

mvn_distribution

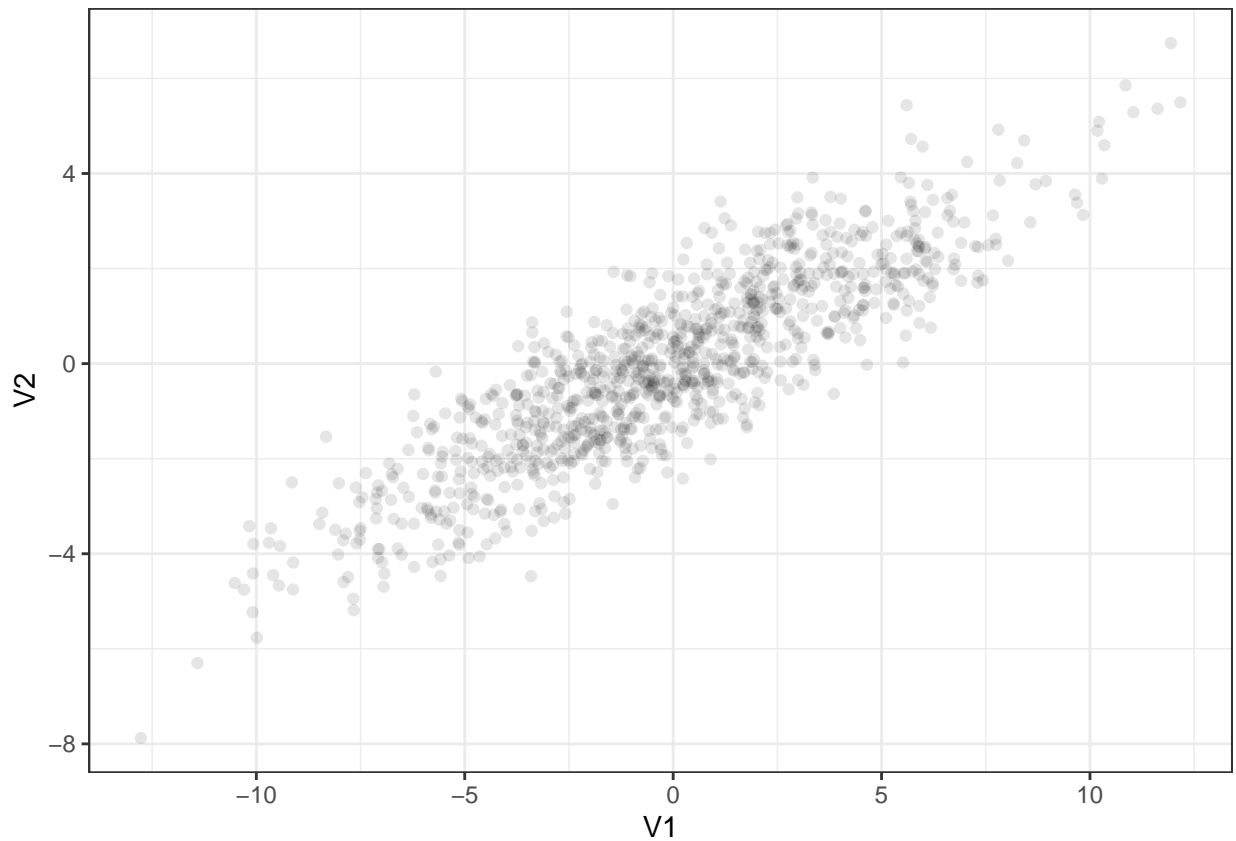
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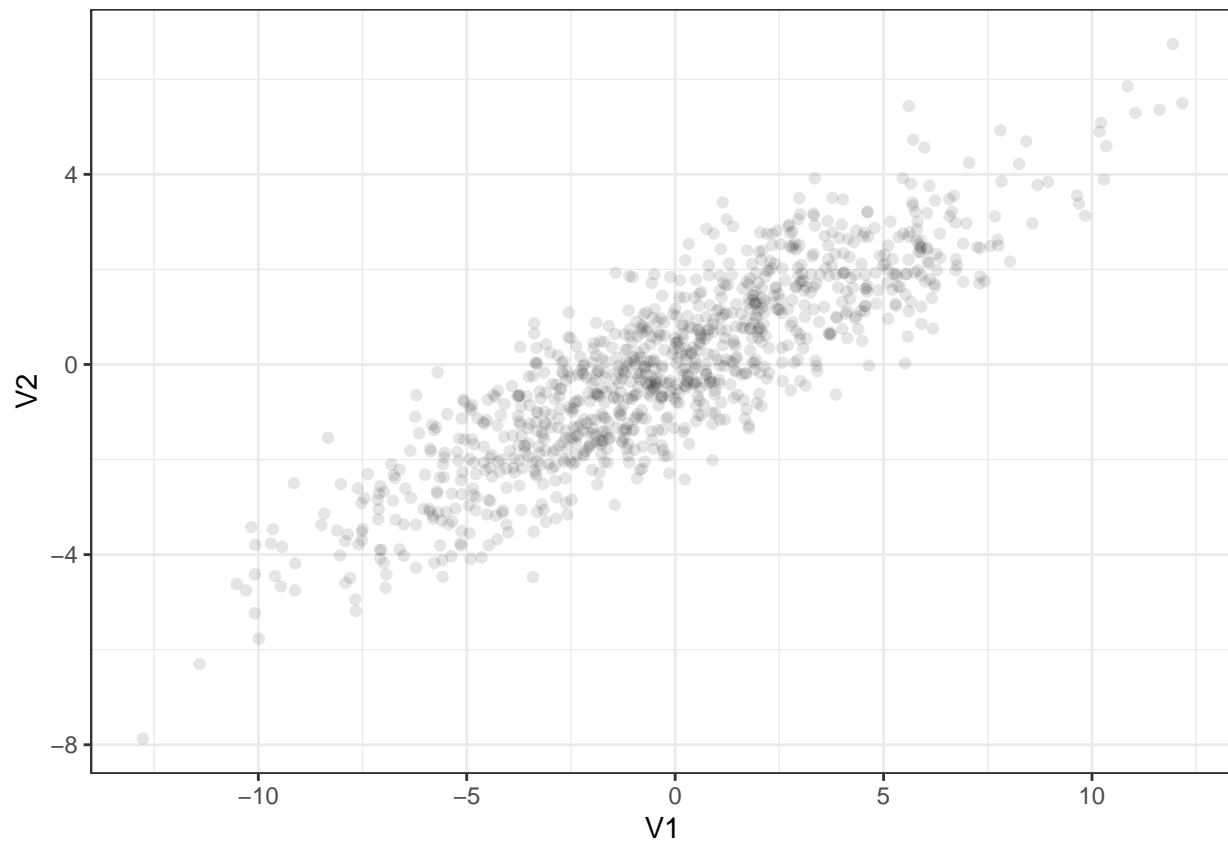
```
library(ggplot2)
library(mvtnorm)
library(MASS)

#population
# population cov matrix
v <- matrix(c(16,7,7,4), nrow = 2, ncol = 2 , byrow = TRUE)
# True mean
mu <- c(0,0)
n <- 1000

d1 <- as.data.frame(rmvnorm(n, mean = mu, sigma = v))
ggplot(d1, aes(V1, V2)) +geom_point(alpha = 0.1) + theme_bw()
```



```
d2 <- as.data.frame(rmvnorm(n, mean = mu, sigma = v))
ggplot(d1, aes(V1, V2)) +geom_point(alpha = 0.1) + theme_bw()
```

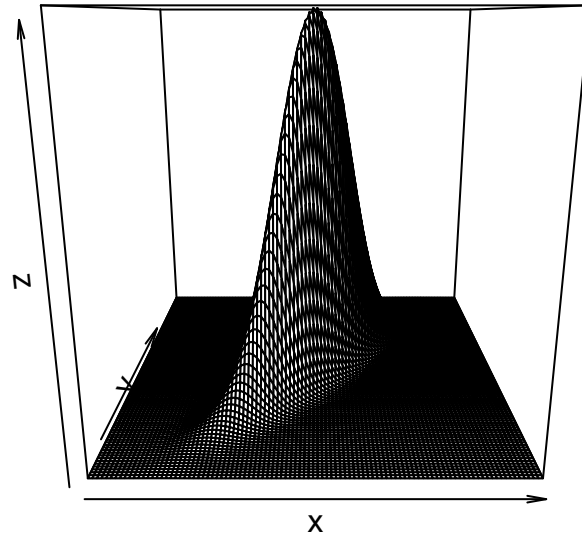


3D Plot

```
x <- seq(-20, 20, length =100)
y <- seq(-8,8, length = 100)

calc.z <- function(x,y,mu,sigma)
{
  z <- matrix(ncol = length(y), nrow = length(x))
  for (i in 1:length(x))
  {
    for (j in 1:length(y)){
      z[i,j] <- dmvnorm(c(x[i],y[j]), mean = mu , sigma = sigma)
    }
  }
  return(z)
}

z <- calc.z ( x,y, mu, v)
persp(x,y,z,theta=0)
```



```
contour(x, y, z, nlevels= 20 )
```

