Biostats week 3: Describing relationships among variables

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Outline

This packet reviews *bivariate* statistics, or statistics examining relationships between two variables:

1. One categorical variable & one continuous variable
2. Two categorical variables
3. Two continuous variables

Packages you will need in this packet:

- vcd
- ggplot2

1. One categorical variable & one continous variable

Open the local health department data at http://tinyurl.com/zn46s6e and use the summary command to examine the data set and the variables in it.

```
# open local health department (LHD) data
lhd <- read.csv("http://tinyurl.com/zn46s6e")
summary(lhd)
```

```
##        id       numserved           state     expenditures
##  AL032  : 1   Min.   :   5152   OH     : 6   Min.   :  145255
##  AR025  : 1   1st Qu.:  20226   AR     : 3   1st Qu.:  856084
##  AR038  : 1   Median :  41133   IL     : 3   Median : 2384860
##  AR066  : 1   Mean   : 105177   MA     : 3   Mean   : 5155926
##  CA015  : 1   3rd Qu.: 107329   IA     : 2   3rd Qu.: 6175087
##  CT021  : 1   Max.   :1135992   ID     : 2   Max.   :51278368
##  (Other):44                     (Other):31   NA's   :15
##     revenues        immunization hivscreen cancerscreen diabetesscreen
##  Min.   :  180455   no : 5       no  :18   no  :25      no  :26
##  1st Qu.:  807600   yes:45       yes :30   yes :22      yes :20
##  Median : 2238886                NA's: 2   NA's: 3      NA's: 4
##  Mean   : 3861264
##  3rd Qu.: 6046167
##  Max.   :16224295
##  NA's   :20
##     services
##  Min.   :0.00
##  1st Qu.:3.00
##  Median :4.00
##  Mean   :4.04
##  3rd Qu.:6.00
##  Max.   :6.00
##
```

Code book:

- id: unique identifier for each health department, starts with state abbreviation
- numserved: number of people served by the health department
- state: state the health department is in
- expenditures: dollars the health department spent in 2015
- revenues: dollars the health department received in 2015
- immunization: does the health department provide immunizations
- hivscreen: does the health department provide HIV screening
- cancerscreen: does the health department provide cancer screening
- diabetesscreen: does the health department provide diabetes screening
- services: number of services the health department provides

More information about this survey and local health departments here: https://nacchoprofilestudy.org/

As a reminder:

- *categorical* variables: Variables with *categories* like marital status, color, sex, alma mater, religion, ethnicity, etc.
- *continuous* variables: Variables with values that can take *any* value along some *continuum* like age, height, weight, distance, blood pressure, temperature, etc.

- *discrete* variables: Variables that are also along a continuum, but can only have certain values like the number of siblings or pets you have, the result of rolling dice, cars on a street, people in a state, etc.

There is quite a bit of evidence that health departments serving more people have more resources and are able to provide more services to their constituents.

In this data set we have a discrete variable showing number of people served (`numserved`) and a categorical variable showing whether or not the health department provides HIV screening (`hivscreen`). We can use bivariate analyses to compare the number of people served by health departments that provide HIV screening with the number of people served by health departments with no HIV screening program.

The mean number of people served by a health department shown in the summary statistics above is 105,177 people. Of the 50 health departments in this sample, 30 provide HIV screening and 18 do not.

Our research question might be:

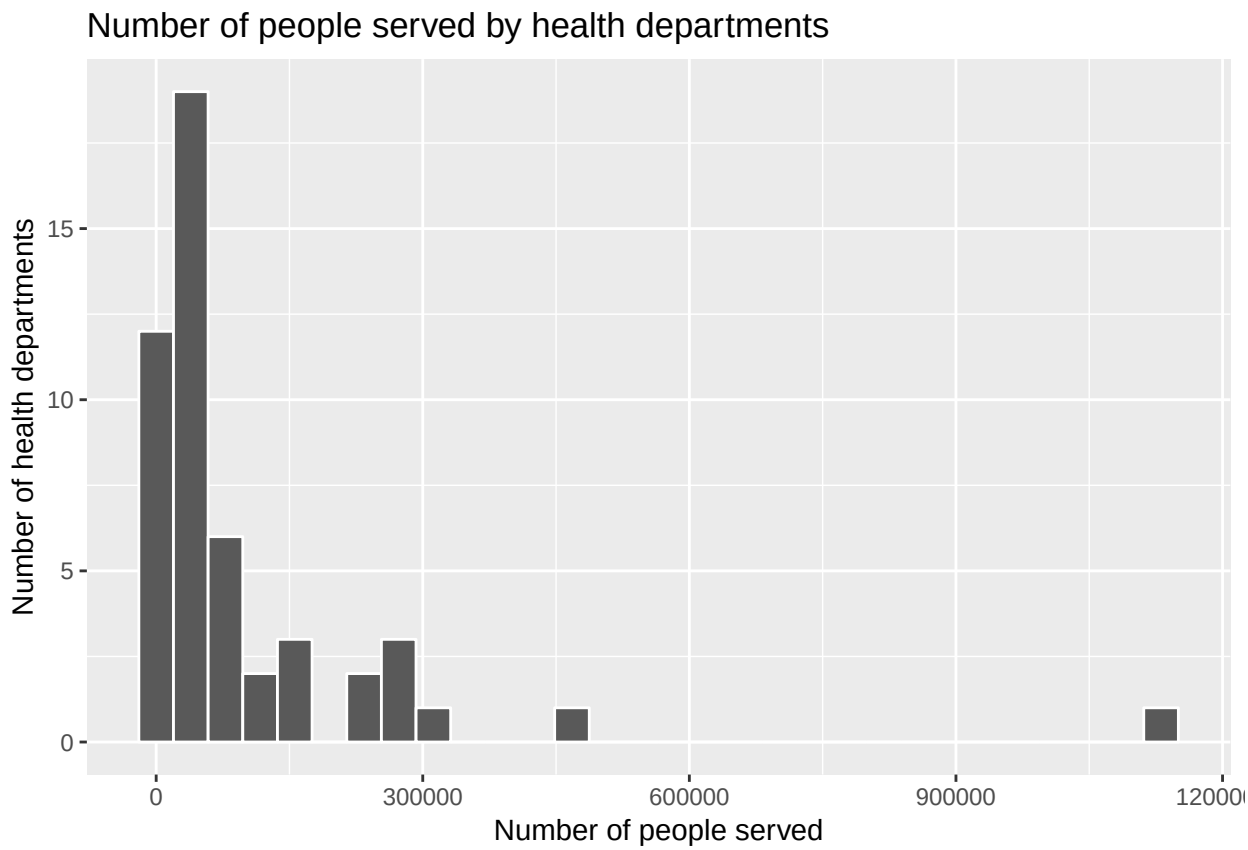
Do health departments that provide HIV screening also serve more people?

First, what measure of central tendency should we use for number of people served? Let's graph it and find out:

```
# open ggplot2 for graphing
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.5.1
```

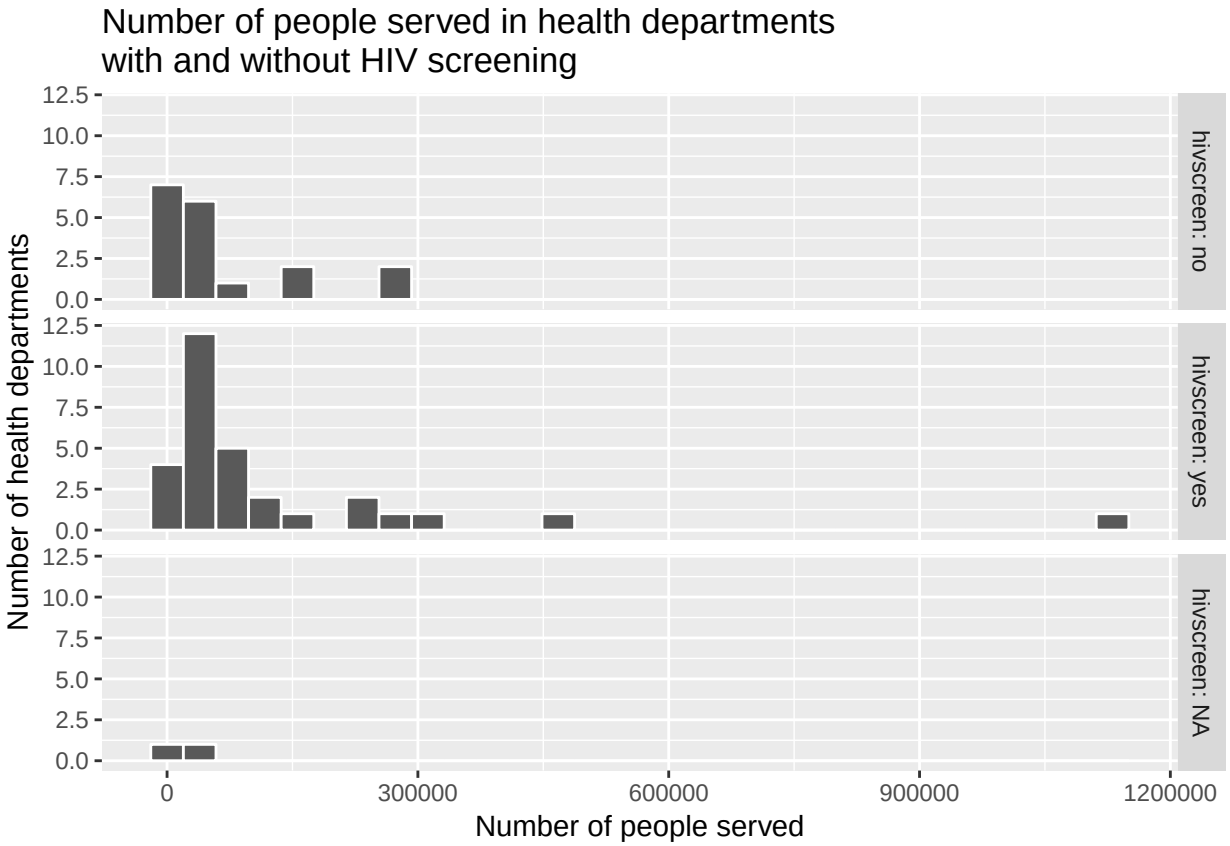
```
# make a histogram
ggplot(data = lhd, aes(x = numserved)) +
  geom_histogram(color=I("white")) +
  xlab("Number of people served") +
  ylab("Number of health departments") +
  ggtitle("Number of people served by health departments")
```



It looks right skewed, so the mean is probably not the best measure of central tendency. To be sure, see if number served is skewed within each HIV screening group. There are multiple ways to do this, we will use `facet_grid`.

Adding `facet_grid()` to a `ggplot` allows you to plot different groups in separate sections of a plot, like this:

```
# graph with facets to see health depts
# with and without HIV programs
ggplot(data = lhd, aes(x=numserved)) +
  geom_histogram(color=I("white")) +
  facet_grid(rows = vars(hivscreen), labeller = label_both) +
  xlab("Number of people served") +
  ylab("Number of health departments") +
  ggtitle('Number of people served in health departments\nwith and without HIV screening')
```



Both groups look right skewed, so we should use the median rather than the mean. One way to get the median for each group is to use the `by` command.

The `by` command takes three arguments to get the median for each group:

- data: The data argument is the data to be analyzed, in this case the `numserved` variable from the lhd data frame
- INDICES: These are the groups the data should be divided up by, in this case the `hivscreen` variable
- FUN: The function argument is what procedure you want to do to the data from each group. In this case, we want the median.

```
# get the median for numserved by hivscreen
by(data = lhd$numserved,
   INDICES = lhd$hivscreen,
   FUN = median)
```

```
## lhd$hivscreen: no
## [1] 33088
## ------------------------------------------------------------
## lhd$hivscreen: yes
## [1] 48049
```

Intepreting the results: The health departments providing HIV screening serve a median of 48,049 people, while the health departments not providing HIV screening serve a median of 33,088 people.

The answer to our original research question is *yes*. In this data, health departments with HIV screening serve more people.

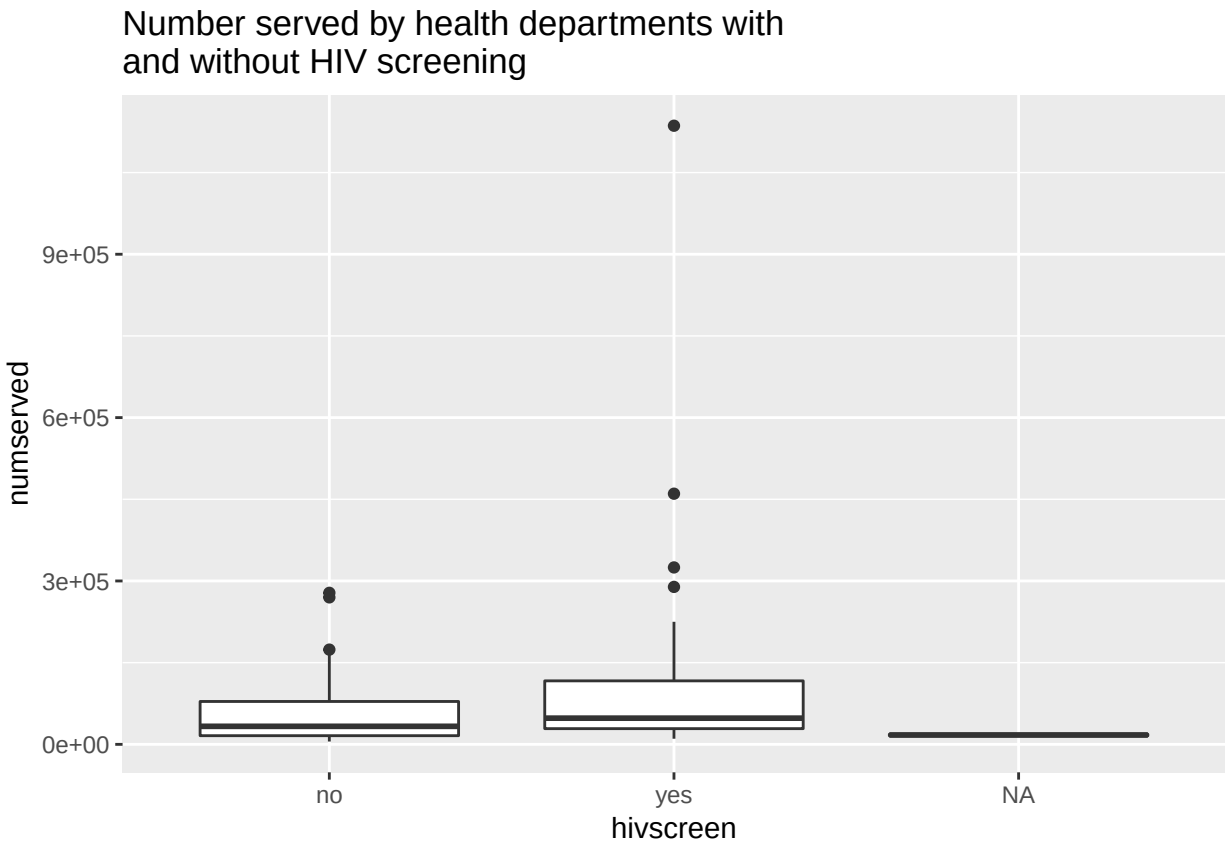
The `by` command works with many different kinds of functions. For example, use `summary` instead of median to get more information:

```r
# get the summary for numserved by hivscreen
by(data = lhd$numserved,
   INDICES = lhd$hivscreen,
   FUN = summary)
```

```
## lhd$hivscreen: no
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    5152   15880   33088   72042   78700  278246
## ------------------------------------------------------------
## lhd$hivscreen: yes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   10326   28818   48049  130926  116594 1135992
```

Numbers are ok for conveying information, but visuals are often easier to interpret and can be more impactful. Try a box plot to visualize differences among groups:

```r
# boxplot of numserved by hivscreen
ggplot(data = lhd, aes(x = hivscreen, y = numserved)) +
  geom_boxplot() +
  ggtitle("Number served by health departments with\nand without HIV screening")
```



It is a little hard to see with all of the dots representing outliers and the NA box. We may want to hide the missing values box since it is not really important to our research question.

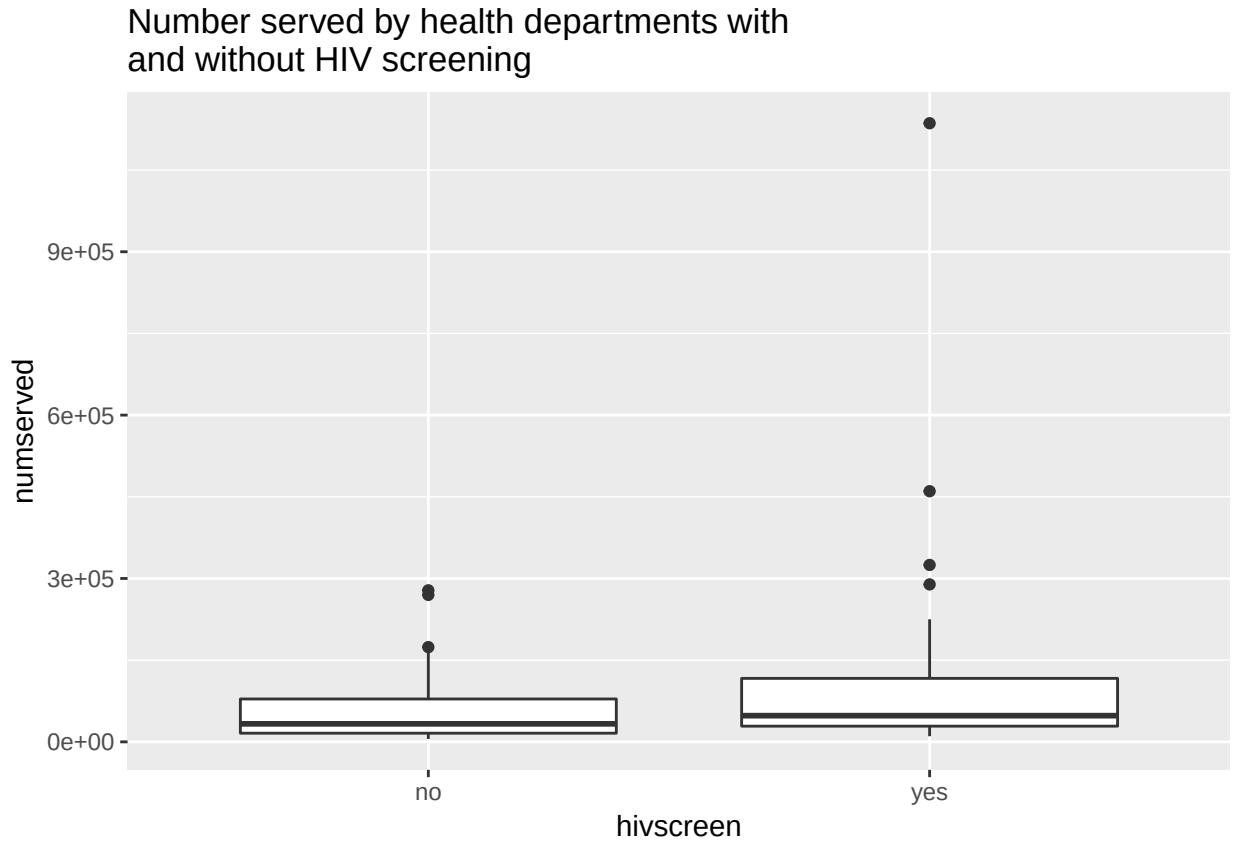
There is no easy way to do this in the ggplot command, but we can remove NA values from the data using subset and then plot it again.

```r
# take a subset of the lhd data where hivscreen
# is not NA
lhd.noNA <- subset(x = lhd, hivscreen!='NA')

# check the hivscreen variable in the new data frame
summary(lhd.noNA$hivscreen)
```

```
##  no yes
##  18  30
```

```r
# plot it again
ggplot(data = lhd.noNA, aes(x = hivscreen, y = numserved)) +
  geom_boxplot() +
  ggtitle("Number served by health departments with\nand without HIV screening")
```

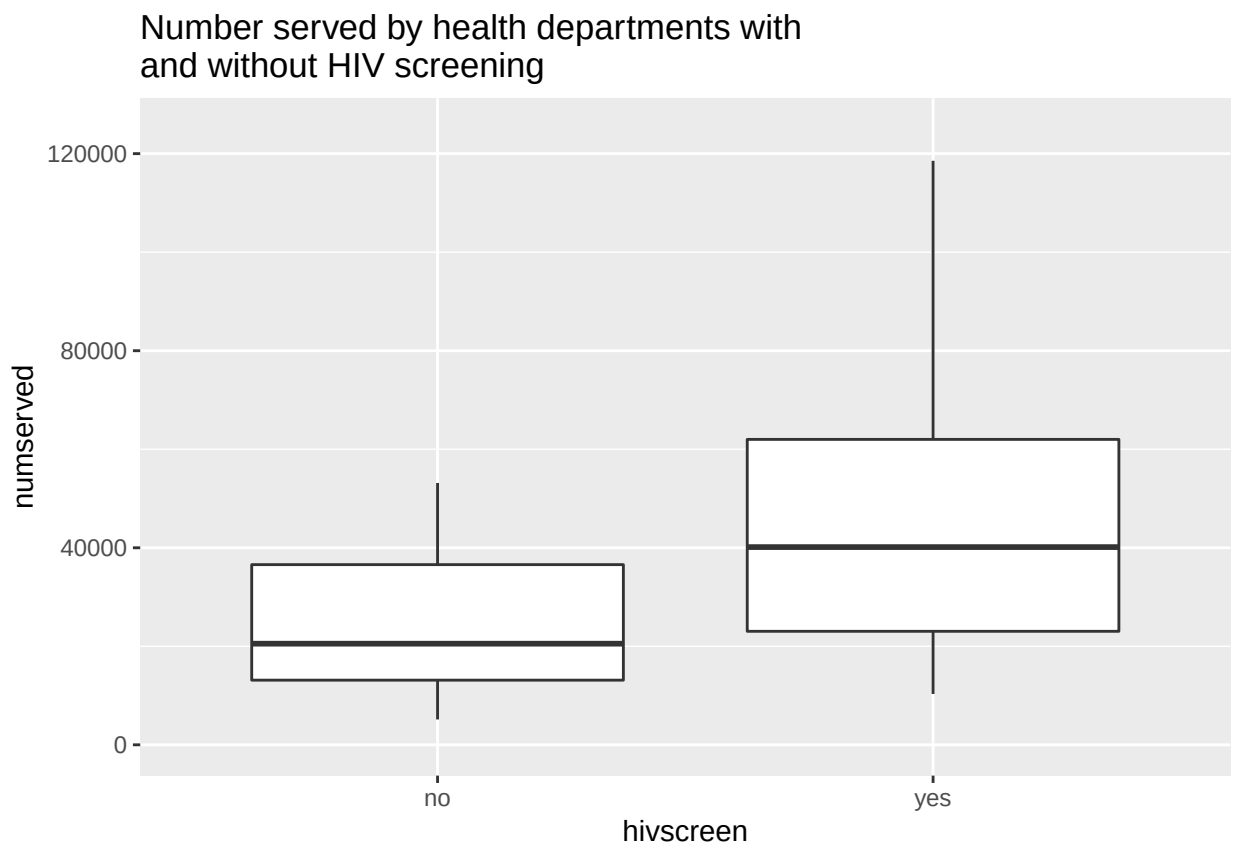


The outliers still seem to be crowding the boxes and making it difficult to see whether there is a difference. Use an option to hide outliers and change the y-axis limits for better interpretation.

Note: Make sure the upper limit you set for the y-axis is above the highest value you display. If it is lower, R will truncate your data and only show you part of the boxplots.

```r
# plot it again without the outliers
# add ylim to change the y-axis limits
ggplot(data = lhd.noNA, aes(x = hivscreen, y = numserved)) +
  geom_boxplot(outlier.shape = NA) +
  ylim(0, 125000) +
  ggtitle("Number served by health departments with\nand without HIV screening")
```

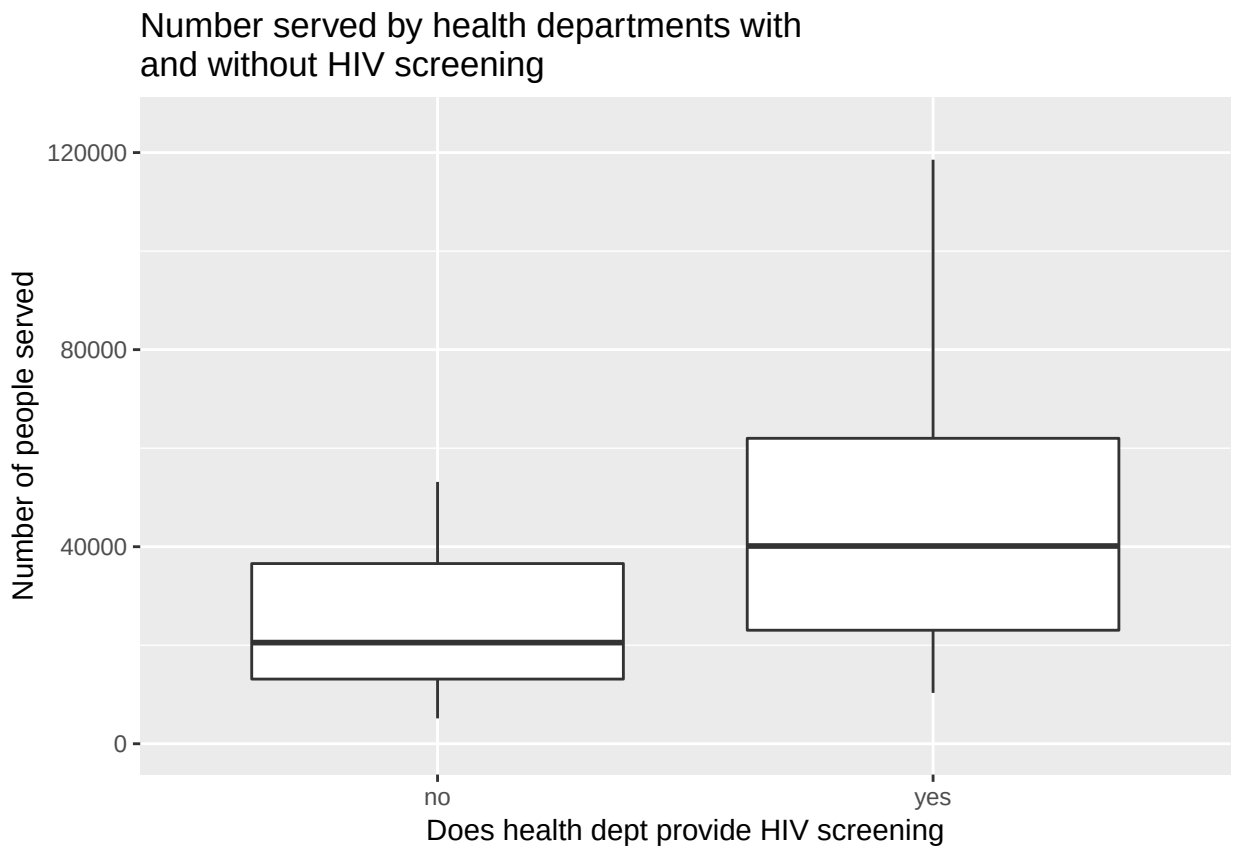
```
## Warning: Removed 11 rows containing non-finite values (stat_boxplot).
```



The warning message tells us that we removed 11 outlier values! The boxplots look great but for anyone but the analyst to know what the heck it means, it needs better labels on the axes.

```
# add axis labels to plot
ggplot(data = lhd.noNA, aes(x = hivscreen, y = numserved)) +
  geom_boxplot(outlier.shape = NA) +
  ylim(0, 125000) +
  ylab("Number of people served") +
  xlab("Does health dept provide HIV screening") +
  ggtitle("Number served by health departments with\nand without HIV screening")
```

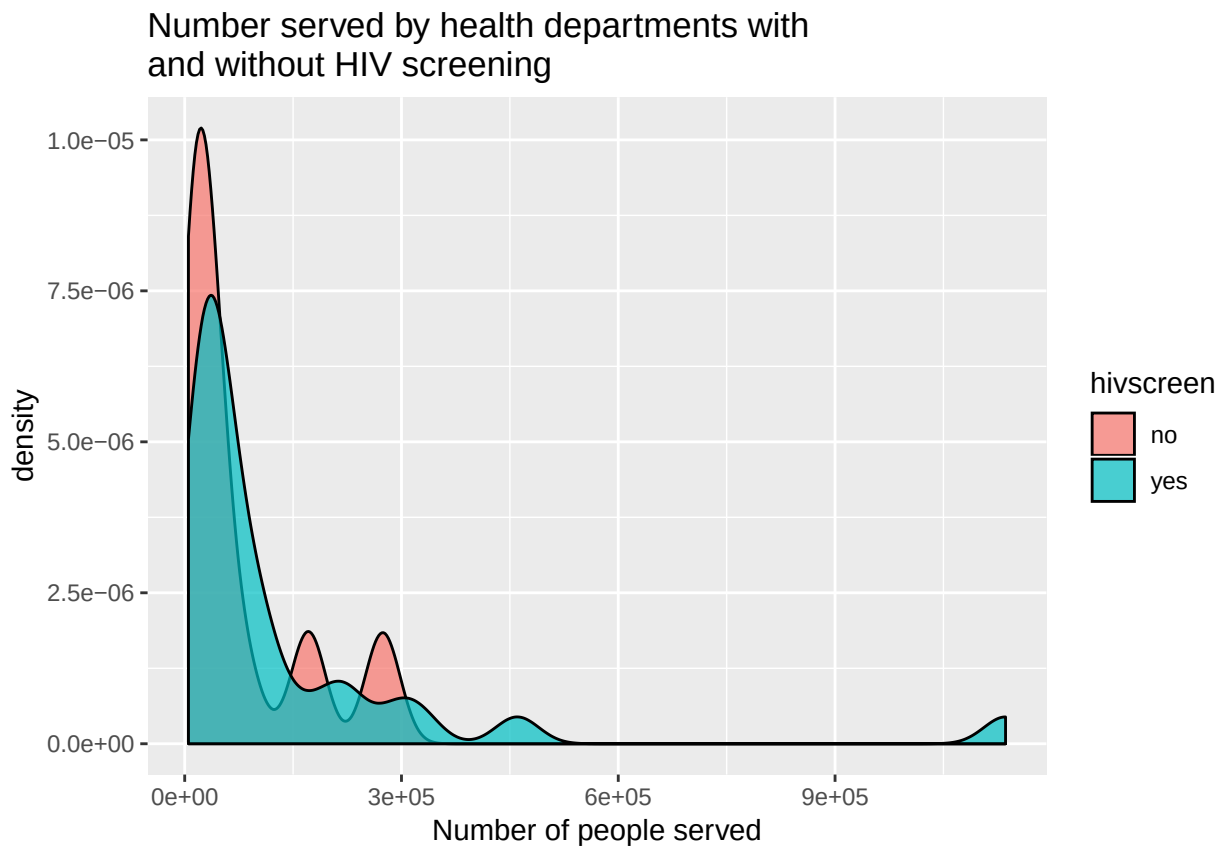
```
## Warning: Removed 11 rows containing non-finite values (stat_boxplot).
```



Interpreting the plot: Health departments that provide HIV screening serve more people than health departments that do not provide HIV screening.

Another option for visualizing the distribution of a continuous or discrete variable across groups is the petal plot, which is essentially a layered density plot. Try it:

```
# use the density geom to make a petal plot
# add alpha for transparency
ggplot(data = lhd.noNA,
       aes(x = numserved, fill = hivscreen)) +
  geom_density(alpha=I(.7)) +
  xlab("Number of people served") +
  ggtitle("Number served by health departments with\nand without HIV screening")
```



2. Two categorical variables

Sometimes we may want to know how two categorical variables are related. For example, are the health departments with no HIV screening also the health departments with no cancer screening? To figure this out, we want to know how many:

- health departments with both HIV and cancer screening (yes for both)
- health departments with HIV screening but no cancer screening
- health departments with cancer screening but no HIV screening
- health departments with neither type of screening (no for both)

Using the table function in R to find these numbers...

```
# table of hiv and cancer screening
table(lhd$hivscreen, lhd$cancerscreen)
```

```
##
##       no yes
##   no  15   3
##   yes 10  19
```

Well, those are the numbers! But, which is which? Are the rows HIV screening and the columns cancer screening? There must be a way that shows us more information. Try adding names to label the parts of the `table` command:

```
# add row and column names to table
table(hiv = lhd$hivscreen, cancer = lhd$cancerscreen)
```

```
##      cancer
## hiv   no yes
##   no  15   3
##   yes 10  19
```

Better! But still not perfect. It would be great to know the percentages instead to be able to compare how people are distributed across categories.

```
# find percentages
prop.table(table(hiv = lhd$hivscreen,
                 cancer = lhd$cancerscreen))
```

```
##      cancer
## hiv           no        yes
##   no  0.31914894 0.06382979
##   yes 0.21276596 0.40425532
```

Interpretation: Just over 40% of health departments in the sample have both services, while 31.9% have neither service. Of the health departments 21.3% have HIV screening but no cancer screening and 6.4% have cancer screening but no HIV screening.

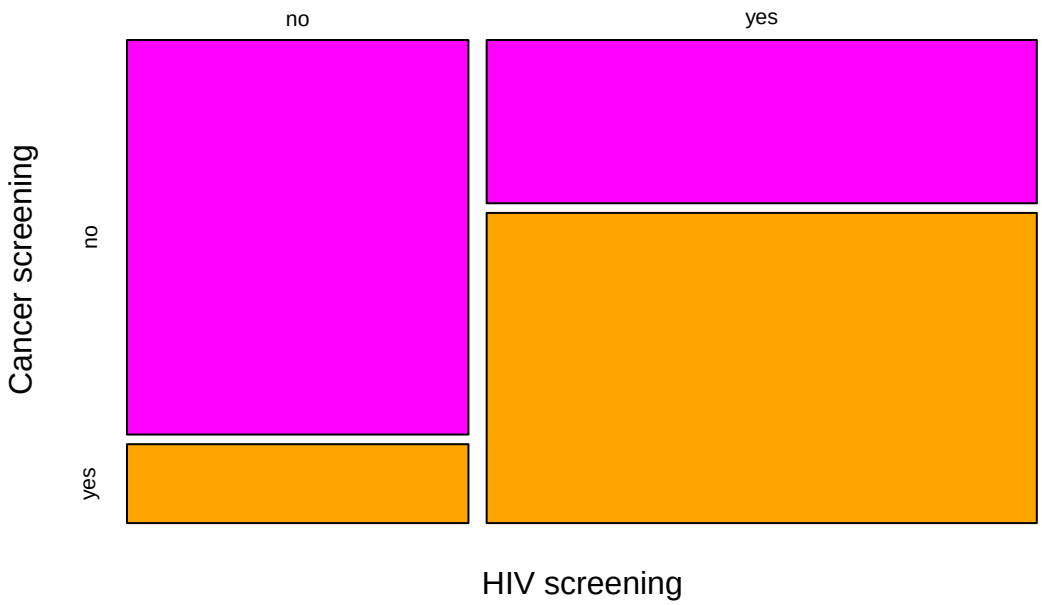
Visually, a `facet_grid`, grouped bar plot, or mosaic works well to display the relationship between two categorical variables. Install the package vcd to use the mosaic plot commands.

```
# open vcd package
library(vcd)
```

```
## Warning: package 'vcd' was built under R version 3.5.1
```

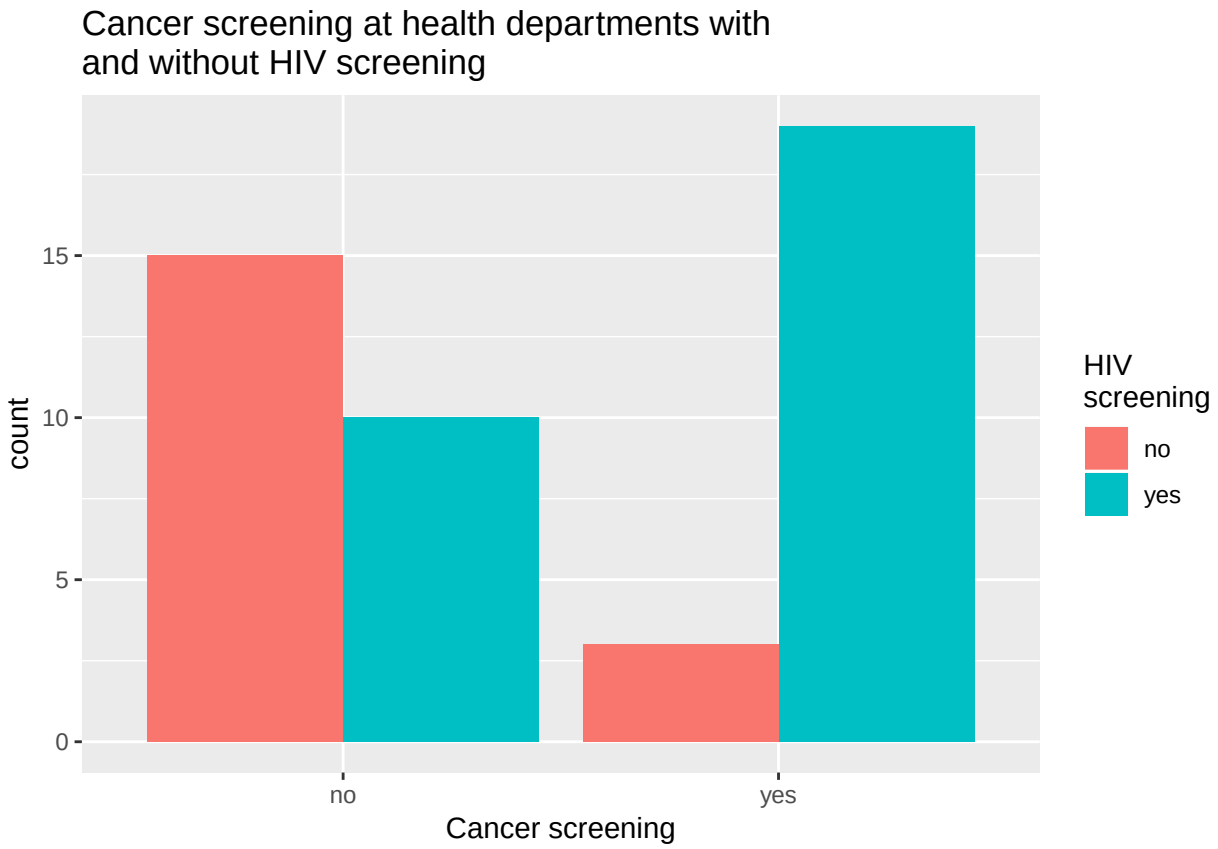
```
## Loading required package: grid
```

```
# make the mosaic plot
mosaicplot(~ hivscreen + cancerscreen,
       data = lhd, color = c("magenta","orange"),
       xlab = "HIV screening", ylab = "Cancer screening",
       main = "HIV screening and cancer screening in LHDs")
```

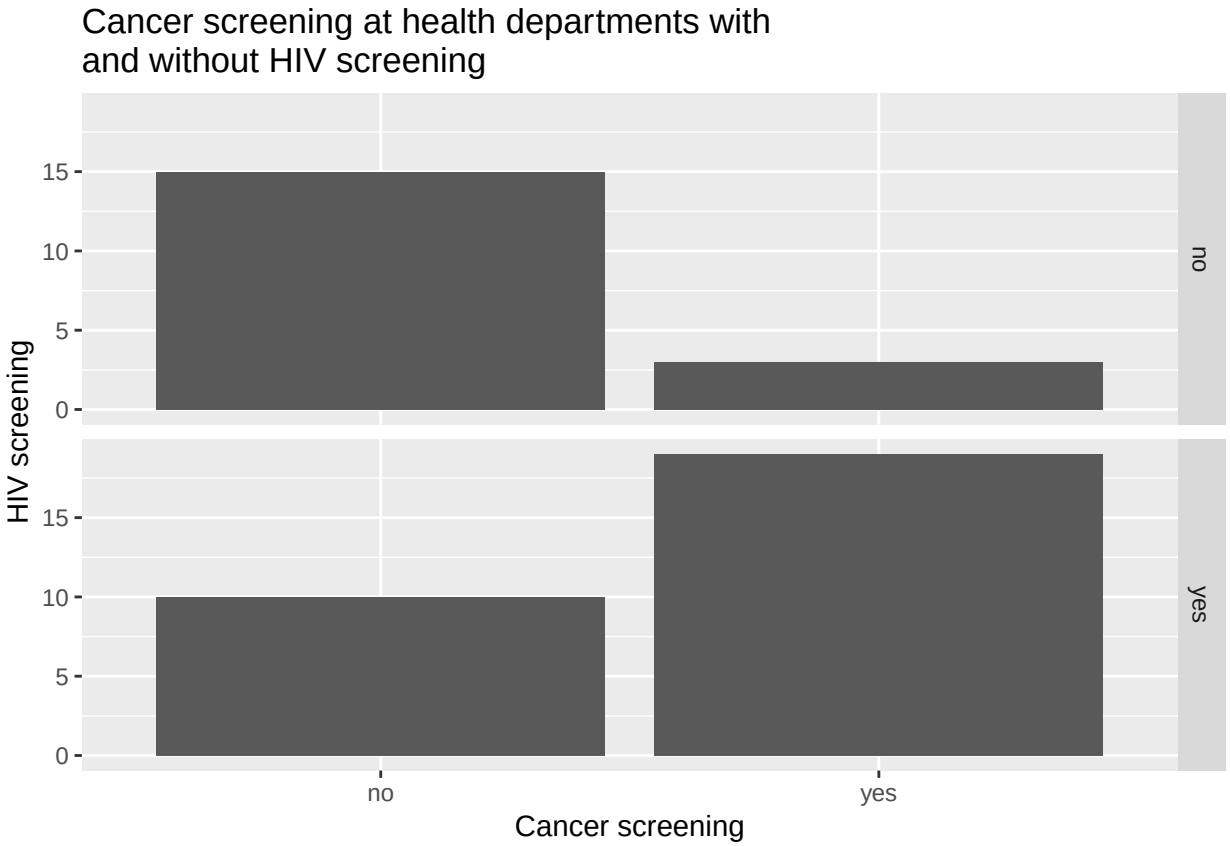



```
# try bar plots with facets or groups
# subset data so there are no NA values in cancer screen
lhd.noNA.screen <- subset(lhd.noNA, cancerscreen != 'NA')

# bar plot with groups
ggplot(data = lhd.noNA.screen,
       aes(x = cancerscreen, fill = hivscreen)) +
  geom_bar(position = "dodge") +
  xlab("Cancer screening") +
  labs(fill = "HIV\nscreening") +
  ggtitle("Cancer screening at health departments with\nand without HIV screening")
```




```
# bar plot with facets
ggplot(data = lhd.noNA.screen,
       aes(x = cancerscreen)) +
  geom_bar() +
  facet_grid(rows = vars(hivscreen)) +
  xlab("Cancer screening") +
  ylab("HIV screening") +
  ggtitle("Cancer screening at health departments with\nand without HIV screening")
```



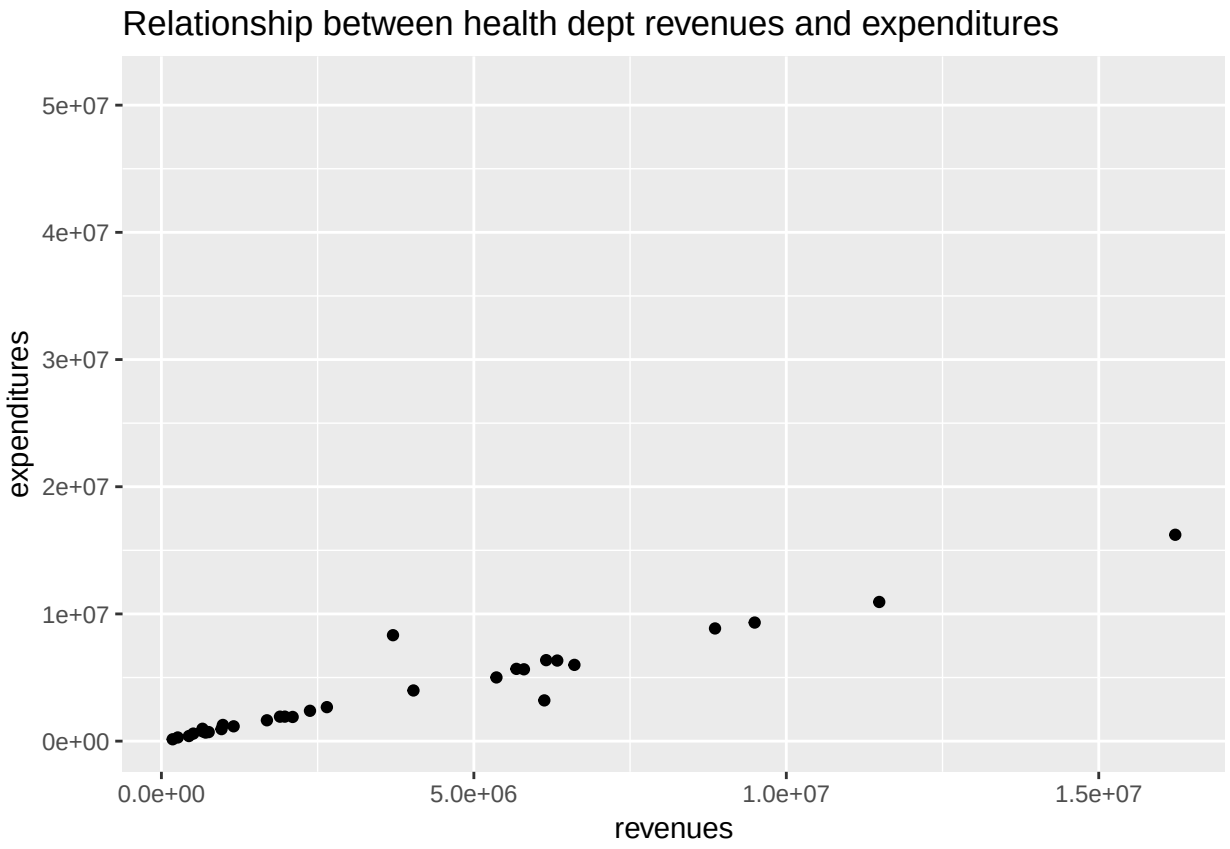
Interpretation of plots: Consistent with the numbers in the table, the plots show that the largest group is health departments with both services. Health departments that have neither service is also a large group. There is a smaller group that has HIV screening but no cancer screening. The smallest group has no HIV screening but does do cancer screening.

3. Two continuous variables

It would make sense that health departments that bring in more revenues would use that money and have higher expenditures. Let's see if that is the case:

```
# graph revenues by expenditures
ggplot(data = lhd, aes(x = revenues, y = expenditures)) +
  geom_point() +
  ggtitle("Relationship between health dept revenues and expenditures")
```

```
## Warning: Removed 20 rows containing missing values (geom_point).
```



It looks like, as revenues go up, expenditures go up!

We can check this numerically using several different methods. The first method is covariance, which measures whether two variables vary together (co-vary) using this formula:

$$cov_x y = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{n-1}$$

If the covariance is a positive number, there is a positive relationship between the two variables. Revenues and expenditures looked like it had a positive relationship; the covariance can help quantify it. Note that the *covariance* command is like the *mean* command in that it needs to know what to do with missing values. In this case, instead of na.rm, the *cov* command uses *use* to determine which values to use. See the help documentation for information on all the possible options for *use*.

```
# covariance of revenues and expenditures
cov(lhd$revenues,lhd$expenditures, use='complete')
```

```
## [1] 1.439844e+13
```

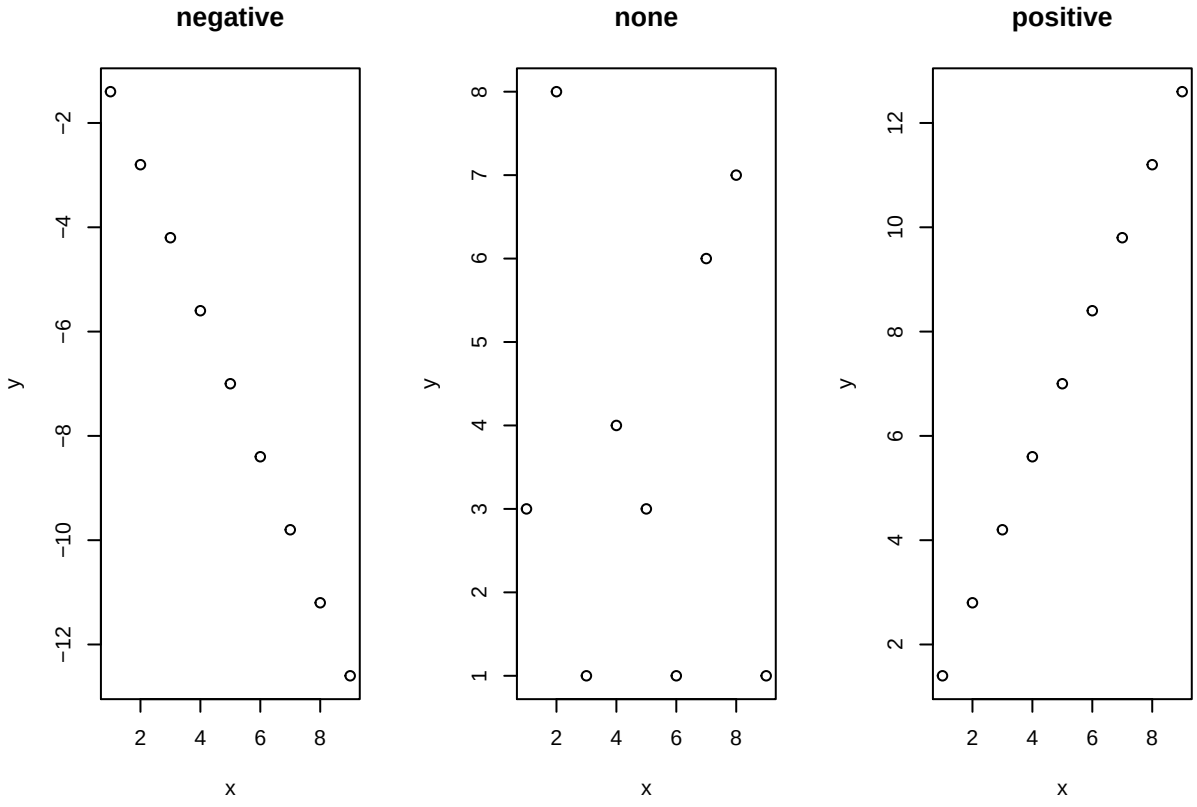
Well, this seems a little strange. The e+13 is scientific notation indicating that the decimal place should be moved 13 places to the right of where it currently is, so the variance is actually 1,440,543,000,000. A number this big is not really very useful beyond being able to say that the relationship is positive.

Because the covariance measure is highly influenced by the size of the numbers used to compute it (we had very large numbers for revenues and expenditures, so we had a very large covariance), it is not all that useful. Instead we use a version of the covariance divided by the standard deviations of x and y. This is called a correlation coefficient and is computed:

$$r_{xy} = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{(n-1)s_x s_y}$$

This version of the correlation coefficient is called Pearson's r and can range from -1 (a perfect linear negative relationship) to 0 (no relationship) to 1 (a perfect linear positive relationship).

- *Negative correlations* are when one variable goes up, the other goes down
- *No correlation* is when there is no discernable pattern in how two variables vary
- *Positive correlations* are when one variable goes up, the other also goes up (or when one goes down the other does too); both variables move together in the same direction



A correlation coefficient can help us quantify the relationship:

```
# correlation between revenues and expenditures
cor(lhd$revenues, lhd$expenditures, use='complete')
```

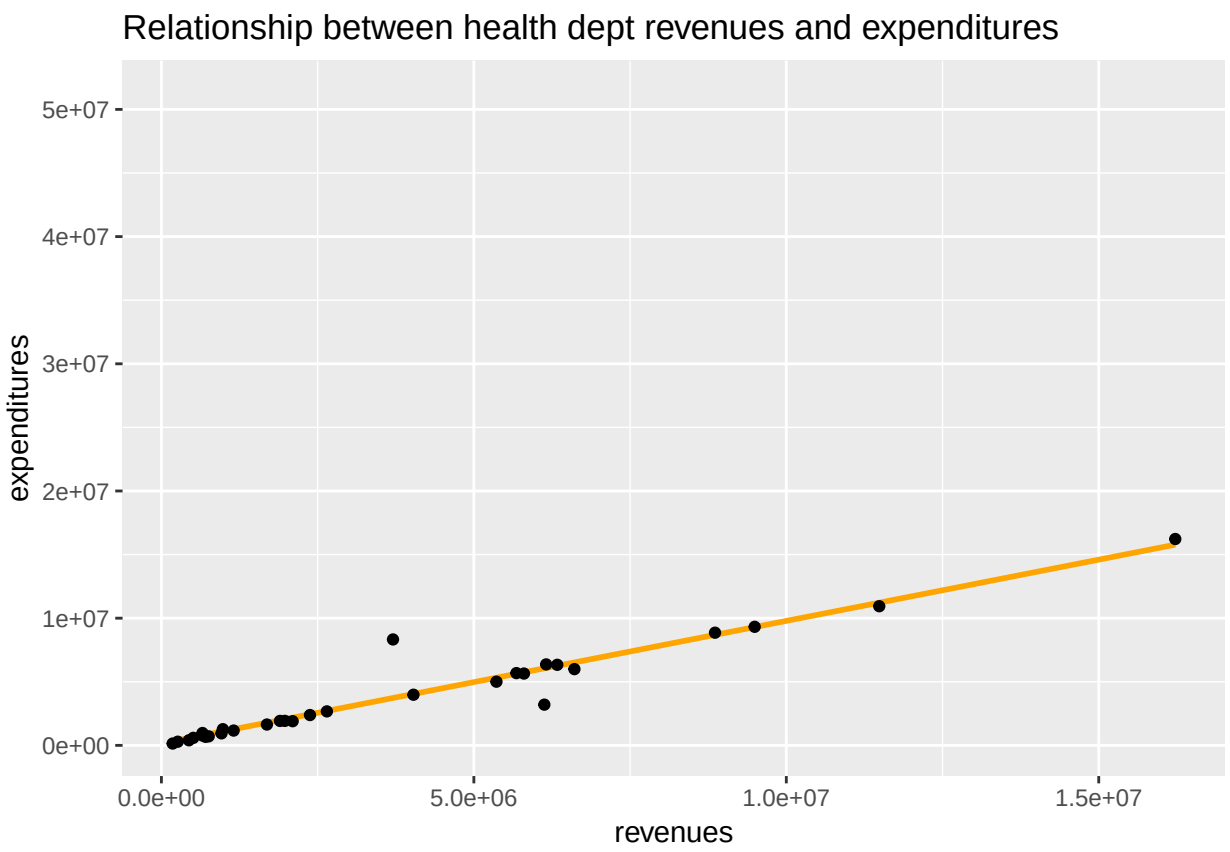
```
## [1] 0.9641266
```

A correlation of .96 is positive and very strong since 1.0 is the largest positive correlation possible.

Interpretation: Health department revenues are strongly and positively correlated with health department expenditures (r=.96). As revenues go up, expenditures also go up.

If we look again at the graph of revenues and expenditures and use the geom_smooth option to add a line to show the relationship, we can confirm that it is a strong positive relationship, which makes sense given the very high correlation:

```
# scatterplot of revenues and expenditures
ggplot(data = lhd, aes(x = revenues, y = expenditures)) +
  geom_smooth(method = "lm", se = FALSE, color = "orange") +
  geom_point()+
  ggtitle("Relationship between health dept revenues and expenditures")
```



Occasionally there are values included in the data that do not makes sense. For example, a data entry error or something else could cause a health department to show revenues that make no sense. The data shown here do not have any problem values, but imagine that the point shown on the far right side of the scatter plot is a mistake and you need to remove it. The `subset` command can be used to remove values that are incorrect (or just to limit the data to examine a specific group). Try subsetting the `revenues` variable so that it only includes revenue values that are less than 10,000,000:

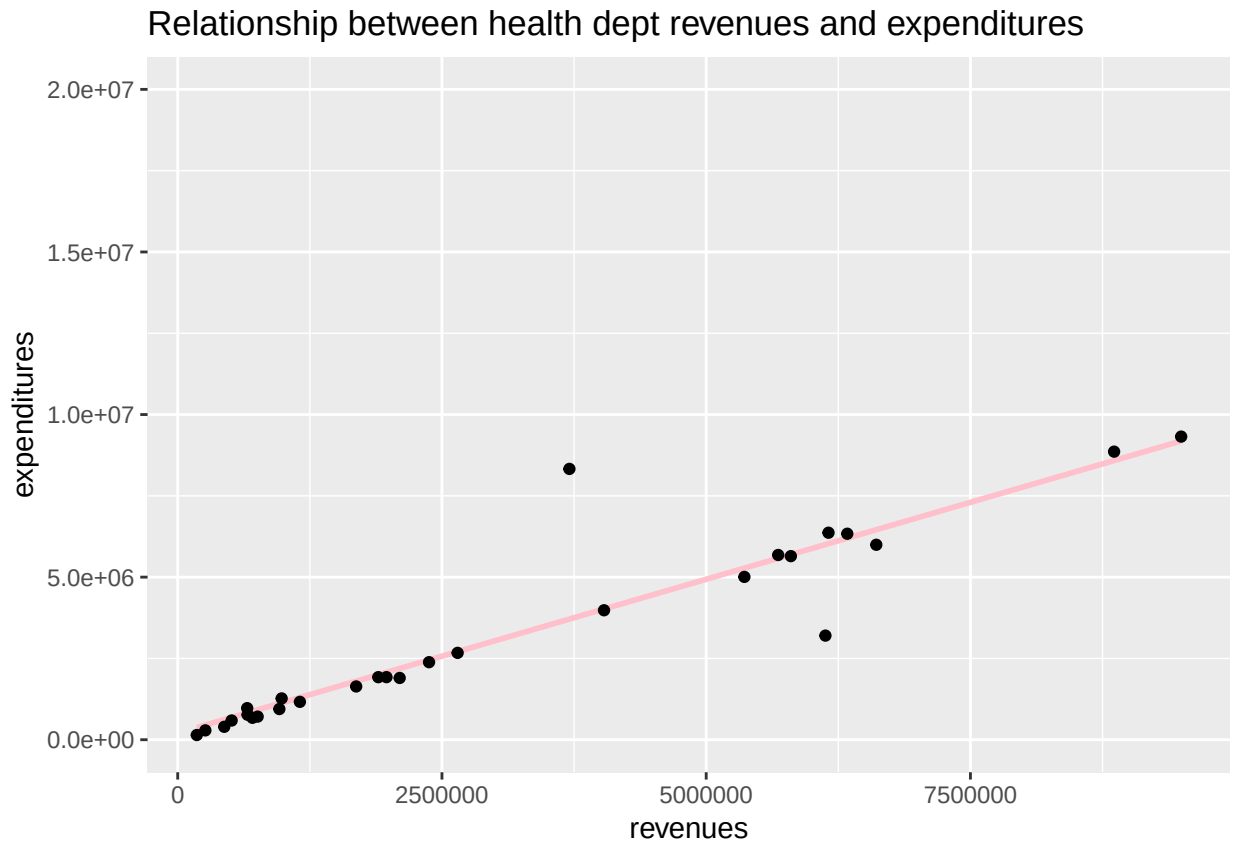
```
# subset revenues to less than 10 million
lhd.subset <- subset(x = lhd, revenues < 10000000)
summary(lhd.subset$revenues)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
```

```
##  180455  743957 2037501 3147370 5711111 9493792
```

It looks like the health departments with revenues greater than 10000000 were removed. The new data frame shows just 28 health departments are left. Try graphing it with the same code from above and the new data frame:

```
# graph with limits on y-axis
ggplot(data = lhd.subset, aes(x = revenues, y = expenditures)) +
  geom_smooth(method = "lm", se = FALSE, colour = "pink") +
  geom_point()+
  ggtitle("Relationship between health dept revenues and expenditures")+
  ylim(0,20000000)
```



It looks like a few observations were removed, but not enough to go from 50 to 28. A quick look at both data frames shows that the `NA` values were also dropped for the subset.

Challenge 3

Install the `rmarkdown` package.

Download the standard or hacker version of the Challenge from GitHub and follow the instructions.

Upload whichever version you chose **before the next class meeting**.