

point estimate: single number that is our best guess for the population	(1 - alpha)100% CI with length <= D, n >= (2 * t(n-1, 1-alpha/2) * s / D)^2	shapiro-wilk test: when p-value is small, it does not follow a normal distribution
parameter	Hypothesis testing: using probability to quantify how plausible a value for a parameter is	response variable OR dependent variable OR target variable OR output variable
<ul> <li>it varies from sample to sample as we are not taking the mean of the</li> </ul>	hypothesis: statement about a population, claiming that a parameter takes a particular value or	explanatory OR regressor OR independent OR predictor OR input OR covariate
population and we are taking a random sample each time.	falls in a certain range of data.	regression: mathematical relationship between the mean of Y and the different values of X
<ul> <li>it does not provide an idea about how close it is to the true value.</li> </ul>	step 1: assumptions	linear regression: the relationship is linear, Y = B0 + B1*X + E
<ul> <li>p_hat is a point estimate for p</li> </ul>	- data must come from randomisation	assumption of a simple linear regression model, Y ~ X
<ul> <li>X_bar is the point estimate for mu (mean)</li> </ul>	- sample size must be large enough or shape of the population distribution is symmetric.	- data obtained by randomization
<ul> <li>S^2 is the point estimate for Var(X)</li> </ul>	step 2: stating hypotheses	- relationship between X and Y is linear
<ul> <li>S is the point estimate for standard deviation</li> </ul>	null hypothesis: statement that the parameter takes a particular value	<ul> <li>error term, E, ~N(0, sigma^2) and sigma^2 is a constant</li> </ul>
<ul> <li>X(0.5) is the point estimate for q0.5(50th percentile)</li> </ul>	alternative hypothesis: statement that the parameter falls in some alternative range of values.	these assumptions implies that for any X value, Y ~ N(B0 + B1*X, sigma^2), hence
interval estimate: an interval of numbers which the parameter value is	- H0 usually represents no effect and H1 represents effect of some type.	variance is always the same and mean of Y is (B0 + B1*X)
believed to fall	- right sided test: H1 parameter is larger than the value in H0	the fitted regression line gives Y_hat and it is the point estimate for the mean of Y
- indicates precision by giving an interval of numbers around the point	- left sided test: H1 parameter is smaller than the value in H0	interpolation: estimating the mean response for an X value that had not been observed,
estimate	- two sided test: H1 parameter is not equal to the value in H0	but it is within the range of observed values
- made up of numbers that are the most believable values for the	step 3: test statistic (describes how far the point estimate falls from the value in H0)	extrapolation: estimating the mean response for an X value that is outside the range.
unknown parameter, based on the data observed.	- we need the value of point estimate from the sample and its sampling distribution	sigma^2 gives us the idea of the variability of the response values around the fitted line
confidence interval: interval containing the most believable values for a parameter.	- parameter value specified under H0. step 4: p-value (probability that the test statistic receives the value as observed for more	smaller variance, closer to the fitted line
confidence level: the probability that this method produces an interval that	extreme, given that H0 is true)	in simple linear model, the F-test is equivalent to the t-test
contains the parameter.	- when it is small, either H0 is rejected or sample is not representative of the population	t-test tests for the significance of the coefficients of the regressor terms.
- point estimate +- margin of error	- small p-value provides strong evidence against H0.	- H0: regressor is not significant, H1: regressor is significant - t = B1 hat / SE(B1 hat)
margin of error: measures how accurately the point estimate is likely to be	- small p-value provides strong evidence against no two sided test: p-value is left and right tail probabilities	- t = B1_nat / SE(B1_nat) - for a simple linear model, the null distribution of t is t(n-2)
in estimating a parameter, it is a multiple of the standard deviation.	- right sided test: p-value is the area on the right side of the test statistic	F-test: tests for the significance of the whole model
- for sample proportion: sqrt(p*(1-p)/n)	- left sided test: p-value is the area on the left of the test statistic	- H0: model is not significant, OR H0: all coefficients except intercept are zero,
for population proportion, p hat ~ N(p, p*(1-p)/n)	step 5: conclusion: if p-value <= alpha, we reject H0 as we have strong evidence against H0.	- H1: model is significant OR at least one coefficient except intercept is non-zero
- n*p hat*(1-p hat) must >= 5	for proportions, variable measured is categorical	- if we do not reject the H0, Y = B0 + E, Y hat = B0 hat, Y does not depend on any
- 95%: p hat +- 1.96 * sqrt(p hat*(1-p hat)/n)	- distribution assumption fulfilled when n*p0*(1 - p0) >= 5, p0 is value in H0.	checking for assumptions
- 99%: p_hat +- 2.58 * sqrt(p_hat*(1-p_hat)/n)	- H1: p > p0 OR p < p0 OR p!= p0	- normality and constant variance: checked using residuals of built model
- 80%: p_hat +- 1.28 * sqrt(p_hat*(1-p_hat)/n)	$-Z = (p \text{ hat } - p0) / \text{sgrt}(p0 * (1 - p0) / n) \sim N(0, 1)$	- linearity: checked using scatter plot between response and regressor
- 100%: [0, 1] can have this without any sample, a lower CI can	for means, variable measures is quantitative	- randomisation: checked in the steps of data collection
significantly narrow down the range of values for the parameter.	- normal assumption is crucial when n is small	if linearity assumption is violated, can add higher order terms in X like X^2 to the model
% that the proportion of in the population falls in (,)	- H1: mu > mu0 OR mu < mu0 OR mu != mu0	if variance is not constant, can transform the response like ln(Y), sqrt(Y) and 1/Y
confidence: refers to a long-run interpretation, describes how well the	- T = (X_bar - mu0) / (s / sqrt(n)), follows t-distribution with (n-1) degrees of freedom.	standardised residuals: Y - Y_hat / SE of (Y - Y_hat)
method performs over many different random samples	type I error: occurs when we reject H0 when it is in fact true. denoted by alpha	plot of SR against Y_hat or X: points scatter randomly about 0, within (-3, 3)
- if we form many 95% CI for p, then in the long run, 95% of these	type II error: occurs when we do not reject H0 when it is in fact false. denoted by beta	<ul> <li>funnel shape means the constant variance assumption is violated.</li> </ul>
intervals will contain the true p	power of the test: probability of correctly rejecting H0 when it is in fact false. denoted by 1-beta	histogram and QQ plot of SR: normally distributed
error probability: 1 - CI probability that it does not contain the true value.	two independent samples	- non-normal means normality assumption violated
<ul> <li>we can increase the CI but the interval will become wider.</li> </ul>	- in an experimental study, study units are assigned randomly to different treatments	when sample size n is large, expect SR to show randomness
factors affecting the length of CI	- in an observational study, we draw a random sample from the population, and then observe	linear scatter plot of Y against X
- sample size: larger n, smaller interval	variables. OR we draw a random sample from a population and then a sample from another	- curved band means the linearity assumption is violated
- CI: higher the CI, smaller alpha, wider interval	population to observe the variable of interest.	outliers have SR greater than 3 or less than -3
- the true value of p in the underlying population (cannot change)	two dependent samples: when we have two samples comprises the same set of subjects	influential points: one that affect the parameter greatly and can test with Cook's distance
- variance (sigma^2) of the population distribution (cannot change)	- arise when the measurements are taken from the same set of subjects before and after a	- if cooks distance > 1, which is the effect of deleting the point, it is an influential point
(1 - alpha)100% CI with length <= D, n >= (2 * q1-alpha/2 / D)^2 * p(1-p) - if p is unknown, use p = 0.5 and it gives largest possible margin of error	treatment to see how effective the treatment is	- not all outliers are influential points
<ul> <li>if p is unknown, use p = 0.5 and it gives largest possible margin of error</li> <li>will give us the smallest possible n we need for the sample.</li> </ul>	equal variance test: var.test(x, y) and it is not equal if the p-value is small independent sample with equal variances	R^2: proportion of total variation of the response that is explained by the model
for population mean, X bar ~ N(mean, sigma^2/n)	- quantitative response variable for both groups and the samples are independent.	- takes on values between 0 and 1
- sample must be obtained by randomisation	- quantitative response variable for both groups and the samples are independent.  - population distribution of each group is approximately normal and it is crucial when n is small	- if there are repeated values of X with different Y values, it can never be 1 - in a simple model, one regressor, R =  Cor(x, y)
- distribution of data should be approximately normal or symmetric	- variances are equal	- in a simple model, one regressor, $R =  Cor(x, y) $ - used to comment on the goodness of fit of the model
- (X bar - mean) / (s / sgrt(n)) ~ t(n - 1) t-distribution with df of n - 1	- S^2p = ((n1 - 1)*S^2x + (n2 - 1)*S^2y) / (n1 + n2 - 2)	adjusted R^2: measure of fit
- 95%: X bar +- t(n-1, 0.975)* s/sgrt(n)	$-T = (X \text{ bar} - Y \text{ bar}) / \text{Sp*sgrt}(1/n1 + 1/n2) \sim t(n1 + n2 - 2)$	- use this to compare multiple linear regression models
t-distribution is also symmetric about 0, just like N(0, 1)	independent samples with unequal variances	- 1 - (1 - R^2)*(n - 1) / (n - k - 1), k is the number of regressors
- probabilities under this depends on the degrees of freedom	- variances are unequal	indicator variables: categorical variables in the model
- has thicker tails and more variability than N(0,1)	$-T = (X \text{ bar - } Y \text{ bar}) / \text{sqrt}(S^2x/n1 + S^2y/n2)$	- I(Xn = 1) include into the model only if the Xn variable is 1
- the larger the value of df, the closer it is to N(0,1)	dependent samples	Interaction term: interaction between the two variables
- when df is 30 or more, it is nearly identical to N(0, 1)	- get the set of n differences, D1,, Dn and treat it as one-sample data, H0: mu = 0	- add Xi * Xj into the model
robust: when respect to a particular assumption if it performs adequately	Normality assumption to check if the population distribution is approximately Normal	
even when that assumption is modestly violated.	- checked using the sample distribution using histogram gg plots or shapiro-wilk test	
- randomisation assumption: not robust	gg plot	
- data distribution assumption: is robust	- might tail below straight line or left tail above straight line: longer than normal	
- sample size is large enough, we only need to ensure no extreme outlier	- right tail above the straight line or left tail below the straight line: shorter than normal	