Hypothesis testing

Null hypothesis H_0 and alternative hypothesis H_1 . Simple and compound hypotheses.

Simple : the probabilistic model is specified completely.

Compound : the probabilistic model is not specified completely (generally it will contain parameters to be estimated).

Example 1: we want to test whether data are compatible with the assumption that their true mean is μ_0 . Then it could be set as:

*H*₀:
$$X_1, \ldots, X_n \sim N(\mu_0, \sigma_0^2)$$
 and independent. [simple if σ^2 known];

*H*₁:
$$X_1, \ldots, X_n \sim N(\mu, \sigma_0^2)$$
 and independent, with $\mu \neq \mu_0$. [compound]

Rejection region

Example 2: we have two groups, and we wish to test whether they can be considered as samples from the same population, or from two populations with different means. General assumption:

$$X_1, \ldots, X_n \sim N(\mu_X, \sigma^2), Y_1, \ldots, Y_m \sim N(\mu_Y, \sigma^2), \text{ and independent.}$$

 $H_0: \mu_X = \mu_Y, \sigma^2 > 0.$
 $H_1: \mu_X \neq \mu_Y, \sigma^2 > 0.$

Both are compound, but H_0 is 'simpler' than H_1 .

How does a test work? We select a *rejection region* C: if data fall in C, we reject H_0 (and accept H_1); if data do not fall in C, we accept (do not reject) H_0 .

Error of first species: rejecting H_0 if H_0 is true; **Error of second species**: accepting H_0 if H_1 is true.

A smaller rejection region C decreases error of first species, but increases those of second species; a larger C vice versa.

A test of hypothesis is a region C: it will have a *level* (the risk I take of errors of 1st species) and a *power* (the probability of not making errors of 2nd species).

Level and power of a test

Level The probability of an error of 1st species, i.e. to reject H_0 when H_0 is true.

Power 1- the probability of an error of 2st species, i.e. to reject H_0 when H_0 is false.

If hypotheses were simple, level and power could be computed exactly.

In actual tests, the level can often be computed or bounded from above; the power will depend on exact parameter value.

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Ideally the level should be close to 0 and the power close to 1. But to decrease the level, we should reject H_0 less often, thus decrease the power.

Solution? Choose the level α [often 5%]. Then among all possible tests of level α (i.e. rejection regions s.t. $\mathbb{P}(X \in C | H_0) \leq \alpha$) choose the one of highest power [*uniformly most powerful test*]; this is not always possible, but it is the rationale for many well known tests.

One-sample test on the mean

Example 1: (with σ^2 unknown).

 $H_0: X_1, \ldots, X_n \sim N(\mu_0, \sigma^2)$ and independent, where $\sigma^2 > 0$.

 H_1 : $X_1, \ldots, X_n \sim N(\mu, \sigma^2)$ and independent, where $\mu \neq \mu_0, \sigma^2 > 0$. The test quantity used is $T = \frac{\bar{X} - \mu_0}{S/\sqrt{n}}$ where S^2 is the sample variance.

It is natural (and can be justified rigorously) to reject H_0 when T is far away from 0.

Under H_0 , T follows a t(n-1) distribution. Then we find t_α s.t. $\mathbb{P}(|t(n-1)| > t_\alpha) = \alpha$. Reject H_0 if $|T| > t_\alpha$, accept it otherwise.

One-sample test on the mean. II

If [unilateral alternative]

 $H_1: X_1, \ldots, X_n \sim N(\mu, \sigma^2)$ and independent, where $\mu > \mu_0, \ \sigma^2 > 0$,

then the rejection region is for T positive and large. Hence we find t'_{α} s.t. $\mathbb{P}(t(n-1) > t_{-}\alpha) = \alpha$. Reject H_0 if $T > t'_{\alpha}$, accept it otherwise. Vice versa if the alternative hypothesis is $\mu < \mu_0$.

Often programs (e.g. R) return the *p*-value = $\mathbb{P}(|t(n-1)| > T)$ (for a bilateral test), [or $\mathbb{P}(t(n-1) > T)$ against $\mu > \mu_0$]. If the *p*-value is less than the level we chose, reject H_0 ; otherwise accept.

Observations: unilateral alternatives make it easier rejecting the null hypothesis (hence they are seldom used). In practice, border-line results suggest further research.

Independent samples (e.g. 2 groups with different treatments)

$$egin{aligned} X_1,\ldots,X_n &\sim \mathcal{N}(\mu_X,\sigma^2), \ Y_1,\ldots,Y_m &\sim \mathcal{N}(\mu_Y,\sigma^2), \ ext{and independent.} \ &\mathcal{H}_0: \ \mu_X = \mu_Y, \ \sigma^2 > 0. \ &\mathcal{H}_1: \ \mu_X
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Independent samples (e.g. 2 groups with different treatments) $X_1, \ldots, X_n \sim N(\mu_X, \sigma^2), Y_1, \ldots, Y_m \sim N(\mu_Y, \sigma^2), \text{ and independent.}$ $H_0: \mu_X = \mu_Y, \sigma^2 > 0.$ $H_1: \mu_X \neq \mu_Y, \sigma^2 > 0.$ Estimate of $\sigma^2: S_{X,Y}^2 = \frac{1}{n+m-2} \left((n-1)S_X^2 + (m-1)S_Y^2 \right)$

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Under H_0 $T = \frac{\bar{Y} - \bar{X}}{s_{X,Y}\sqrt{\frac{1}{n} + \frac{1}{m}}}$ follows a t(m + n - 2) distribution.

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Assumptions: normality, independence, equality of variances (should be checked [sometimes variable transformations help]).

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Assumptions: normality, independence, equality of variances (should be checked [sometimes variable transformations help]). A modified version (Welch *t*-test) works without assuming equal variances.

Paired samples (e.g. same individuals before/after treatment)

General assumption

$$D_i = Y_i - X_i \sim N(\mu, \sigma^2), \quad i = 1 \dots n.$$

No assumption on X_i and Y_i , but only on their differences (the effect of treatment).

$$H_0: \ \mu = 0, \ \sigma^2 > 0.$$
 $H_1: \ \mu \neq 0, \ \sigma^2 > 0.$

This is simply a test that the true mean of D = Y - X is 0.

It will be easier rejecting H_0 because generally s_D is much smaller than $\sqrt{2}s_{X,Y}$.

Basic assumption: the effect of treatment is additive (does not depend on the original value of X_i).

Paires samples. An example

hot outside temperature:

Body and encephalus temperature measured on 6 ostriches kept at

Body T	encephalus T
38.51	39.32
38.45	39.21
38.27	39.20
38.52	38.68
38.62	39.09
38.18	38.94
	38.51 38.45 38.27 38.52 38.62

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	2	38.45	39.21
hot outside temperature:	3	38.27	39.20
	4	38.52	38.68
	5	38.62	39.09
	6	38.18	38.94

 $ar{X} = 38.425$ $ar{Y} = 39.073$ $S_D = 0.283$ $T = \sqrt{n} \frac{ar{Y} - ar{X}}{S_D} = 5.6099.$ p-value = $\mathbb{P}(|t(5)| > 5.6099) = 0.00249.$

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Reject $\mu_{Y-X} = 0$.

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Under H_0 , $\mathbb{P}(D_i > 0) = \mathbb{P}(D_i < 0) = \frac{1}{2}$. Count number of positive n_+ and negative n_- observations: if they are far from $\frac{n}{2}$, reject H_0 .

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-value = 3.125%.

Sign test is very robust, but not very powerful (*rejecting* H_0 is difficult).

There exist intermediate tests such as Wilcoxon's test, that use not only signs, but also **ranks** of observations.

Chi-square test

General chi-square test:

We have k types of events that can occur in each trial, with a priori probabilities for them

$$p_1^0,\ldots,p_k^0$$
 with $p_1^0+\cdots+p_k^0=1.$

After n trials, we observe

 n_1 events of type 1, n_2 of 2,..., n_k of k, with $n_1 + \cdots + n_k = n$.

Are data compatible with expectations? (k = 2 is binomial)

Classical test: **chi-square**: Set $E_i = np_i^0$ (expected number of events of type *i* under H_0),

$$X^2 = \sum_{i=1}^k \frac{(n_i - E_i)^2}{E_i} \sim \chi^2(k-1)$$
 for *n* large.

Find c_{α} s.t. $\mathbb{P}(\chi^2(k-1) > c_{\alpha}) = \alpha$. If $X^2 > c_{\alpha}$, reject H_0 ; accept it otherwise.

Chi-square for data fit to a distribution

The values p_1^0, \ldots, p_k^0 can be those arising from some distribution. Often the distribution will contain parameters to be estimated (e.g. λ of Poisson).

One can use the chi-square: if *m* parameters are estimated, $X^2 \sim \chi^2(k - m - 1)$ (of course m < k - 1). Example: data (Von Bortkiewicz, 1898) on Prussians soldiers kicked to death by horses:

i (deaths)	<i>n_i</i> (number of corps/years)
0	109
1	65
2	22
3	3
4	1
Total	200

Chi-square example (continued)

Estimate λ with the sample mean $\hat{\lambda} = (1 \cdot 65 + 2 \cdot 22 + 3 \cdot 3 + 4 \cdot 1)/200 = 0.61$. Compute E_i . Join the classes ≥ 3 (rule of thumb: $E_i \geq 5$) to obtain:

i	ni	Êi
0	109	108.67
1	65	66.29
2	22	20.22
\geq 3	4	4.82
Total	200	

Compute $X^2 \approx 0.32$. *p*-value = $\mathbb{P}(\chi^2(2) > 0.32) = 85.2\%$.

A classical use of chi-square is when we observe two qualitative variables X and Y.

 H_0 : variables are independent; H_1 : they are not independent. X: k levels, Y: l levels (if k = l = 2, a 2 × 2 contingency table). Data: n_{ij} (# of observ. with X = i and Y = j).

Chi-square test of independence

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 H_0 : variables are independent; H_1 : they are not independent. X: k levels, Y: l levels (if k = l = 2, a 2 × 2 contingency table). Data: n_{ij} (# of observ. with X = i and Y = j). H_0 : $\mathbb{P}(X = i, Y = j) = p_i q_i$ for all i and j

 $p_i, i = 1 \dots k - 1, q_j, j = 1 \dots l - 1$ to be estimated from data.

$$H_1: \mathbb{P}(X=i, Y=j) \neq p_i q_j.$$

Computations in test of independence

Row totals:
$$n_{i\bullet} = \sum_{j=1}^{l} n_{ij}$$

column totals: $n_{\bullet j} = \sum_{i=1}^{k} n_{ij}$
grand total: $n_{\bullet \bullet} = \sum_{i=1}^{k} n_{i\bullet} = \sum_{j=1}^{l} n_{\bullet j}$.

$$\hat{E}_{ij} = \frac{n_{i\bullet}n_{\bullet j}}{n_{\bullet\bullet}}$$
 so that $X^2 = \sum_{i,j} \frac{(n_{ij} - \hat{E}_{ij})^2}{\hat{E}_{ij}}$

This to be compared with $\chi^2(k \cdot l - k - l + 1) = \chi^2((k-1)(l-1)).$

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Chi-square is only an approximation. One can perform exact tests based on binomial (Fisher's test)

Example of test of independence

In a (hypotethical) study a set of individuals was treated with an antiviral or a placebo, and then experimentally infected with a mild strain of influenza. From following analyses, individuals were classified as "No virus", "Virus but no symptoms", "severe infections" obtaining the table:

	NV	VNS	SI	Total
Antiviral	8	21	4	33
Placebo	6	14	12	32
Total	14	35	16	65

Example: computations

VNS SI Total NV
 8
 21
 4
 33

 6
 14
 12
 32
 14 35 16 65 $\frac{33\cdot14}{65} = 7.1$ $\frac{33\cdot35}{65} = 17.8$ $\frac{33\cdot16}{65} = 8.1$ Expected values: $\frac{32.14}{65} = 6.9$ $\frac{32.35}{65} = 17.2$ $\frac{32.16}{65} = 7.9$ $X^{2} = \frac{(8-7.1)^{2}}{7.1} + \frac{(21-17.8)^{2}}{17.8} + \frac{(4-8.1)^{2}}{8.1} + \frac{(6-6.9)^{2}}{6.9}$ $+\frac{(14-17.2)^2}{17.2}+\frac{(12-7.9)^2}{7.0}=5.605.$

p-value = $\mathbb{P}(\chi^2(2) > 5.605) = 6.1\%$. We cannot reject independence, though it is a borderline case. Comparison of means of multiple groups

When we have many (more than 2) groups, we may think to perform *t*-tests for $\mu_1 = \mu_2$, then $\mu_1 = \mu_3$, then $\mu_2 = \mu_3 \dots$

Comparison of means of multiple groups

When we have many (more than 2) groups, we may think to perform *t*-tests for $\mu_1 = \mu_2$, then $\mu_1 = \mu_3$, then $\mu_2 = \mu_3 \dots$ Why is this not appropriate? not optimal? When we have many (more than 2) groups, we may think to perform *t*-tests for $\mu_1 = \mu_2$, then $\mu_1 = \mu_3$, then $\mu_2 = \mu_3 \dots$ Why is this not appropriate? not optimal? If we perform many tests, we need to correct probability levels. If we perform 20 tests, each with 5% probability of being positive, we suspect some may become positive just for chance... When we have many (more than 2) groups, we may think to perform *t*-tests for $\mu_1 = \mu_2$, then $\mu_1 = \mu_3$, then $\mu_2 = \mu_3 \dots$ Why is this not appropriate? not optimal? If we perform many tests, we need to correct probability levels. If we perform 20 tests, each with 5% probability of being positive, we suspect some may become positive just for chance... Tests are not independent... When we have many (more than 2) groups, we may think to perform *t*-tests for $\mu_1 = \mu_2$, then $\mu_1 = \mu_3$, then $\mu_2 = \mu_3 \dots$ Why is this not appropriate? not optimal? If we perform many tests, we need to correct probability levels. If we perform 20 tests, each with 5% probability of being positive, we suspect some may become positive just for chance... Tests are not independent...

Proper way to correcting for this: analysis of variance.