

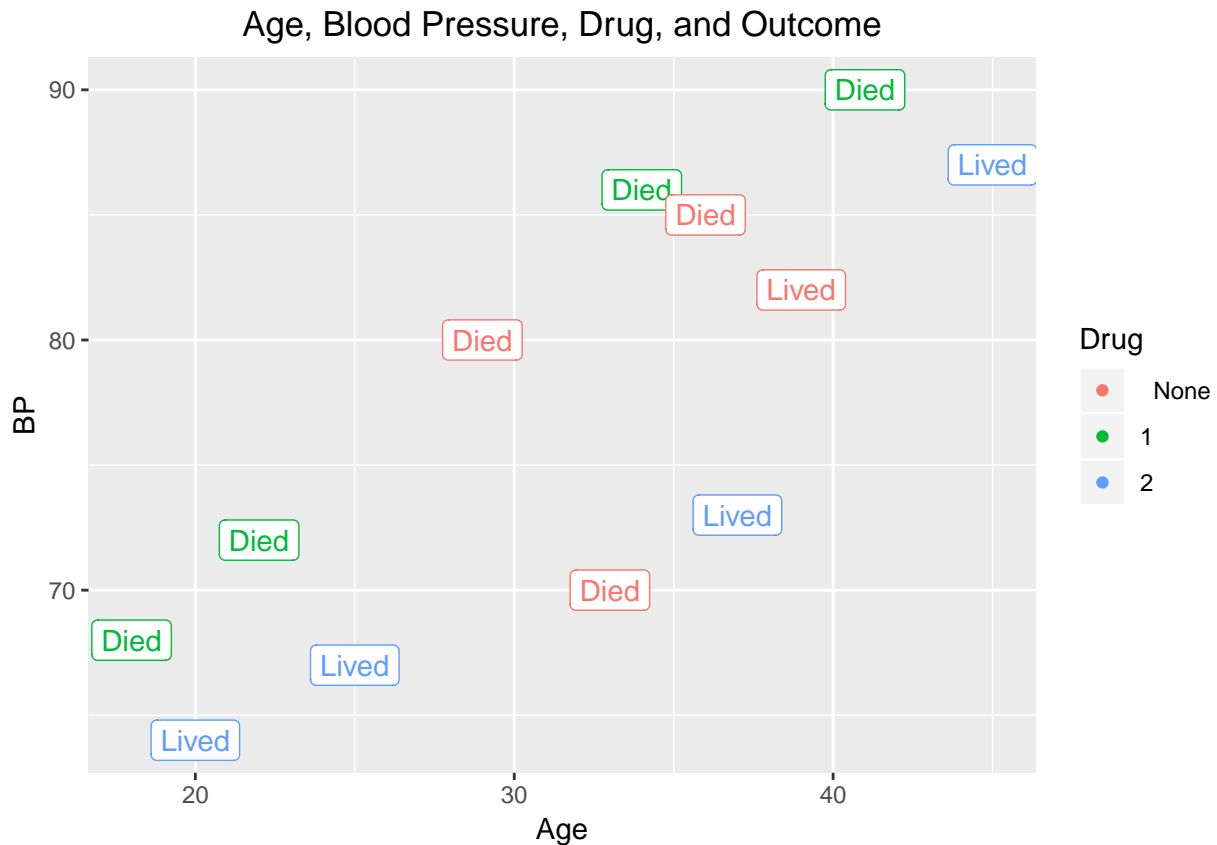
# Consulting Homework 6

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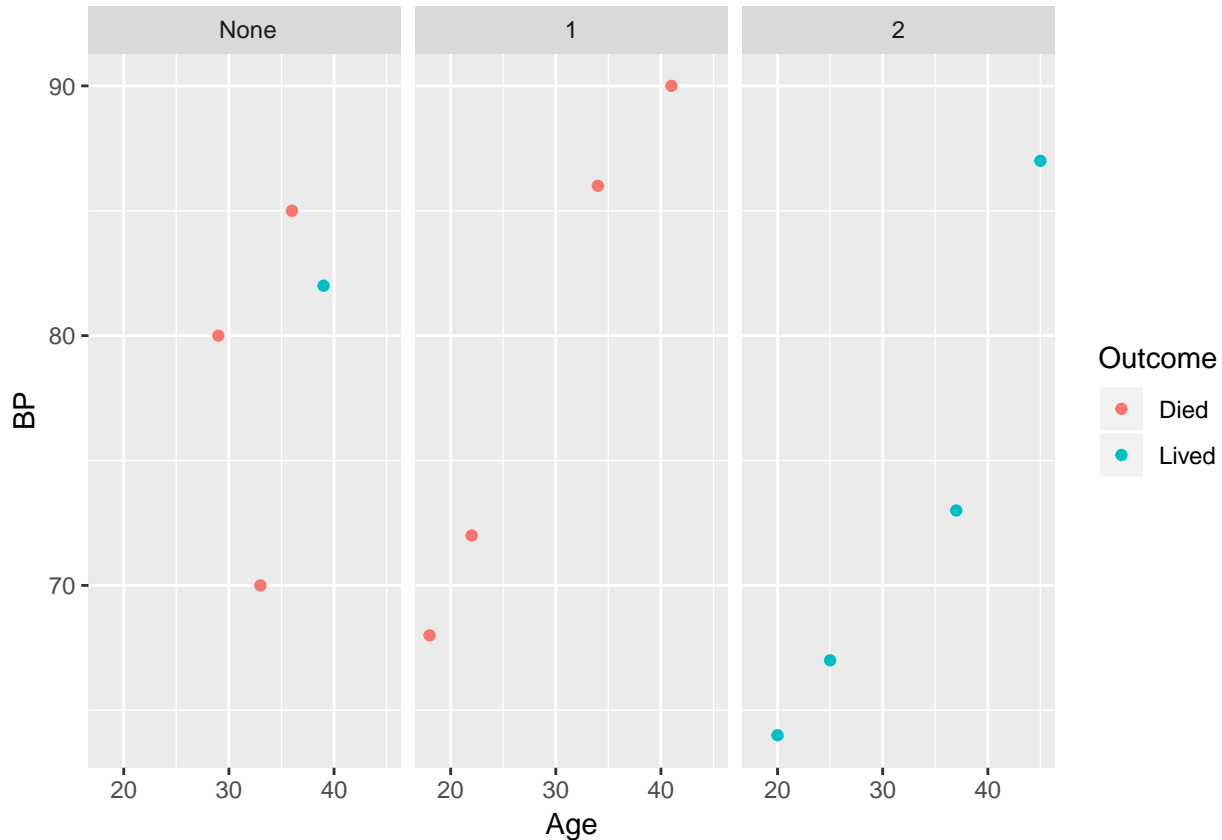
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```
# Load the libraries.
library(ggplot2)

# Read in data saved as a CSV file.
dat <- read.csv("/Users/timvigers/Documents/School/UC Denver/Biostatistics/Statistical Consulting 1/Homework 6/Assignment 6/Assignment 6 Data.csv")
# Change D and L to "Died" and "Lived" for clearer graphing.
dat$L.D[dat$L.D == " D"] <- "Died"
dat$L.D[dat$L.D == " L"] <- "Lived"
# Plot everything on one graph.
everything <- ggplot(data = dat, aes(x = Age, y = BP, color = Drug, label = L.D)) +
  geom_point() +
  geom_label(show.legend = F) +
  ggtitle("Age, Blood Pressure, Drug, and Outcome") +
  theme(plot.title = element_text(hjust = 0.5))
everything
```



```
# Plot using panels.
panels <- ggplot(data = dat, aes(x = Age, y = BP, color = L.D)) +
  geom_point() +
  labs(color = 'Outcome')
panels + facet_wrap(~ Drug)
```



The first plot without panels is a little difficult to read, probably because it's trying to cram too much information into one plot. However, when you use a separate panel for each drug, the results seem a little clearer. It appears that the no drug group have a fairly high mortality rate, but it might actually be better than drug 1. Participants on drug 1 had higher blood pressure overall than those on drug 2, and everyone on drug 1 died while everyone on drug 2 lived. These results are pretty interesting, but it's difficult to make any conclusions based on such a small sample size and without any statistical tests. Also, if you add a linear regression to the plot, it appears that no drug and drug 2 might have lower slopes than drug 1, which would mean that drug 1 actively increases BP as patients get older. Again, it's hard to make any conclusions, but the plots suggest it's worth investigating further.

```
panels +
  geom_smooth(method='lm',se = F,color = "grey") +
  facet_wrap( ~ Drug)
```

