

Univariate test vs multivariate test

immediate

```
library(mvtnorm)
library(data.table)
library(ggplot2)
library(ggforce) # install.packages("ggforce")
```

1 One-dimensional test

Create a 1D-grid of values corresponding to the possible values of the 1D statistic test:

```
grid1D <- seq(-3,3,0.025)
```

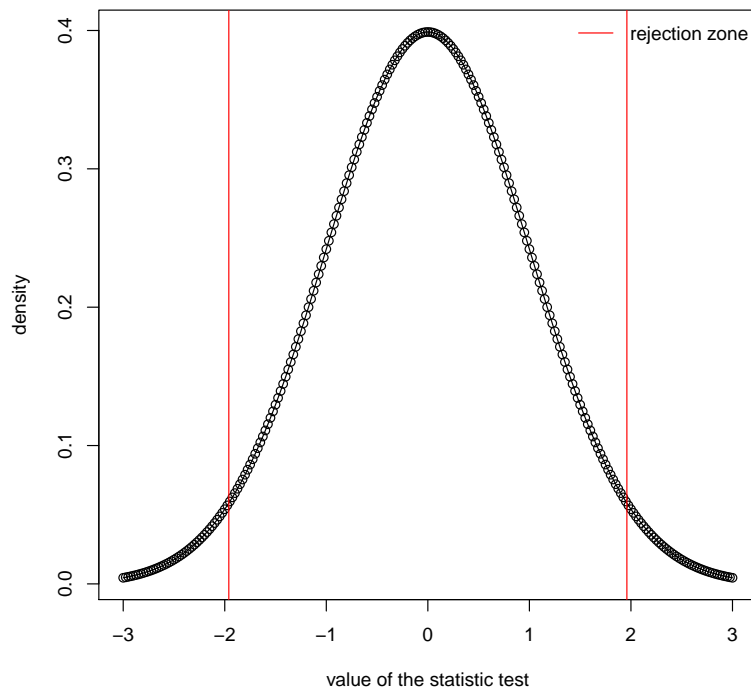
The rejection region at 5% is defined by the 0.025 and 0.975 quantiles of the normal distribution:

```
rejection1D <- c(qnorm(0.025), qnorm(0.975))
rejection1D
```

```
[1] -1.959964  1.959964
```

```
plot(grid1D, dnorm(grid1D), type = "o", xlab = "value of the statistic test",
     ylab = "density")
abline(v = rejection1D, col = "red")
legend("topright", col = "red", lty = 1, legend = "rejection zone", bty = "n")
```

We can then plot the values of the statistic tests and the rejection region:



2 2 dimensional test

Create a 2D-grid of values corresponding to the possible values of the 2D statistic test:

```
grid2D <- as.data.table(expand.grid(beta1 = grid1D, beta2 = grid1D))
grid2D[, density := dmvnorm(cbind(beta1, beta2))]
range(grid2D$density)
```

```
[1] 1.964128e-05 1.591549e-01
```

If we would do two univariate tests (not accounting for multiple testing), the rejection region at 5% would be a square whose size is defined the 0.025 and 0.975 quantiles of the normal distribution:

```
rejection2D.2uni <- data.table(xmax = qnorm(0.975, mean = 0, sd = 1),
                              ymax = qnorm(0.975, mean = 0, sd = 1),
                              xmin = qnorm(0.025, mean = 0, sd = 1),
                              ymin = qnorm(0.025, mean = 0, sd = 1))
rejection2D.2uni
```

```
      xmax      ymax      xmin      ymin
1: 1.959964 1.959964 -1.959964 -1.959964
```

When we account for multiple comparison we get:

```
rejection2D.2uniadj <- data.table(xmax = qmvnorm(0.95, mean = c(0,0), sigma = diag(1,2)
, tail = "both")$quantile,
                                ymax = qmvnorm(0.95, mean = c(0,0), sigma = diag(1,2)
, tail = "both")$quantile,
                                xmin = -qmvnorm(0.95, mean = c(0,0), sigma = diag
(1,2), tail = "both")$quantile,
                                ymin = -qmvnorm(0.95, mean = c(0,0), sigma = diag
(1,2), tail = "both")$quantile)
rejection2D.2uniadj
```

```
      xmax      ymax      xmin      ymin
1: 2.236422 2.236422 -2.236422 -2.236422
```

If we do a bivariate test, the rejection region at 5% would be a circle whose radius is the 0.95 quantile of a chi-squared distribution with 2 degrees of freedom:

```
rejection2D.chisq <- sqrt(qchisq(0.95, df = 2))
rejection2D.chisq
```

```
[1] 2.447747
```

```
gg2D <- ggplot() + labs(x=expression(beta[1]), y=expression(beta[2]))
gg2D <- gg2D + geom_raster(data = grid2D, aes(x=beta1, y=beta2, fill = density))
gg2D <- gg2D + scale_fill_gradient(low="white", high="blue")

## gg2D <- gg2D + geom_rect(data = rejection2D.2adj,
##                          aes(xmin = xmin, xmax = xmax, ymin = ymin, ymax = ymax,
##                              colour = "2 univariate Wald tests (non-adjusted)",
##                              size = 2,
##                              fill = NA)
gg2D <- gg2D + geom_rect(data = rejection2D.2uniadj,
                        aes(xmin = xmin, xmax = xmax, ymin = ymin, ymax = ymax,
                            colour = "2 univariate Wald tests (adjusted)",
                            size = 2,
                            fill = NA)
gg2D <- gg2D + geom_circle(aes(x0=0, y0=0, r = rejection2D.chisq,
                              color = "1 Chi-2 test"),
                          size = 2)
gg2D <- gg2D + labs(color = "critical quantile")
gg2D
```

