```r
# Sample size
n <- 500

# A vector of means of our two variables
mu <- c(1000, 2000)

# Covariance of our 2 variables is equal to Pearson's R * SD_var1 *
# SD_var2. If we know the variance for each of our variables we can
# calculate the sd. We can then use these values to work out the
# covariance we need for any particular Pearson's r value

# For the below example to give us a Pearson's r of .5 and variance for
# var1 = 100, and variance of var2 = 50 we have covariance = .5 *
# sqrt(100) * sqrt(50) which gives us 35.35534
myr <- 35.35534

# The 2 x 2 covariance matrix where we have the variance of variable 1,
# the covariance of variables 1 and 2, the covariance of variables 1
# and 2 and the variance of variable 2
mysigma <- matrix(c(100, myr, myr, 50), 2, 2)
```

```
set.seed(1234)
data <- data.frame(mvrnorm(n, mu, mysigma, empirical = TRUE))
colnames(data) <- c("Var_1", "Var_2")

ggplot(data, aes(x = Var_1, y = Var_2)) +
  geom_point() +
  geom_smooth(method = "lm")

rcorr(data$Var_1, data$Var_2)
```

```
      x   y
x 1.0 0.5
y 0.5 1.0


n= 500


P
    x   y
x       0
y   0
```