

Master Program in *Data Science and Business Informatics*

Statistics for Data Science

Lesson 33 - Multiple comparisons. Fitting distributions

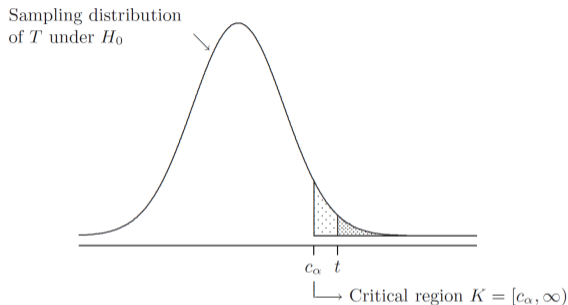
Salvatore Ruggieri

Department of Computer Science

University of Pisa

salvatore.ruggieri@unipi.it

Critical values and p-values



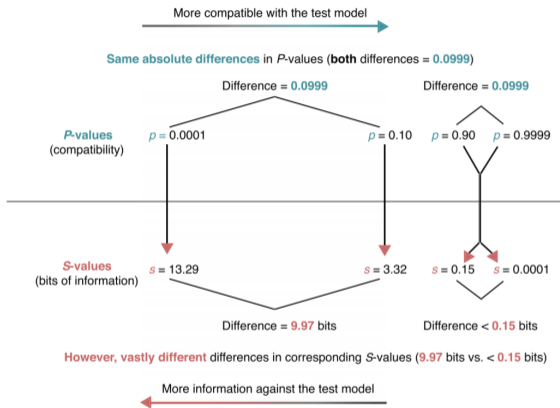
- *Critical region K* : the set of values that reject H_0 in favor of H_1 at significance level α
- *Critical values*: values on the boundary of the critical region
- *p-value*: the probability of obtaining test results at least as extreme as the results actually observed, under the assumption that H_0 is true
- $t \in K$ iff $p\text{-value} \leq \alpha$

Misues of p -values

Misinterpretations of p -values, [[Greenland et al, 2016](#)]

- ~~The p value is the probability that the null hypothesis is true, or the probability that the alternative hypothesis is false.~~ A p -value indicates the degree of compatibility between a dataset and a particular hypothetical explanation
- ~~The 0.05 significance level is the one to be used:~~ No, it is merely a convention. There is no reason to consider results on opposite sides of any threshold as qualitatively different.
- ~~A large p value is evidence in favor of the test hypothesis:~~ A p -value cannot be said to favor the test hypothesis except in relation to those hypotheses with smaller p -values
- ~~If you reject the test hypothesis because $p \leq 0.05$, the chance you are in error is 5%:~~ No, the chance is either 100% or 0%. The 5% refers only to how often you would reject it, and therefore be in error.

s-values



- Shannon information value or surprisal value (**s-value**) is $-\log_2 p$
- $p = 0.05 \Rightarrow s = 4.3$ - no more surprising than getting all heads on 4 fair coin tosses.
- $p = 0.005 \Rightarrow p = 7.64$ - no more surprising than getting all heads on 8 fair coin tosses.

The multiple comparisons problem

- Single test $H_0 : \theta = 0$, with significance level $\alpha = 0.05$ *[false positive rate]*
 - ▶ test is called *significant* when we reject H_0
 - ▶ α is Type I error, probability of rejecting H_0 when it is true
- Multiple tests, say $m = 20$
 - ▶ E.g., $H_0^i : \theta_i = 0$ for $i = 1, \dots, m$ where θ_i is the **expectation of a subpopulation**
- What is the probability of rejecting at least one H_0^i when all of them are true?

$$P(\text{at least one reject}) = P(\cup_{i=1}^m \{p_i \leq \alpha\}) = 1 - P(\cap_{i=1}^m \{p_i > \alpha\}) = 1 - (1 - \alpha)^m$$

and then $1 - (0.95)^{20} \approx 0.64$

Family-wise error rate (FWER)

The FWER is the probability of making at least one Type I error in a family of n tests. If the tests are independent:

$$\alpha_{FWER} = 1 - (1 - \alpha)^m$$

If the test are dependent: $\alpha_{FWER} \leq m \cdot \alpha$

Multiple comparisons: corrections

- *Bonferroni correction* (most conservative one):

$$\alpha = \frac{\alpha_{FWER}}{m}$$

Hence, $p < \alpha$ iff $p \cdot m < \alpha_{FWER}$

- *Šidák correction* (exact for independent tests):

$$[\text{invert } \alpha_{FWER} = 1 - (1 - \alpha)^m]$$

$$\alpha = 1 - (1 - \alpha_{FWER})^{1/m}$$

Hence, $p < \alpha$ iff $1 - (1 - p)^m < \alpha_{FWER}$

See R script

False Discovery Rate and q -values

		True state of nature	
		H_0 is true	H_1 is true
Our decision on the basis of the data	Reject H_0	False Positive	True Positive
	Not reject H_0	True Negative	False Negative

- False Positive Rate: $FPR = FP / (FP + TN)$
 - ▶ Corrections control for FPR since $FWER = P(FP > 0 | H_0^i \ i = 1, \dots, m)$
- Drawback: acting on α increases $FNR = FN / (FN + TP)$
- False Discovery Rate: $FDR = FP / (FP + TP)$ [Korthauer et al, 2019]
 - ▶ $FDR = 0.05$ means 5% of rejected H_0 's are actually true
- **q -value** is $P(H_0 | T \geq t)$ [vs. $p = P(T \geq t | H_0)$]
 - ▶ FDR can be controlled by requiring $q \leq \text{threshold}$

See R script

Distribution fitting and quality of fitting

- Dataset x_1, \dots, x_n realization of $X_1, \dots, X_n \sim F$
- **Distribution fitting:** What is a plausible F ?
 - ▶ Parametric approaches:
 - Assume $F = F(\lambda)$ for some family F , and estimate λ as $\hat{\lambda}$
 - Maximum Likelihood Estimation (point estimate):
$$\hat{\lambda} = \operatorname{argmax}_{\lambda} L(\lambda)$$
 - Parametric bootstrap (p -value):
$$T_{ks} = \sup_{a \in \mathbb{R}} |F_n^*(a) - F_{\hat{\lambda}^*}(a)|$$
 - ▶ Non-parametric approaches:
 - Empirical distribution
 - Kernel Density Estimation
- **Quality of fitting:** Among several fits F_1, \dots, F_k , which one is the best?
 - ▶ Goodness of fit: how good is F_i in fitting the data?
 - ▶ Comparison: which one between two F_1 and F_2 is better?

Quality of fitting

- Loss functions (to be minimized)

- ▶ Akaike information criterion (AIC), balances model fit against model simplicity

$$AIC(F(\lambda)) = 2|\lambda| - 2\ell(\lambda)$$

- ▶ Bayesian information criterion (BIC), stronger balances over model simplicity

$$BIC(F(\lambda)) = |\lambda| \log n - 2\ell(\lambda)$$

- Statistics (continuous data):

- ▶ **KS test** $H_0 : X \sim F$ $H_1 : X \not\sim F$ with Kolmogorov-Smirnov (KS) statistic:

$$D = \sup_{a \in \mathbb{R}} |F_n(a) - F(a)| \sim K$$

- ▶ **LR test** $H_0 : X \sim F_1$ $H_1 : X \sim F_2$ with the likelihood-ratio test:

$$\lambda_{LR} = \log \frac{L(F_1(\lambda_1))}{L(F_2(\lambda_2))} = \ell(F_1(\lambda_1)) - \ell(F_2(\lambda_2)) \quad \text{with} \quad -2\lambda_{LR} \sim \chi^2$$

See R script

Chi-square distribution

The Chi-square distribution with k degrees of freedom $\chi^2(k)$ has density:

$$f(x) = \frac{1}{2^{k/2}\Gamma(k/2)} x^{k/2-1} e^{-x/2}$$

Let $X_1, \dots, X_k \sim N(0, 1)$. Then $Y = \sum_{i=1}^k X_i^2 \sim \chi^2(k)$

- Statistics (discrete data):

- ▶ **Pearson's Chi-Square test** $H_0 : X \sim F$ $H_1 : X \not\sim F$ with χ^2 statistic:


$$\chi^2 = \sum_{N_i > 0} \frac{(N_i - n_i)^2}{n_i} = n \cdot \sum_{N_i > 0} \frac{(N_i/n - p(i))^2}{p(i)} \sim \chi^2(df)$$

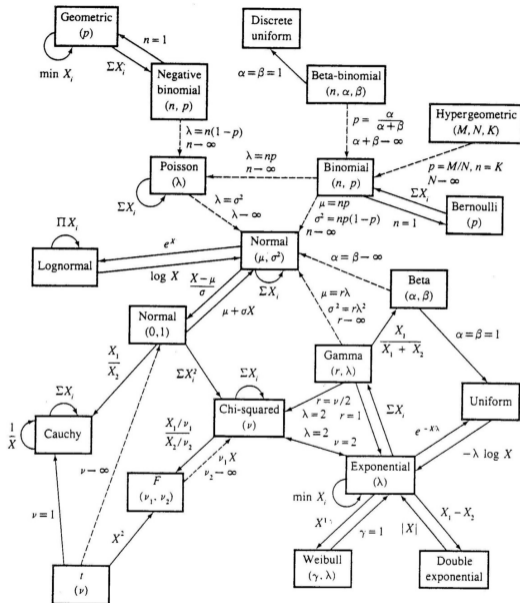
where N_i number of observations of value i , $n_i = n \cdot p(i)$ expected number of observations (rescaled), and $df = |\{i \mid N_i > 0\}| - 1$ is the number of observed values minus 1.

$\chi^2 = \infty$ if for some i : $n_i = 0$

See R script

Common distributions

- Probability distributions at Wikipedia
- Probability distributions in R
-  C. Forbes, M. Evans, N. Hastings, B. Peacock (2010) Statistical Distributions, 4th Edition Wiley



Relationships among common distributions. Solid lines represent transformations and special cases, dashed lines represent limits. Adapted from Leemis (1986).

Comparing two datasets

- Dataset x_1, \dots, x_n realization of $X_1, \dots, X_n \sim F_1$
- Dataset y_1, \dots, y_m realization of $Y_1, \dots, Y_n \sim F_2$
- $H_0 : F_1 = F_2$ $H_1 : F_1 \neq F_2$
- Continuous data: KS statistics

$$D = \sup_{a \in \mathbb{R}} |F_1(a) - F_2(a)| \sim K$$

- Discrete data: χ^2 statistics

$$\chi^2 = \sum_{R_i > 0 \vee S_i > 0} \frac{(\sqrt{\frac{m}{n}} R_i - \sqrt{\frac{n}{m}} S_i)^2}{R_i + S_i} \sim \chi^2(df)$$

where R_i (resp., S_i) is the number of observations in x_1, \dots, x_n (resp., y_1, \dots, y_m) of value i ,
 $df = |\{i \mid R_i > 0 \vee S_i > 0\}| - 1$

- Useful to detect **covariate drift** (data stability) from source to target datasets (training set vs deployment set) *[See also Lessons 16 and 35 for association measures]*

See R script

Optional references



Keegan Korthauer, Patrick K. Kimes, Claire Duvallet, Alejandro Reyes, Ayshwarya Subramanian, Mingxiang Teng, Chinmay Shukla, Eric J. Alm, and Stephanie C. Hicks (2019)

A practical guide to methods controlling false discoveries in computational biology.

Genome Biology 20, article 118



Sander Greenland, Stephen J. Senn, Kenneth J. Rothman, John B. Carlin, Charles Poole, Steven N. Goodman, and Douglas G. Altman (2016)

Statistical tests, P values, confidence intervals, and power: a guide to misinterpretations.

European Journal of Epidemiology 31, pages 337–350