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Calculating covariance of joint probability mass function in R

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I have a joint probability mass function of two variables X,Y like here







			r		
		0	1	2	$f_G(g)$
	0	$\frac{\binom{4}{3}}{\binom{9}{3}} = \frac{4}{84}$	$rac{inom{2}{1}inom{4}{2}}{inom{9}{3}}=rac{12}{84}$	$\frac{\binom{2}{2}\binom{4}{1}}{\binom{9}{3}} = \frac{4}{84}$	$\frac{20}{84}$
g	1	$\frac{\binom{3}{1}\binom{4}{2}}{\binom{9}{3}} = \frac{18}{84}$	$\frac{\binom{2}{1}\binom{3}{1}\binom{4}{1}}{\binom{9}{3}}=\frac{24}{84}$	$rac{inom{2}{2}inom{3}{1}}{inom{9}{3}}=rac{3}{84}$	45 84
	2	$rac{inom{3}{2}inom{4}{1}}{inom{9}{3}}=rac{12}{84}$	$rac{inom{2}{1}inom{3}{2}}{inom{9}{3}}=rac{6}{84}$	0	18 84
	3	$rac{inom{3}{3}}{inom{9}{3}}=rac{1}{84}$	0	0	1 84
	$f_R(r)$	$\frac{35}{84}$	$\frac{42}{84}$	$\frac{7}{84}$	

How can I calculate the covariance in R?

I created two vectors x,y and fed them into cov(), but I get the wrong result.

How can I do this right?

Thanks in advance and happy coding!

r statistics probability Edit tags

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asked May 31, 2018 at 10:51



This is probably better at home on CrossValidated, the statistics website on the SE network. – JAD May 31, 2018 at 11:13

ah thanks, I'll ask there then! – nequalstim May 31, 2018 at 11:14

As far as an R implementation is concerned, please take a look my step-by-step answer below. – Maurits Evers May 31, 2018 at 12:56 🖍

1 Answer

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Since SO is a coding forum, I'll leave working out the math/stats details up to you. Here is an implementation in R.



1. We start by noting the sample spaces for X and Y



For G G <- 0:3;



For R R <- 0:2;



2. The joint probability mass function is given by the following matrix

```
joint_pmf <- matrix(
    c(4/84, 12/84, 4/84,
        18/84, 24/84, 3/84,
        12/84, 6/84, 0,</pre>
```

```
1/84, 0, 0),
ncol = 3, byrow = T);
```

3. We calculate the population means

```
# For G
mu_G <- rowSums(joint_pmf) %*% G;
# For R
mu_R <- colSums(joint_pmf) %*% R;</pre>
```

4. We can make use of the theorem Cov(X, Y) = E[XY] - E[X]E[Y] to calculate the covariance

```
cov_GR <- G %*% joint_pmf %*% R - mu_G * mu_R;
# [,1]
#[1,] -0.1666667</pre>
```

where we have used the fact that $E[G] = mu_G$ and $E[R] = mu_R$ are the respective population means.

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edited May 31, 2018 at 12:51

answered May 31, 2018 at 12:32

