Hypotheses tests with continuous variables

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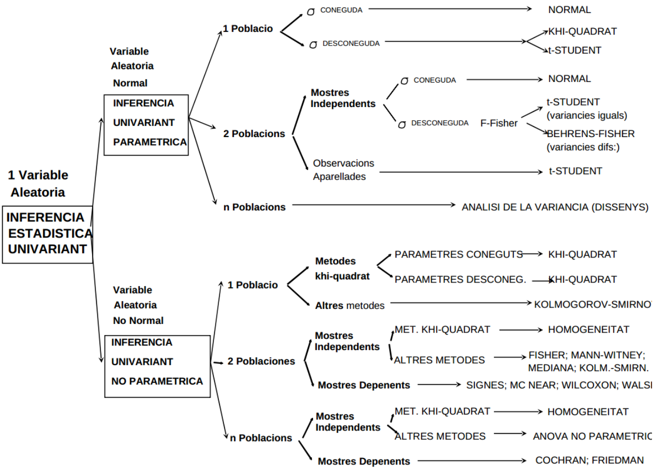
Outline

Introduction

- Once the concept of hypothesis testing is established,
- Researchers face the problem of *which test should be applied at every possible situation*.
- Best solution:
  - understand the problem and the questions addressed
  - know available tests for each problem
  - be aware of applicability assumptions of each test and how to check them.
- Easier to say than to do.
  - Sometimes cheatsheets may be helpful, but be warned against a blind use, that is understand and be critic with the steps.

Which test is appropriate for which problem



Example situation

- A study was designed to compare two distinct hypertension control programs.
- 60 individuals with HTA were randomly assigned to either one or the other group (30 per group)
- Blood pressure was measured each month during a year

```r
hta <- read_excel("datasets/hta.xls")
print(head(hta[,1:7]))
```

```
## # A tibble: 6 x 7
##   numero sexo  grupo  tas1  tad1  tas2  tad2
##    <dbl> <chr> <chr> <dbl> <dbl> <dbl> <dbl>
## 1      1 VARON B       150   100   150    90
## 2      2 MUJER B       160    90   170    90
## 3      3 MUJER B       150    90   110    90
## 4      4 VARON A       120    80   140    90
## 5      5 MUJER A       150    85   145    85
## 6      6 MUJER B       140    75   160    70
```

Always start looking at the data

```r
oldpar<-par(mfrow=c(1,1)) # Guarda los parámetros para el dibgujo
par(mfrow=c(2,2)) # Dibuja cuatro gráficos por grafico
with(hta, boxplot(tas1, main="Box-plot") )
with(hta, hist(tas1) )
with(hta, qqnorm(tas1, main="Normal QQplot") );with(hta, qqline(tas1) )
par(oldpar) # Vuelve a los parámetros de dibujo originales
```

Normality Test

```
with(hta,shapiro.test(tad1) ) # Shapiro Wilk test
```

```
##
##  Shapiro-Wilk normality test
##
## data:  tad1
## W = 0.96622, p-value = 0.09512
```

One sample Test

```
with(hta,t.test(tad1,mu=90) ) # One sample T.test
```

```
##
##  One Sample t-test
##
## data:  tad1
## t = -1.2137, df = 59, p-value = 0.2297
## alternative hypothesis: true mean is not equal to 90
## 95 percent confidence interval:
##  85.80626 91.02707
## sample estimates:
## mean of x
##  88.41667
```

Homogeneity variance Test

```
library(car)
hta%>%
  group_by(sexo) %>%
  summarise(var = sd(tas1))
```

```
## # A tibble: 2 x 2
##   sexo    var
##   <chr> <dbl>
## 1 MUJER  17.6
## 2 VARON  22.1
```

```
with(hta,leveneTest(tad1~factor(sexo),center="median"))
```

```
## Levene's Test for Homogeneity of Variance (center = "median")
##       Df F value Pr(>F)
## group  1  1.3506 0.2499
##       58
```

- p value is over 0.05
- We can assume homogeneity of variances

T test when variances are equal

```
with(hta,t.test(tas1~factor(sexo),var.equal=TRUE ))
```

```
##
##  Two Sample t-test
##
## data:  tas1 by factor(sexo)
## t = -0.2471, df = 58, p-value = 0.8057
## alternative hypothesis: true difference in means between grou
## 95 percent confidence interval:
##  -11.603461   9.053519
## sample estimates:
## mean in group MUJER mean in group VARON
##            149.5946            150.8696
```

- Type I Error is over than 0.05
- We cannot reject mean equality

T test when variances are unequal

```
with(hta,t.test(tas1~factor(sexo),var.equal=FALSE ))
```

```
##
##  Welch Two Sample t-test
##
## data:  tas1 by factor(sexo)
## t = -0.23436, df = 39.098, p-value = 0.8159
## alternative hypothesis: true difference in means between grou
## 95 percent confidence interval:
##  -12.277927   9.727986
## sample estimates:
## mean in group MUJER mean in group VARON
##            149.5946            150.8696
```

- Same conclusions as before
- Test is also known as Welch test

U Mann-Whitney or Sum Rank non parametric test

```
with(hta,wilcox.test(tad1~factor(sexo)
    ,alternative='two.sided',exact=TRUE, correct=FALSE))
```

```
##
##  Wilcoxon rank sum test
##
## data:  tad1 by factor(sexo)
## W = 434, p-value = 0.8955
## alternative hypothesis: true location shift is not equal to 0
```

```
hta%>%
  group_by(sexo) %>%
  summarise(median = median(tad1))
```

```
## # A tibble: 2 x 2
##   sexo  median
##   <chr>  <dbl>
## 1 MUJER     90
## 2 VARON     90
```

- Null Hypothesis cannot be rejected

Paired T-test

```r
with(hta,t.test(tas1,tas12,paired=TRUE))
```

```
##
##  Paired t-test
##
## data:  tas1 and tas12
## t = 6.0672, df = 51, p-value = 1.609e-07
## alternative hypothesis: true mean difference is not equal to
## 95 percent confidence interval:
##   8.518285 16.943253
## sample estimates:
## mean difference
##        12.73077
```

```r
summary(hta$tas1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   100.0   140.0   145.0   150.1   160.0   210.0
```

```r
summary(hta$tas12)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
```

Paired Sign-Rank Wilcoxon Test

```
with(hta,wilcox.test(tad1,tad12,
     exact=TRUE, paired=TRUE))
```

```
##
##  Wilcoxon signed rank test with continuity correction
##
## data:  tad1 and tad12
## V = 478.5, p-value = 0.05333
## alternative hypothesis: true location shift is not equal to 0
```

Read diabetes data

```
library(readxl)
library(dplyr)
library(magrittr)
diabetes <- read_excel("datasets/diabetes.xls")
sapply(diabetes, class)
```

```
##    numpacie        mort    tempsviu        edat         bmi    edatdiag
##   "numeric" "character"   "numeric"   "numeric"   "numeric"   "numeric"
##       tabac         sbp         dbp         ecg         chd
## "character"   "numeric"   "numeric" "character" "character"
```

```
diabetes_factor <- diabetes %>%
  mutate_if(sapply(diabetes, is.character), as.factor) %>%
  select (-numpacie)

diabetes%>%
  group_by(ecg) %>%
  summarise( n=n(),
    mean = mean(edat),
            sd=sd(edat))
```

```
## # A tibble: 3 x 4
##   ecg           n  mean    sd
##   <chr>     <int> <dbl> <dbl>
## 1 Anormal      11  64.9  6.76
## 2 Frontera     27  53.8 11.4
## 3 Normal      111  50.5 11.5
```

ANOVA

```
anova<-aov(edat~ecg,data=diabetes_factor)
summary(anova)
```

```
##              Df Sum Sq Mean Sq F value  Pr(>F)
## ecg           2   2166  1083.0   8.619 0.00029 ***
## Residuals   146  18347   125.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

Multicomparison

```
library(multcomp)
tuk <- glht(anova, linfct = mcp(ecg = "Tukey"))

  print(summary(tuk)) # pairwise tests
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = edat ~ ecg, data = diabetes_factor)
##
## Linear Hypotheses:
##                         Estimate Std. Error t value Pr(>|t|)
## Frontera - Anormal == 0  -11.094      4.010  -2.767 0.016446 *
## Normal - Anormal == 0    -14.405      3.543  -4.065 0.000222 ***
## Normal - Frontera == 0    -3.310      2.405  -1.376 0.345709
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
print(confint(tuk, level=0.95)) # confidence intervals
```

```
##
##   Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = edat ~ ecg, data = diabetes_factor)
##
## Quantile = 2.3458
## 95% family-wise confidence level
##
##
## Linear Hypotheses:
##                         Estimate lwr      upr
## Frontera - Anormal == 0 -11.0943 -20.5002  -1.6883
## Normal - Anormal == 0   -14.4046 -22.7167  -6.0925
## Normal - Frontera == 0   -3.3103  -8.9530   2.3324
```

Multicomparison plot

```
plot(confint(tuk))
```

Kruskal-Wallis Test

```
diabetes_factor%>%
  group_by(ecg) %>%
  summarise(median = median(edat))
```

```
## # A tibble: 3 x 2
##   ecg      median
##   <fct>     <dbl>
## 1 Anormal      64
## 2 Frontera     53
## 3 Normal       49
```

```
kruskal.test(edat~ecg,data=diabetes_factor)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  edat by ecg
## Kruskal-Wallis chi-squared = 17.483, df = 2, p-value = 0.0001
```

Dunn Test for multiple comparison

```
library(dunn.test)
with(diabetes_factor,dunn.test(edat,ecg,method="bonferroni"))
```

```
##   Kruskal-Wallis rank sum test
##
## data: edat and ecg
## Kruskal-Wallis chi-squared = 17.4826, df = 2, p-value = 0
##
##
##                             Comparison of edat by ecg
##                                   (Bonferroni)
## Col Mean-|
## Row Mean |    Anormal   Frontera
## ---------+----------------------
## Frontera |   2.721182
##          |    0.0098*
##          |
##   Normal |   4.075469   1.467464
##          |    0.0001*     0.2134
##
```