2-sample t-test

 $\bar{y} = \frac{1}{n} \sum_{i=1}^{n} y_i$ Estimates the population mean μ . $S^2 = \frac{1}{n-1} \sum_{i=1}^{n} (y_i - \bar{y})^2$ Estimates the variance σ^2 . The Hypothesis test is: H_0 : $\mu_1 = \mu_2$; H_a : $\mu_1 \neq \mu_2$, or < (left-tailed) or > (right-tailed).

Known Variances use the z test; $Z=(\bar{y}_1-\bar{y}_2)/\sqrt{\frac{\sigma_1^2}{n_1}+\frac{\sigma_2^2}{n_2}}$ (two population means), or $Z=(\bar{y}-\mu_0)/\frac{\sigma}{\sqrt{n}}$ (one). $100(1-\alpha\%)$ C.I. for $\mu_1-\mu_2$: $(\bar{y}_1-\bar{y}_2)\pm Z_{\alpha/2}\sqrt{\frac{\sigma_1^2}{n_1}+\frac{\sigma_2^2}{n_2}}$. C.R. where H_a : $\neq \implies Z_{\alpha/2}$. $<\implies Z_{\alpha}$. $>\implies Z_{\alpha}$

Unknown Variances $(\sigma_1^2 = \sigma_2^2)$ $t = (\bar{y}_1 - \bar{y}_2)/S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}, d.f = v = n_1 + n_2 - 2.$ $S_p^2 = \frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{n_1 + n_2 - 2}$ $(S_p = \sqrt{S_p^2})$ $100(1 - \alpha)\%$ C.I. for $\mu_1 - \mu_2$: $(\bar{y}_1 - \bar{y}_2) \pm t_{\alpha/2,v} S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$ (two means), or $\bar{y} \pm t_{\alpha,n-1} \frac{\sigma}{\sqrt{n}}$ (one mean).

Unknown Variances $(\sigma_1^2 \neq \sigma_2^2)$ $t = (\bar{y}_1 - \bar{y}_2) / \sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}, d.f = v = \frac{((S_1^2/n_1) + (S_2^2/n_2))^2}{\frac{(S_1^2/n_1)^2}{n_1 - 1} + \frac{(S_2^2/n_2)^2}{n_2 - 1}}.$ (round down v to the nearest int.) C.R. where H_a : $\neq \implies t_{\alpha/2,v}$. H_a : $< \implies -t_{\alpha,v}$. H_a : $> \implies t_{\alpha,v}$

Tests on Variances The Hypothesis test is: H_0 : $\sigma_1^2 = \sigma_2^2$; H_a : $\sigma_1^2 \neq \sigma_2^2$, or < (left-tailed) or > (right-tailed). two-tailed(\neq): $F = \frac{S_1^2}{S_2^2} > F_{\alpha/2,n_1-1,n_2-1}$, left-tail(<): $F = \frac{S_2^2}{S_1^2} > F_{\alpha,n_2-1,n_1-1}$, right-tail (>): $F = \frac{S_1^2}{S_2^2} > F_{\alpha,n_1-1,n_2-1}$.

Paired t-test (2 measurements From Each Exp Unit)

Advantage: less variability than a design with 2 separate samples, test is more sensitive, ie more powerful. Hypothesis: H_0 : $\mu_{\delta} = 0$. H_a : $\mu_{\delta} \neq 0$. Where $\mu_{\delta} = \mu_2 - \mu_1$ (before - after). Test statistic: $t = \frac{\bar{d}}{S_d/\sqrt{n}}$ Where $\bar{d} = \frac{1}{n} \sum_{j=1}^n d_j$ is the sample mean. And $S_d^2 = \frac{1}{n-1} \sum_{j=1}^n (d_j - \bar{d})^2$. (note: use $S_d = \sqrt{S_d^2}$) Reject H_0 if $|t| > t_{\alpha/2, n-1}$.

ANOVA

The overall mean μ is $\frac{1}{a}\sum_{i=1}^{a}\mu_{i}$. Note that $\sum_{i=1}^{a}\tau_{i}=0$. LS estimates: $\hat{\mu}=\bar{y}_{..}, \hat{\mu}_{i}=\bar{y}_{i}, \hat{\tau}=\bar{y}_{i}, -\bar{y}_{..}$, to estimate common population variances σ^{2} , use $S_{p}^{2}=\frac{\sum_{i=1}^{a}(n_{i}-1)s_{i}^{2}}{\sum_{i=1}^{a}(n_{i}-1)}$

Anova Table (One-way Layout)

Source	df	SS	MS	F	Note: N is the total number of observations,
Treatments	a-1	SSTr	$MSTr = \frac{SSTr}{a-1}$	$F = \frac{MSTr}{MSE}$	Pooled sample variance $S_p^2 = \frac{SSE}{N-g} = MSE$.
Error	N-a	SSE	$MSE = \frac{\widetilde{SSE}}{N-a}$		Reject H_0 if $F > F_{\alpha,a-1,N-a}$, or p-value $< \alpha$.
Total	N-1	SST			

Hypotheses: H_0 : $\mu_1=\mu_2=\cdots=\mu_a$. H_a : Not all μ_i are equal. Or H_0 : $\tau_1=\tau_2=\cdots=\tau_a=0$. H_a : Not all $\tau_i=0$.

$$100(1-\alpha)\%$$
 C.I. for μ_i : $\bar{y}_{i.} \pm t_{\alpha/2,N-a} \sqrt{\frac{MSE}{n}}$

To check model assumptions use a normal probability plot and normality test (Anderson-Darling or some other), and a plot of residuals vs. predicted value (residual plot). The residuals should look like they are from a normal distribution if the model assumptions were met. If the model assumptions were met, the residual plot should look like a random scatter. if the plot shows a 'funnel' shape, this is an indication of non-constant variance (heteroscedasticity). The remedy is typically a transformation of the response.

Normal Probability Plot

To estimate the standard deviation σ , note that the slope $\approx \frac{1}{\sigma}$, only with z-score. Or you can estimate the distance from 16% to 50% as one standard deviation. To estimate the mean μ look at the 50th percentile. Hypotheses: H_0 : The data are drawn from a normal distribution. Large p-value means normal.

Standard to Percentile:
 $\frac{\text{Standard Deviations}}{\text{Percentile}}$ $\frac{-2}{2.27\%}$ $\frac{-1}{1.88\%}$ $\frac{0}{50\%}$ $\frac{1}{84.23\%}$ $\frac{2}{97.72\%}$

Note that Φ (standard deviation) = percentile, and Φ^{-1} (percentile) = standard deviation.

Contrasts

 $\Gamma = \sum_{i=1}^{a} c_i \mu_i$, where c_i 's are constants such that $\sum_{i=1}^{a} c_i = 0$. To estimate Γ use $\hat{\Gamma} = \sum_{i=1}^{a} c_i \bar{y}_i$. Hypotheses: H_0 : $\sum_{i=1}^{a} c_i \mu_i = 0$. H_a : $\sum_{i=1}^{a} c_i \mu_i \neq 0$. (or < or >).

Test statistic: $t = (\sum_{i=1}^{a} c_i \bar{y}_{i\cdot})/(\sqrt{\frac{MSE}{n}} \sum_{i=1}^{a} c_i^2)$. Reject H_0 if t in C.R. of $t_{\alpha,N-a}$ (or $\alpha/2$ for 2-tail) or if p-value $< \alpha$. Note: $F = (\sum_{i=1}^{a} c_i \bar{y}_{i\cdot})^2/(\frac{MSE}{n} \sum_{i=1}^{a} c_i^2)$ can be used to test 2-tailed. Reject H_0 if $F > F_{\alpha,1,N-a}$ or if p-value $< \alpha$.

Pairwise comparisons

Note: LSD is most powerful, but worst at guarding against Type I errors. Tukey's is most balanced for equal sample sizes. And Bonferroni's is least likely to make a Type I error.

Fishers LSD For every pair of treatments test the hypothesis at α . H_0 : $\mu_i = \mu_j$. H_a : $\mu_i \neq \mu_j$.

Test statistic $t = |\bar{y}_{i\cdot} - \bar{y}_{j\cdot}| / \sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}$. Reject H_0 is $|t| > t_{\alpha/2, N-a}$.

Therefore, The two treatment means are significantly different if $|\bar{y}_{i\cdot} - \bar{y}_{j\cdot}| > t_{\alpha/2,N-a} \sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}$.

Bonferroni's Method Denote the FWE by α . Identical to Fisher's LSD except that

$$|\bar{y}_{i\cdot} - \bar{y}_{j\cdot}| > t_{\alpha/2k,N-a} \sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}$$
. Where $k = \binom{a}{2}$.

(4)

Tukey's Method Means are significantly different at $FWE\alpha$ when: $|\bar{y}_{i\cdot} - \bar{y}_{j\cdot}| > q_{\alpha,a,N-a} \sqrt{\frac{MSE}{2} \left(\frac{1}{n_i} + \frac{1}{n_j}\right)}$.

 $100(1-\alpha)\%$ Simultaneous C.I's for all possible treatment differences $\mu_i - \mu_j$ using Tukeys Method:

$$\bar{y}_{i\cdot} - \bar{y}_{j\cdot} \pm q_{\alpha,a,N-a} \sqrt{\frac{MSE}{2} \left(\frac{1}{n_i} + \frac{1}{n_j}\right)}$$

Graphical results Note that a line under the treatments indicates that they are not significantly different.

 $(2) \qquad \qquad (1)$

 $(3) \qquad \qquad (5)$

Treatments should be ordered from the smallest sample mean to the largest sample mean. This graph indicates that treatment 2 and 1 are not significantly different, and 4 and 3, and 5 are not significantly different.

Test of Equality of Variances

Hypothesis: H_0 : $\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_a^2$. H_a : at least one σ_i^2 is different.

Bartlett's test (use if data is normal) assumes normality for each treatment. Very sensitive to non-normality.

Modified Levene's test (use if data \approx normal) robust for non-normality. For data from a normal dist, not as powerful as Bartlett's.

Confidence Interval Derivation

Note that $\frac{\bar{d}-\delta}{S_d/\sqrt{n}} \sim t(n-1)$ implies $1-\alpha = P\left(-t_{\alpha/2,n-1} \le \frac{\bar{d}-\delta}{S_d/\sqrt{n}} \le t_{\alpha/2,n-1}\right)$ Which simplifies to $\bar{d} \pm t_{\alpha/2,n-1} \frac{S_d}{\sqrt{n}}$.

Conclusions

Rejection Methods Reject H_0 if p-value $\leq \alpha$. Reject H_0 if the test statistic falls within the critical region.

 $100(1-\alpha)\%$ C.I. "We are $100(1-\alpha)\%$ confident that the true {test} is between {upper bound} and {lower bound}."

Reject H_0 "There is enough statistical evidence to support (the statement of H_a)."

Fail to reject H_0 "There is not enough statistical evidence to support (the statement of H_a)." or "The evidence from the data is consistent with (the statement of H_0)"

Type I Error, α , is the mistake of rejecting the null hypothesis when it is true.

Type II Error, β , is the mistake of failing to reject the null hypothesis when it is false.