Clas27-29

October 28, 2020

0.1 Correlation, 2X2 tables, and Regression

0.1.1 Covariance

The **covariance** between two random variables X and Y is computed as

$$\mathrm{Cov}(X,Y) = E\left\{[X - E(X)]\,[Y - E(Y)]\right\} \tag{1}$$

where E is the expectation. The **covariance** describes the distance both X and Y vary from their means.

The covariance is *positive* when samples of X and Y both vary above, or below, their mean respective means. The covariance is *negative* when samples of X vary above their mean and samples of Y vary below their mean or vice-versa.

The covariance, a parameter, is one way to describes the relationship between two different random variables. To estimate the covariance with the **sample covariance**, a statistic, we need the mean of X ($barX$) and the mean of Y ($\bar{Y}$). The covariance can then be estimated from a sample of N pairs (x_i, y_i)

$$\mathrm{cov}(x,y) = N^{-1}\sum_{i=1}^{N}(x_i - \bar{X})\,(y_i - \bar{Y}) \tag{2}$$

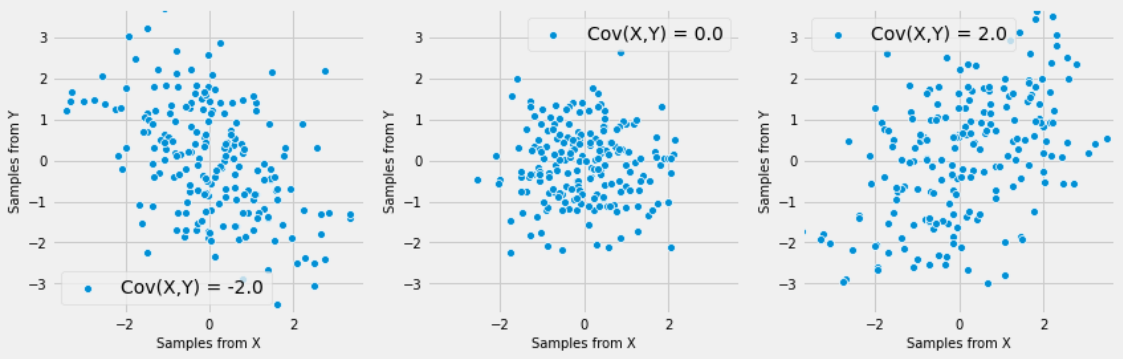
where $\bar{X} = N^{-1}\sum_{i=1}^{N} x_i$ and $\bar{Y} = N^{-1}\sum_{i=1}^{N} y_i$.

Below are three scatterplots where each scatterplot shows 200 sampled pairs (x_i, y_i) with covariances -2, 0 and 2.

[35]:
```
plt.style.use("fivethirtyeight")
fig,axs = plt.subplots(1,3)

covariances = [-2,0,2]

minx,maxX = [],[]
miny,maxY = [],[]

for i in range(3):
    ax = axs[i]
```

```
    cov = covariances[i]

    samples = np.random.multivariate_normal([0,0],[[1,cov],[cov,1]],200)
    x = samples[:,0]
    y = samples[:,1]

    minx.append(min(x))
    maxX.append(max(x))

    miny.append(min(y))
    maxY.append(max(y))

    sns.scatterplot(x,y,ax=ax,label="Cov(X,Y) = {:.1f}".format(cov))
    ax.tick_params(labelsize=10)

    ax.set_xlabel("Samples from X",fontsize=10)
    ax.set_ylabel("Samples from Y",fontsize=10)

    ax.legend()

minv = min( [min(minx), min(miny)] )
maxv = max( [max(maxX), max(maxY)] )

for ax in axs:
    ax.set_xlim(minv,maxv)
    ax.set_ylim(minv,maxv)

fig.set_size_inches(12,4)
fig.set_tight_layout(True)
```

```
/usr/local/lib/python3.7/site-packages/ipykernel_launcher.py:14: RuntimeWarning:
covariance is not positive-semidefinite.
```



0.1.2 Correlation

The covariance can measure the association between two random variables, but it is difficult to interpret. To determine if the association between two variables is strong using the covariance also requires us to understand how X and Y vary by themselves. If, for example, the variance of X is 20 and Y is 30 then a covariance of 2 is not a strong association. If instead the variance of X is 0.5 and the variance of Y is 0.25 then the covariance of 2 is very strong. The **correlation** incorporates information about the covariance between two variables X and Y and also eahc individual random variables variance.

Pearson's The **correlation** between X and Y is computed as

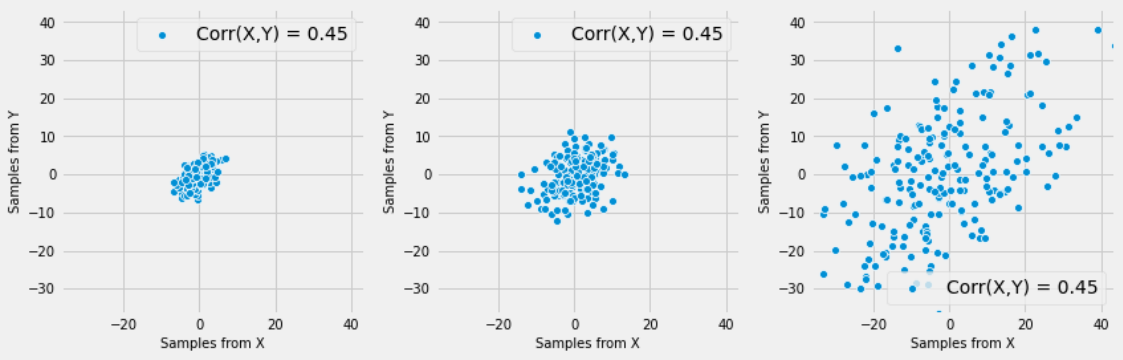
$$\rho_{X,Y} = \text{corr}\,(X,Y) = \frac{\text{cov}(X,Y)}{\text{Std.}(X)\ \text{Std.}(Y)} \tag{3}$$

where $\text{cov}(X,Y)$ is the covariance, and $\text{Std.}(X)$ and $\text{Std.}(Y)$ are the standard deviations of X and Y. This type of correlation is often called Pearson's correlation. Pearson's correlation normalizes the covariance: the smallest correlation is -1 and the largest correlation is +1. Pearon's correlation *linear* relationships between two random variables—a proportional change in both X from it's mean and Y from it's mean.

Below are three plots with the same correlation but the variance of X and Y differ. The variance of X and Y is 2.5 for the 1st plot, 5.0 for the 2nd plot, and 15 for the 3rd plot. The correlation for all three samples of 200 pairs of (x,y) is 0.45.

[34]:
```
plt.style.use("fivethirtyeight")
fig,axs = plt.subplots(1,3)

stds  = [2.5,5,15]
corrs = [0.45,0.45,0.45]

minx,maxX = [],[]
miny,maxY = [],[]

for i,(std,cor) in enumerate(zip(stds,corrs)):
    ax = axs[i]

    samples = np.random.multivariate_normal([0,0],[[ std*std, cor*std*std␣
 ↪],[cor*std*std,std*std]],200)
    x = samples[:,0]
    y = samples[:,1]

    minx.append(min(x))
    maxX.append(max(x))

    miny.append(min(y))
    maxY.append(max(y))
```

```
    sns.scatterplot(x,y,ax=ax,label="Corr(X,Y) = {:.2f}".format(cor))
    ax.tick_params(labelsize=10)

    ax.set_xlabel("Samples from X",fontsize=10)
    ax.set_ylabel("Samples from Y",fontsize=10)

    ax.legend()

minv = min( [min(minx), min(miny)] )
maxv = max( [max(maxX), max(maxY)] )

for ax in axs:
    ax.set_xlim(minv,maxv)
    ax.set_ylim(minv,maxv)

fig.set_size_inches(12,4)
fig.set_tight_layout(True)
```



Spearmans One disadvantage of Pearson's correlation is it can only capture relationships thats are linear. Spearman's correlation is able to assess non-linear relationships between two random variables.

To compute Spearman's correlation we need to assign ranks to samples of X and separately to samples of Y. Then we compute Pearson's correlation on the transformed pairs of ranks. For example, lets look at the data set

$$D = \begin{bmatrix} X & Y \\ \hline 0.1 & 1 \\ -1 & 0 \\ 4.7 & -1.2 \\ 2.3 & 20.4 \end{bmatrix} \tag{4}$$

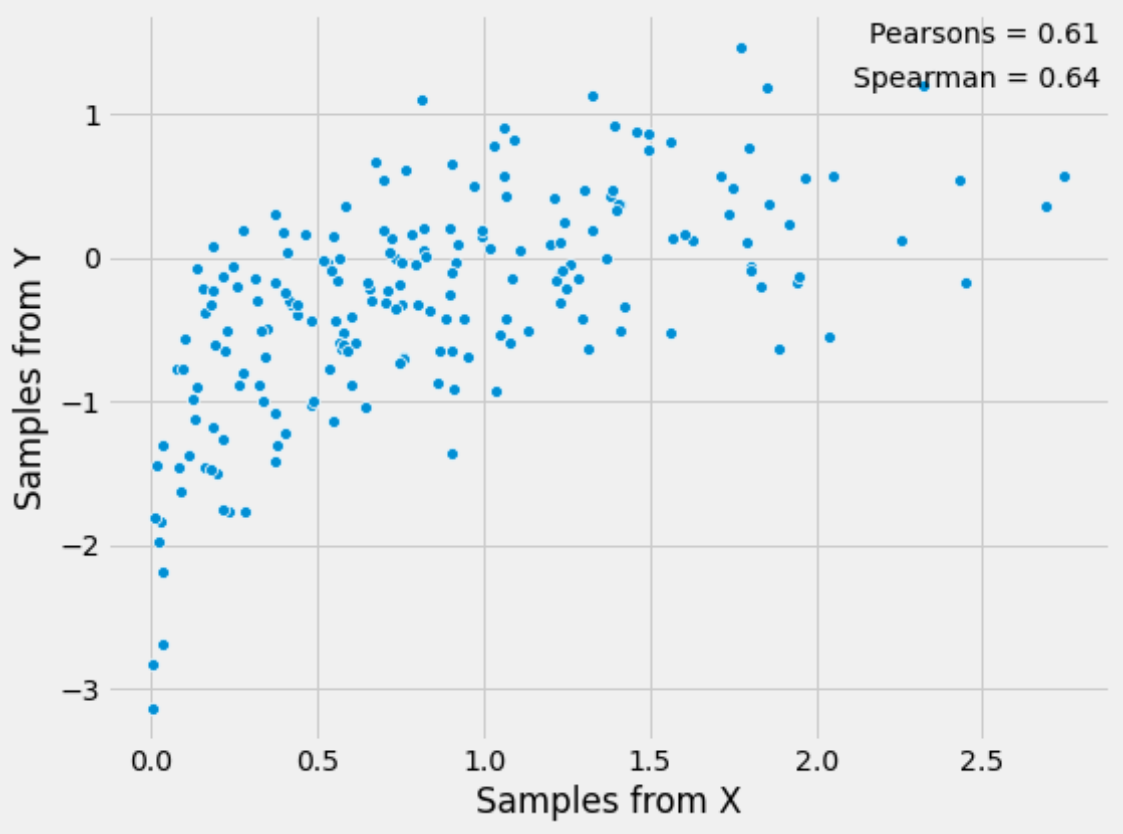
Rank the X samples and separately the Y samples

$$D = \begin{bmatrix} X & Y \\ \hline 2 & 3 \\ 1 & 2 \\ 4 & 1 \\ 3 & 4 \end{bmatrix} \tag{5}$$

and then we compute Pearson's correlation.

Lets look at an example of data with non-linear relationships and compute Pearson's and Spearman's correlation.

[97]:
```
import scipy.stats

fig,ax = plt.subplots()

xs = []
for n in range(200):
    x=-1
    while x<0:
        x = np.random.normal(0,1)
    xs.append(x)
ys = 0.5*np.array([ np.log(x) for x in xs]) + np.random.normal(0,0.5,200)

sns.scatterplot(xs,ys,ax=ax)

r,p = scipy.stats.pearsonr(xs,ys)
s,p = scipy.stats.spearmanr(xs,ys)

ax.text(0.99,0.99,s="Pearsons = {:.2f}".
 ↪format(r),ha="right",va="top",transform=ax.transAxes)
ax.text(0.99,0.93,s="Spearman = {:.2f}".
 ↪format(s),ha="right",va="top",transform=ax.transAxes)

ax.set_xlabel("Samples from X")
ax.set_ylabel("Samples from Y")

fig.set_tight_layout(True)
fig.set_size_inches(8,6)
```



0.1.3 2X2 tables

The 2 X 2 table (sometimes call the cross tabulations) is a classic statistical tool for computing association between categorical random variables. We can compute several different statistics using the 2 X 2 table and assess whether or not two random variables are correlated or associated with one another.

Construction A R X C table, a more general version of a 2 X 2 table, is built by first finding the number of categories possible for th r.v. X and for the r.v. Y. Then build an empty table where the number of rows is the number of categories of X and where the number of columns is the number of categories of Y. For example, if there are 3 possible values of X and 4 possible values of Y then our table is

$$\left[\begin{array}{c|ccc} & & Y & \\ \hline & & A & B & C \\ D & & & & \\ & E & - & - & - \\ - & & & & \\ X & F & - & - & - \\ - & & & & \\ & G & - & - & - \\ - & & & & \end{array}\right] \tag{6}$$

In each cell with, row R and column C, place in the table the number of times R and C occurred together.

How to compute expected values Lets suppose we build a 2X2 table that has the following values

$$\left[\begin{array}{c|cc} & A & B \\ \hline C & 23 & 62 \\ D & 44 & 71 \end{array}\right] \tag{7}$$

We can compute the expected frequency in each cell assuming the two random variables X and Y were independent with these steps:

- Sum all the counts in each cell (23+62+44+71 = 200)
- Sum up the Columns and sum up the Rows

$$\left[\begin{array}{c|cc|c} & A & B & \\ \hline C & 23 & 62 & 85 \\ D & 44 & 71 & 115 \\ \hline & 67 & 133 & 200 \end{array}\right] \tag{8}$$

If X and Y were independent than you could assume the frequency in each cell follows a binomial distribution where the number of trial is the total frequency (200) and the probability of success (the probability two values—for example A and C—occur together) is the probability one value occurs (#As/200) times the probability the other value occurs (#Cs\200). Then the expected value is the total frequency times the probability each value occurs independently.

$$\text{Expected value} = N \times \frac{\#(\text{Value From Y})}{N} \times \frac{\#(\text{Value From X})}{N} \tag{9}$$

$$= \frac{\#(\text{Value From Y}) \times \#(\text{Value From X})}{N} \tag{10}$$

In our example above, the expected frequencies is X and Y were independent are

$$\text{Expected values} = \left[\begin{array}{c|cc} & A & B \\ \hline C & 85 \times 67 \Big/ 200 & 85 \times 133 \Big/ 200 \\ D & 115 \times 67 \Big/ 200 & 115 \times 133 \Big/ 200 \end{array}\right] \tag{11}$$

$$= \left[\begin{array}{c|cc} & A & B \\ \hline C & 28.48 & 56.52 \\ D & 38.52 & 76.48 \end{array}\right] \tag{12}$$

$$\tag{13}$$

Goodness of fit and O-E We can measure the association between X and Y by computing the difference between what we observed versus what we would have expected to see if the two random variables are independent.

$$\left[\begin{array}{c|cc} & A & B \\ \hline C & (23 - 28.48) & (62 - 56.52) \\ D & (44 - 38.52) & (71 - 76.48) \end{array}\right] \tag{14}$$

$$\tag{15}$$

To decide if the differences above are big or small we can divide by the expected frequency and look at the relative difference between observed and expected frequencies.

$$\left[\begin{array}{c|cc} & A & B \\ \hline C & (23 - 28.48) \Big/ 28.48 & (62 - 56.52) \Big/ 56.52 \\ D & (44 - 38.52) \Big/ 38.52 & (71 - 76.48) \Big/ 76.48 \end{array}\right] \tag{16}$$

$$\tag{17}$$

Finally, it doesn't much matter if the observed frequency is smaller or larger than expected. All that matters is that their different. Let's square the numerator.

$$\left[\begin{array}{c|cc} & A & B \\ \hline C & (23 - 28.48)^2 \Big/ 28.48 & (62 - 56.52)^2 \Big/ 56.52 \\ D & (44 - 38.52)^2 \Big/ 38.52 & (71 - 76.48)^2 \Big/ 76.48 \end{array}\right] \tag{18}$$

$$\tag{19}$$

But this is a table of four values. To transform this into a single value how about we add all the squared relative differences together.

$$\chi^2 = (23 - 28.48)^2 \Big/ 28.48 + (62 - 56.52)^2 \Big/ 56.52 + (44 - 38.52)^2 \Big/ 38.52 + (71 - 76.48)^2 \Big/ 76.48 = 2.75 \tag{20}$$

Chisquare distribution and pvalue A formal hypothesis test requires we present a null hypothesis and alternative hypothsis. The null hypothesis for this test, called the "Goodness of fit" test, supposes the observed and expected frequencies are equal. If this was the case, then χ^2 would equal zero. The alternative hypothesis is then that χ^2 is not equal zero.

$$H_{\text{null}} : \chi^2 = 0 \tag{21}$$
$$H_{\text{Alte.}} : \chi^2 \neq 0 \tag{22}$$
$$\tag{23}$$

Our test statistic is the sum of squared relative differences between observed and expected values. But what distribution does our test statistic have? We will need to find out if we want to compute a pvalue—the probability we could observe a test statistic value more extreme than our observed test statistic.

The Z score has a Normal dist and the Z^2 a Chisquare

0.1.4 Simple linear regression

Probabilistic and model form

LINE assumptions

Expected value

Computing b_0 and b_1

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