1, height = 0.4) +
   geom_smooth(aes(color = treatment),
         method = "lm", size = 2)


# Make jittered scatterplot with smoother lines showing the trends for each
# treatment group
dat %>%
   ggplot(aes(x = visit, y = symptoms)) +
   geom_jitter(aes(color = treatment),
         width = 0.1, height = 0.4) +
   geom_smooth(aes(color = treatment),
         size = 2)
```