Course: Univariate Statistics with R

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Like other occult techniques of divination, the statistical method has a private jargon deliberately contrived to obscure its methods from non-practitioners. – Attributed to G. O. Ashley

Which test to use?

It is almost impossible to get by in epidemiology without having at least a cursory understanding of what a null hypothesis, p-value, confidence interval means.

Statistical tests work by calculating a test statistic – a value that indicates how much the relationship between variables in your test differs from the null hypothesis of no relationship. Most, if not all, tests calculates a p-value (probability value) which estimates how likely it is that you would see the difference described by the test statistic if the null hypothesis of no relationship were true. If the p-value is less than 0.05, we reject the null hypothesis that there's no difference between the means and conclude that a **significant** difference does exist. If the p-value is larger than 0.05, we cannot conclude that a significant difference exists. (P value sceptic? https://www.nature.com/articles/d41586-019-00857-9). Statistical tests assume a null hypothesis of no relationship or no difference between groups.

To determine which statistical test to use, you need to know:

- Whether your data meets certain statistical assumptions (Independence of observations, Homoscedasticity and normality of data)
- The types of variables that you're dealing with.

If your data do not meet the assumptions of normality or homogeneity of variance, you may be able to perform a **nonparametric statistical test**.

Parametric tests

Prerequisite: data has to conform to the three assumptions. The most common types of parametric test include regression tests, comparison tests, and correlation tests.

Regression test: used to test cause-and-effect relationships i.e., the effect of one or more continuous (or categorical for logistic regressions) variables on another variable.

Correlation test: used to check whether two variables are related without assuming causeand-effect relationships. e.g How are latitude and temperature related?

Non-parametric tests

Used when many assumptions about the data are not met. Always assess whether data are likely from a normal distribution using either Kolmogorov-Smirnov test, the Anderson-Darling test, or the Shapiro-Wilk test.

There are two kinds of statistics, the kind you look up, and the kind you make up.

- Rex Stou

#T test #Use Shapiro-Wilk normality test as described at: Normality Test in R. - Null #hypothesis: the data are normally distributed - Alternative hypothesis: the data #are not normally distributed. lungcancer <- read.csv("Lungcancer.csv",header = T) # Shapiro-Wilk normality test for Men's weights with(lungcancer, shapiro.test(Weight[Sex == "Male"]))# $p = 0.5$ # Shapiro-Wilk normality test for Women's weights with(lungcancer, shapiro.test(Weight[Sex == "Female"]))# $p = 0.9$ #the two p-values are greater than the significance level 0.05 implying that the distribution of the data are not #significantly different from the normal distribution. In other words, we can assume the normality. # use F-test to test for homogeneity in variances using var.test() res.ftest <- var.test(Weight ~ Sex, data = lungcancer) res.ftest #The F test value is greater than the significance level alpha = 0.05 thus no significant #difference between the variances of the two sets of data. Therefore, we can use the classic t-test witch assume equality of the two variances t test1 <- t.test(Weight ~ Sex, data = lungcancer) t_test1 #The p-value of the test is 0.2858, which is less than the significance level #alpha = 0.05. #We can conclude that men's average weight is not significantly different from #women's average weight# #look at the confidence interval! what can it tell regarding significance? **#Mann-Whitney-Wilcoxon** #suppose the data violated the assumptions we undertake a Mann-Whitney-Wilcoxon #Test using the wilcox.test function wilcox.test(Weight \sim Sex, data = lungcancer) library(datasets) head(mtcars) str(mtcars) **#One way anova** #a one-way ANOVA on mpg (miles per gallon) being dependent on the gear (3, 4 and 5) mtcars\$gear <- as.factor(mtcars\$gear) #always plot your data first $boxplot(mpg\text{-}year, data = mtcars)$ fit \leq aov(mpq \sim gear, data = mtcars) summary(fit) # p value is significant meaning different distribution hence we need to do a post #hoc analysis

```
posthoctukey <- TukeyHSD(fit)
posthoctukey
#plot the pairwise comparison
plot(posthoctukey,las=2,col="black",cex.axis=1,cex.lab =1)
```
#Kruskal wallis

#if the data was not normally distributed, we use a non-parametric test

fit kruskal <- kruskal.test(mpg ~ gear, data = mtcars) fit_kruskal

#post hoc test shoulr use Dunn's pairwise tests or Nemeyi test

pairwise.wilcox.test(mtcars\$mpg, mtcars\$gear, p.adjust.method = "bonferroni")

#Chi-square test

#Chi-square test examines whether rows and columns of a #contingency table are statistically significantly associated.

#Null hypothesis (H0): the row and the column variables of the contingency table are independent. #Alternative hypothesis (H1): row and column variables are dependent #say you want to analyse the distribution of lung cancer cases by sex #rows will be sex (the predictor) and column lung cancer incidence (the response)

#create a 2 by 2 contingency table

tab canc sex <- table(lungcancer\$Sex,lungcancer\$Lungcancer) tab_canc_sex

chisq.test(tab canc sex)

#p value > that 0.05 thus there is no significant relationship between the two categorical variables

#Fisher exact test

#the Fisher's exact test is used when the sample is small #same assumptions as for chi square

tab canc sex <- table(lungcancer\$alcohol,lungcancer\$Lungcancer) fisher.test(tab canc sex)

#linear regression

#The mathematical formula of the linear regression can be written as $y = b0 + b1*x +$ e, where: #b0 and b1 are known as the regression beta coefficients or parameters: #b0 is the intercept of the regression line; that is the predicted value when $x = 0$ #b1 is the slope of the regression line. #e is the error term (also known as the residual errors), the part of y that can be explained by the regression model #Create a scatter plot displaying wt (weight) vs mpg (miles per gallon) in mtcars #dataset library(ggplot2) p scatter \leq - ggplot(mtcars, aes(x = wt, y = mpg)) + geom point(color=c("#00AFBB"), shape = 19 , size =3)+ $\text{labs}(x = "mpg", y = "wt", \text{title} = "Relationship of mpg and wt") +$ theme $bw()$ + theme(plot.title = element text(color = "black", size = 12,hjust = 0.5), $axis.text.x = element_text(color = "black", size = 12),$ $axis.text.y = element_text(color = "black", size = 12),$ axis.title.x= element_text(color = "black", size = 12), axis.title.y = element_text(color = "black", size =12)) p_scatter #run a regression analysis using function lm regress mpg wt <- $lm(mpq\text{-wt},data = mtears)$ regress_mpg_wt # the estimated regression line equation can be written as follow: mpg = 49.65 + (-5.344)*wt #add regression line on the scatter plot p_scatter_regline <- p_scatter+geom_smooth(method = "lm",color="#00AFBB") p_scatter_regline #try mpg and qsec

PS: For those keen on proceeding to intermediate level we will dive deeper into regression analysis.