Into the roots

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General principles

About learning and teaching

> *Bene ascolta chi la nota.*
>
> *("He listens well who takes notes.")*
>
> — *Dante Inferno. 15:99*

> *"The time has come," the Walrus said,*
>
> *"To talk of many things:*
>
> — *Lewis Carroll*
> *Through the Looking-Glass and What Alice Found There*

The nature of truth: Statistics

The scientist’s dilemma

Science believes in generalising the special, to make general rules that apply to everybody, from a *limited* number of observations. This is the only way research is done, because it is not humanly possible to examine every human on this planet to verify if he has a set of femurs. When Vesalius cut up his very first corpse, he *instantly* made the decision that the human *species*, not just the specimen on his table, but the *entirety* of the human species, must have two femurs. Herein lies the scientist’s dilemma. A *formal proof*, as iterated in pure mathematics, should not be based on induction (that is, no one specimen should be held representative of whole of the population). A proof must establish, by rigorous mathematical procedures, an identity between two sides of an equation. This kind of reasoning, however smart it may sound, is absurd in most kinds of research except pure mathematics. For the more mundane kind of research, we can not examine whole populations and we have to deal with samples. A few questions immediately spring up

- what should be the sample size to make a reasonable conclusion (i.e. can I make a statement "every human has two femurs" by examining only one corpse, or do I need more samples)
- what should be the benchmark of 'statistical significance' (i.e. how can I decide if between two events, one is being caused by another, or if its just by chance - there is no real relationship between them)
- what will be the amount of error (how valid will be our research) when we deviate from the mathematical 'formal proof' method (i.e. by doing research on samples)
- how much will the reserach be biased by a distorted sample (i.e. a study done on shoe size on a sample of acromegalics)

Statistics is the answer to these questions.

Measurements

By definition, any set of rules for assigning numbers to attributes of objects is *measurement*. Not all measurement techniques are equally useful in dealing with the world, however, and it is the function of the scientist to select those that are more useful. The physical and biological scientists generally have well-established, standardized, systems of measurement, unlike social scientists.

The issue of measurements were discussed in great detail by S.S.Stevens in an article in 1951.

Properties of measurement scales

Magnitude

The property of *magnitude* exists when an object that has more of the attribute than another object, is assigend a larger number by the rule system, i.e. if A is heavier than B then weight of A is more than weight of B.

Intervals

The property of intervals is concerned with the relationship of differences between objects. If a measurement system possesses the property of intervals it means that the unit of measurement means the same thing throughout the scale of numbers. That is, an inch is an inch is an inch, no matter were it falls - immediately ahead or a mile down the road.

Rational Zero

A measurement system possesses a rational zero if an object that has none of the attribute in question is assigned the number zero by the system of rules. The object does not need to really exist in the "real world", as it is somewhat difficult to visualize a "man with no height". The requirement for a rational zero is this: if objects with none of the attribute did exist would they be given the value zero.

Scale types

In the same article in which he proposed the properties of measurement systems, S. S. Stevens (1951) proposed four scale types. These scale types were Nominal, Ordinal, Interval, and Ratio, and each possessed different properties of measurement systems.

Nominal Scales

Nominal scales are measurement systems that possess none of the three properties discussed earlier. Nominal renaming scales apply random numbers (or words) to objects (i.e. social security numbers, classification of diseases). Nominal categorical scales apply a different number to each category of objects (i.e. Belgians = 1, Indians = 2, Irish = 3).

Ordinal Scales

Ordinal Scales are measurement systems that possess the property of magnitude, but not the property of intervals. The property of rational zero is not important if the property of intervals is not satisfied. Any time ordering, ranking, or rank ordering is involved, the possibility of an ordinal scale should be examined. As with a nominal scale, computation of most of the statistics described in the rest of the book is not appropriate when the scale type is ordinal. Rank ordering people in a classroom according to height and assigning the shortest person the number "1", the next shortest person the number "2", etc. is an example of an ordinal scale.

Interval Scales

Interval scales are measurement systems that possess the properties of magnitude and intervals, but not the property of rational zero (i.e. the height of a person). It is appropriate to compute the statistics described in the rest of the book when the scale type is interval.

NOTE

Quantiles: How to remove the property of intervals

Arranging lists according to centiles (i.e. `X belongs to 91st centile' means that 91% of values fall below X) or quartiles (the list divided in four quarters) or deciles (ten parts) removes the inteval property, and converts an interval scale to an ordinal scale.

Ratio Scales

Ratio scales are measurement systems that possess all three properties: magnitude, intervals, and rational zero. The added power of a rational zero allows ratios of numbers to be meaningfully interpreted; i.e. the ratio of John’s height to Mary’s height is 1.32, whereas this is not possible with interval scales.

Descriptive statistics

Data are the figures you derive directly from the source. Primary data is obtained directly from the population (as in census), and secondary data from a record. Obviously, primary data is always more reliable than secondary.

Data has two parts, i.e. a variable (like age, gender, income, number of spouses etc. - denoted by x) and a value (i.e. 40 years, male, Rs. 3500, 3).

A *variable* may be qualitative (Boolean data, subjective data) or quantitative (numbers). Quantitative data may be further classified as *continuous* (i.e. height, weight - which may have any value) or *discrete* (size of shoes - which can have only a fixed set of values).

Universe is the extent of a statistical survey being undertaken, also called the population. The numerical size of the population is denoted by η. Subgroups in this universe are called samples.

An *event* is just that, an event that has or will occur.

Representation of data: Frequency distribution

This special variety of tables describe frequency of an event within *class intervals* of a universe. Mind that the class intervals (the domains) do not overlap and are of equal width.

Table 1. Frequency distribution table of shoe size in a class

Number of students	Shoe size
7	7
8	7.5
8	8
7	8.5
10	9
6	9.5
5	10
2	10.5

A *histogram* is the representation of an frequency distribution table, so the bars are adjacent (to emphasize the discrete nature of the variable being measured, in this case, shoe size, which can be any value between 7-11). By adding the midpoint of top of these bars – you can get a *frequency polygon*.

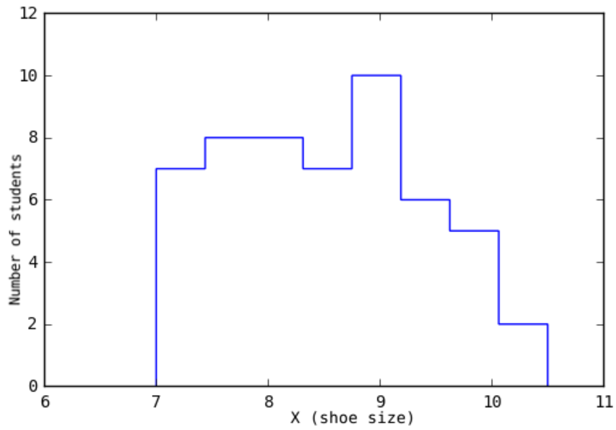


Figure 1. A histogram showing distribution of shoe sizes in a sample of students

Central tendency

1. The **mean** is the arithmetic average, denoted by an X̄ (for a sample) or μ (for the whole population). It is not, however, a very good indicator of the actual distribution of the variable. Suppose you admit a dinosaur (or any fellow with really big feet) in your class, then the mean shoe size will be dramatically altered even though only one member has been added. Mean is affected severly by the values at the end.
2. The **median** is the midpoint value of a distribution arranged in ascending order, or the average of two midpoint values (if number of data is even). The median is not affected by terminal values.
3. The **mode** is the most commonly occurring value in a distribution.

Dispersion

Range

The set of values X can take.

Mean deviation

A particular value x of a variable is said to be deviating from the mean X̄ by an amount x-X̄. This is the deviation of x from mean. The mean deviation is the average of all such deviations. In a population of size η

$$d = \frac{\sum |X - \mu|}{\eta}$$

The mean deviation gives an idea on how widely the data varies. Mind the absolute value sign '|' around the deviations. If we do not ignore the sign of deviations, positive and negative variations tend to cancel each other out.

Variance

For an entire population, variance

$$\sigma^2 = \frac{\sum \left(X - \overline{X}\right)^2}{\eta}$$

For any *sample* of size n , the variance $s^2 \_ n$ is

$$s_n^2 = \frac{\sum \left(X - \overline{X}\right)^2}{n}$$

If the mean of the *population* is unknown, then we must use Bessel’s correction (why? see later).

$$s^2 = \frac{\sum \left(X - \overline{X}\right)^2}{n-1}$$

The variance of a sample shows how widely it is distributed. Suppose, in two different classes, the mean show size is same. In this case, the class with the more variance has a more varying set of students (i.e. there are more number of students who have a very small or very large shoe size) than the class with less variance. Variance is only a number, and its unit is the square of the unit of the thing we want to measure.

Standard deviation

This is important. Standard deviation is the positive square root of variance.

$$\sigma = \sqrt{\frac{\sum \left(X - \mu\right)^2}{\eta}}$$

when dealing with the whole population, or

$$s_n = \sqrt{\frac{\sum \left(X - \overline{X}\right)^2}{n}}$$

when in a sample. If the mean of the population is unknown, Bessel’s correction must be applied

$$s = \sqrt{\frac{\sum \left(X - \overline{X}\right)^2}{n-1}}$$

Properties of standard deviation

For constant c and random variable X,

- $\sigma(X + c) = \sigma(X)$; the SD is not changed if each value is incremented by same amount
- $\sigma(cX) = |c| \times \sigma(X)$; i.e. if each value of a population gets multiplied, the SD is also multiplied

Importance of standard deviation

The standard deviation serves as the 'unit' of variability. We speak 'the shoe size of this student is 3 standard deviations more than the mean, i.e. the shoe size is mean + 3 × standard deviation = 7.818 + 3 × 1.266 = 11.616

Example 1. An example: Finding the mean and SD of a population

Say the shoe sizes in a class of 101 are distributed as follows.

Number of students	Shoe size (X)
5	5.5
6	6
9	6.5
13	7
17	7.5
13	8
13	8.5
10	9
8	9
5	10
2	10.5

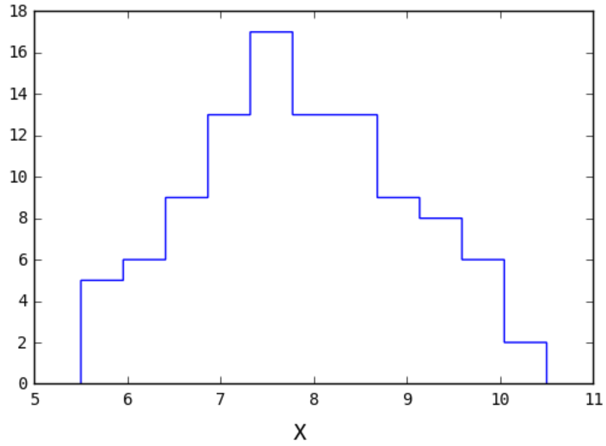


Figure 2. Histogram of the shoe sizes in this class

In this population

- size of population N = 101
- **mean** of the population μ = 7.85
- **variance** of the population $\frac{(X-\mu)^2}{\eta}$ = 1.41
- **standard deviation** σ = $\sqrt{variance}$ = 1.19

NOTE

What is this degree of freedom thing? A fine example from David Lane,

Some estimates are better than others. An estimate based on 100 samples is better than that based on of 5. The **degrees of freedom (df)** of an estimate is the number of *independent* pieces of information that has gone into it.

As an example, let's say that we know that the mean height of Martians is 6 and wish to estimate the variance of their heights. We randomly sample one Martian and find that its height is 8. so variance $(8-6)^2$ = 4, is an estimate of the mean squared deviation for *all* Martians. Therefore, based on this sample of one, we would estimate that the population variance is 4. This estimate is based on a *single* piece of information and therefore has 1 df.

If we sampled another Martian and obtained a height of 5, then we could compute a second estimate of the variance, $(5-6)^2$ = 1. We could then average our two estimates (4 and 1) to obtain an estimate of 2.5. Since this estimate is based on *two* independent pieces of information, it has two degrees of freedom.

However, mostly we are not aware of the population mean when we are estimating the variance. Instead, we have to first estimate the population mean (μ) with the sample mean ($\overline{X}$). The process of estimating the mean affects our degrees of freedom. We have sampled two Martians and found that their heights are 8 and 5. Therefore $\overline{X}$, our estimate of the population mean, is

$$\overline{X} = \frac{8+5}{2} = 6.5$$

We can now compute two estimates of variance:

1. Estimate 1 = $(8-6.5)^2$ = 2.25
2. Estimate 2 = $(5-6.5)^2$ = 2.25

Now for the key question: *Are these two estimates independent*? The answer is *no* because each height contributed to the calculation of $\overline{X}$. Since the first Martian's height of 8 influenced $\overline{X}$, it also influenced Estimate 2. Another way to think about the non-independence is to consider that if you knew the mean and one of the scores, you would know the other score. For example, if one score is 5 and the mean is 6.5, you can compute that the total of the two scores is 13 and therefore that the other score must be 13-5 = 8.

In general, the degrees of freedom for an estimate is equal to the number of values minus the number of parameters estimated en route to the estimate in question. In the Martians example, there are two values (8 and 5) and we had to estimate one parameter (μ) on the way to estimating the parameter of interest (σ^2). Therefore, the estimate of variance has 2 - 1 = 1 degree of freedom. If we had sampled 12 Martians, then our estimate of variance would have had 11 degrees of freedom. Therefore, the degrees of freedom of an estimate of variance is equal to n - 1, where n is the number of observations.

“

NOTE

Bessel's correction

Lets pick a sample of eleven (11) random students from this population. For the sake of argument, we'll assume that we do not know the entire population yet. We just have the sample at hand.

Serial no	Shoe size (X)	Mean ($\overline{X}$)	Deviation $X - \overline{X}$	$\lvert X - \overline{X} \rvert$	Mean deviation ($\frac{\sum \lvert X - \overline{X} \rvert}{n}$)	$(X - \overline{X})^2$	Variance $s^2\_n = \frac{\sum (X - \overline{X})^2}{n-1}$	Standard deviation s_n
		7.818			12.182/11 = 1.107		17.63/ (11-1) = 1.763	$\sqrt{1.763}$ = 1.32
1	6		-1.818	1.818		3.3		
2	6		-1.818	1.818		3.3		
3	7		-0.818	0.818		0.67		
4	7		-0.818	0.818		0.67		
5	7		-0.818	0.818		0.67		
6	8		0.182	0.182		0.03		
7	8		0.182	0.182		0.03		
8	9		1.182	1.182		1.39		
9	9		1.182	1.182		1.39		
10	9		1.182	1.182		1.39		
11	10		2.182	2.182		4.76		

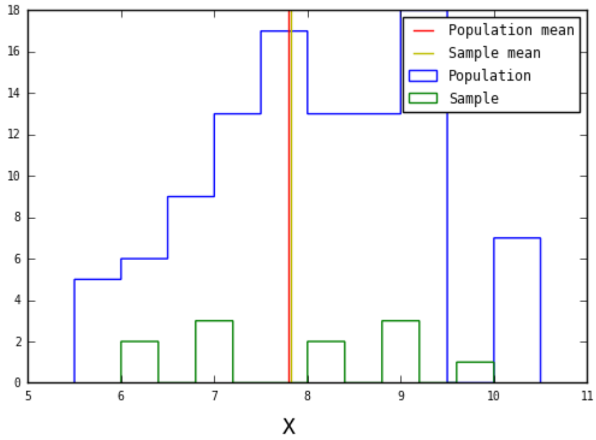


Figure 3. Histogram of population and sample of shoe sizes

We assume now, that the sample mean is a good approximate of population mean (given that the sample is sufficiently random), and thus try to calculate the variance of the sample, which by way of extension, should serve as variance of the entire *population*.

$$s^2 = \sum \frac{(X - \overline{X})^2}{n} = \frac{17.63}{11} = 1.6033$$

vNow let's look back at the population, its mean is 7.8. If we do the same calculation with the population mean

$$s^2 = \sum \frac{(X - \mu)^2}{n} = 1.6035$$

This is bigger (and will always be bigger, as can be proved) from the variance which is derived from the population mean. Our purpose is to calculate sum of the squared distance from the population mean, $X - \mu$, which can be written as

$$\sum (X - \mu)^2 = \sum (X - \overline{X} + \overline{X} - \mu)^2 = \sum (X - \overline{X})^2 + \sum 2(X - \overline{X})(\overline{X} - \mu) + \sum (\overline{X} - \mu)^2$$

The sum of $(X - \overline{X})$, i.e. sum of distances from mean, will naturally be 0, so the entire middle term is 0; thus continuing

$$\sum (X - \mu)^2 = \sum (X - \overline{X})^2 + \sum (\overline{X} - \mu)^2$$

Which proves that calculating from the sample mean will always produce a result smaller than calculating from the population mean.

The root cause of the issue

When population mean is fixed, the n elements of a sample are not free to have any value. The first n - 1 elements might take on any value, but the last one has to conform to regress to the population mean. Thus, the *degree of freedom* is reduced to (n - 1).

Sampling

The use of sampling has already been underlined.

Random sampling

Random sampling is left entirely to nature's own laws of entropy, and everyone has equal probability of being selected. It provides the greatest number of possible samples, but it is also most prone to produce a distorted sample. For example, out of fifty girls and fifty boys, a random sample of 20 has to be chosen. Now it is perfectly possible that the sample of 20 that we choose has exactly 10 girls and 10 boys. It is. however, much more probable for our sample to be distorted either way, i.e. we could select more girls than boys or vice versa. It is, by sheer chance, also possible that we select only girls, and that would be an embarassaingly distorted sample, not even close to represantating the population.

Matched random sampling

If we really want to do a scientific study, let's say about the pattern recognition skill differences between boys and girls, we must select pairs of a boy and a girl, who are identical in all aspects (age, mental growth, family background etc) except that one is a boy and other a girl. We could make a comparison only if such matching has been done.

Systematic sampling

Suppose we pick every 10th person from our hundred (i.e. 1, 11, 21, 31 … or 4, 14, 24 etc), which reduces the number of possible samples (in our particular case, only 10 samples can now be chosen, beginning from 1, 11, 21 to 9, 19, 29). However, if the boys and girls are so arranged that every 10th person is a girl (i.e. if there is periodicity in the population and we resonate with that periodicity), we would end up with 10 girls again. This is the drawback of systematic sampling. Stratified sampling

We could divide the population into reasonable groups (strata) and then takes samples from each group so that no group gets predilected (we could split our hundred into 'boys' stratum and 'girls' stratum, and then go on random/ systematic sampling within each stratum; this way ensure that we do not end up with only girls or only boys in our sample). Stratification can be done on the basis fo age, sex, religion or any other attribute.

Cluster sampling

We could also set up groups of 10 among our hundred (each group may include both boys and girls) and select one from each group. This kind of sampling is used in immunisation survey among children.

Errors in sampling

Sampling error

Each sample of a universe differs from another sample, and this is unavoidable, omnipresent whim of nature.

Non sampling errors

1. Overcoverage: Inclusion of data from outside of the population.
2. Undercoverage: Sampling frame does not include elements in the population.
3. Measurement error: The respondent misunderstand the question.
4. Processing error: Mistakes in data coding.
5. Non-response: People unwilling to take part in a survey may get included in the sample.

Calculation of sample size

Where the sample and population are identical in characteristic, statistical theory yields exact recommendations on sample size. However, where it is not straightforward to define a sample representative of the population, it is more important to understand the cause system of which the population are outcomes and to ensure that all sources of variation are embraced in the sample. Large number of observations are of no value if major sources of variation are neglected in the study.

Cross sectional studies

Qualitative variables

You need

1. the Z score for an alpha error; if the alpha error is selected to be 0.05, then z = 1.96
2. prevalence p of the variable in population
3. precision d to be decided by you; a nice choice is 0.05

Suppose you want to estimate the number of acromegalics in the population. In pilot studies, the prevalence has come to be around 1% (0.01). Thus sample size n

$$n = \frac{z^2 p(1-p)}{d^2}$$

which comes around to be 15. However, if the same study were conducted to estimate malnutrition in children, which has an approximate prevalence of 10%, then the figure would turn out to be 138.

Quantitative variables

$$n = \frac{z^2 \cdot \sigma^2}{d^2}$$

where σ is the known standard deviation of the varible (from previous pilot studies).

Case control studies

Qualitative varibles

Supposing

1. r = ratio of cases to controls
2. p_exp = (prevalence of the exposure in cases + prevalence of the variable in control) / 2 (from pilot studies)
3. z_β = the z score for the power of a test; for a power (1-β) of 80%, z_β = 0.84; if power is increased to 90%, z_β = 1.28
4. z_α = the z score for any α; for α = 0.05, z - 1.96
5. p_c = prevalence of disease in cases (from pilot studies)
6. p_o = prevalence of disease in controls (from pilot studies)

Then

$$n = \left(\frac{r+1}{r}\right) \cdot p_{\exp} . (1 - p_{\exp}) \cdot \frac{\left(z_\beta + z_\alpha\right)^2}{\left(p_c - p_o\right)^2}$$

Quantitative variables

If d is the mean difference between cases and controls and σ is the SD of the variable (both from previosu studies)

$$n = \left(\frac{r+1}{r}\right) \cdot \sigma^2 \frac{\left(z_\beta + z_\alpha\right)^2}{d^2}$$

Cohort studies

Given

1. r = ratio of controls to experimental group
2. p_e = prevalence of disease in experimentl group (from previous studies)
3. p_c = prevalence of disease in control group (from previous studies)
4. p = (p_e + r*p_c) / (r+1)

Then

$$n = \frac{\left(z_\alpha \cdot \sqrt{1 + \frac{1}{r}} \cdot p(1-p) + z_\beta \cdot \sqrt{p_c} \cdot \frac{1-p_c}{r} + p_e(1-p_e)\right)^2}{\left(p_c - p_e\right)^2}$$

Diagnostic test studies

If the sensitivity of the gold standard is sn and specificity sp , then calculate (as always, assume for a p 0.05, z=1.96)

$$n_{sn} = \frac{z^2 sn(1-sn)}{d^2} \; n_{sp} = \frac{z^2 sp(1-sp)}{d^2}$$

Whichever is greater is sample size.

Inferential statistics

Probability

As much as we are fond of data and patterns of data, there is always a limit to how much data we can collect, and at some point of time, we have to stop collecting data and do some hypothesizing. It would have been very fortunate if we could measure all the data about every aspect of everybody, but until that happens, we have to indulge in speculation and forecasting. The beauty of inferential statistics is that, not only does it allow you to make a reasonable prediction, but also allows you to specify the possible amount of error (i.e. "I am 93% sure that there is 13% chance of rain today"). Probability is a theory of uncertainty which deals with these speculations. It is a necessary concept because the world according to the scientist[23] is unknowable in its entirety. However, prediction and decisions are obviously possible. Probability theory is a rational means of dealing with an uncertain world.

Probabilities are numbers associated with events that range from zero to one (0-1). A probability of zero means that the event is impossible. For example, if I were to flip a coin, the probability of a leg is zero, due to the fact that a coin may have a head or tail, but not a leg. Given a probability of one, however, the event is certain. For example, if I flip a coin the probability of heads, tails, or an edge is one, because the coin must take one of these possibilities.

In real life, most events have probabilities between these two extremes. For instance, the probability of rain tonight is 0.40; tomorrow night the probability is 0.10. Thus it can be said that rain is more likely tonight than tomorrow.

The 'odds' of an event

Probability of an event happening / the probability of it *not* happening. If the probability of rain tonight is 0.3, the odds of rain tonight are 0.3 / (1 − 0.3) or 0.3/0.7.

> *The meaning of the term probability depends upon one's philosophical orientation. In the CLASSICAL approach, probabilities refer to the relative frequency of an event, given the experiment was repeated an*

infinite number of times. For example, the .40 probability of rain tonight means that if the exact conditions of this evening were repeated an infinite number of times, it would rain 40% of the time.

*In the SUBJECTIVE approach, however, the term probability refers to a "degree of belief/ confidence." That is, the individual assigning the number .40 to the probability of rain tonight believes that, on a scale from 0 to 1, the likelihood of rain is .40. This leads to a branch of statistics called "Bayesian statistics." [1] This has lead to the term **confidence intervals** for the zones in the normal curve (i.e. that a 95% of values lie within 2 standard deviation means that I am 95% confident any value in this interval belongs to the population)*

— *David W. Stockburger*
Introductory Statistics: Concepts Models and Applications

The probability of an event is the expected number of events among all possible events.

Some basic rules

1. The probability of nothing happening is 0
2. The probability of *something* happening is 1.
3. The probability of two independent events $p(A \cap B) = p(A)p(B)$
4. The probability of *either of* two mutually exclusive events $p(A \cup B) = p(A) + p(B)$
   a. If however, the events are *not* mutually exclusive, $p(A \cup B) = p(A) + p(B) - p(A \cap B)$
5. For opposite events, $p(X) = 1 - p(\neg X)$
6. If an event A implied that some other event B has already occured, then $p(A) < p(B)$
   a. $p(A \mid B) = \dfrac{p(A \cap B)}{p(B)}$

The probability mass function (PMF) for discrete variables (X can have only certain values)

For a variable X, the PMF takes one of the possible values 'x' and retuns the probability $p(X = x)$. For a coin, p(X='heads') is 0.5; and thus for a die, p(X=1) is 1/6.

1. p(X) must always be 0
2. The sum of p(X=x) for all possible x must be 1

The probability density function (PDF) for continuous variables

The function accepts a *range* of [a,b] rather than a single value, and returns a probability p(X in range [a,b])

1. For all x, p(X in [a,b]) must be more than 0
2. The area under the function must be 1

Probability distributions and Models

Models are the necessary abstractions to make any sense of an inherently uncertain world. Models are generated from the *belief* that a few algebraic equations underlie the endless variability observed in the real world. **Probability distributions** is the name given to a table of *all* possible values of a varibale X and their probability, and not just the ones observed. Because probability distributions are all inclusive, the sum of all probabilities (and thus, the area under the graph), is 1.

Every probability distribution has two characteristics

Expectance

The **expectance** $E(X)$, also called the *theoretical mean* (μ), or the most expected value X should take; it is not always the commonest, or even possible, value of X; it is the $\sum x \cdot p(x)$, where x is the set of all values X can have. It represents the center of mass of a physical object, if probabilities are though of solid bar graphs.

In the general case of a discrete distribution,

$$E(f(X)) = \sum f(X) \cdot p(X)$$

In a *continuous* distribution, where the probability P(X=x) is given by a function f(x)

$$E(X) = \int_{-\infty}^{\infty} x f(x) dx$$

Variance

The variance (σ^2), in a *discrete* distribution is the square notation of the average deviation from the mean

$$\sigma^2 = \sum (X - \mu)^2 = \sum (x - \mu)^2 \cdot p(x)$$

which can be shown to be the same as

$$\sigma^2 = E(X^2) - [E(X)]^2 = E(X^2) - \mu^2$$

The variance of a *continuous* distribution of the function f(x) is

$$\sigma^2 = \int (x-\mu)^2 f(x)dx$$

Example: variance of a die roll

For a 6 sided die, the expectance (theorteticla mean) $E(X) = 1x\frac{1}{6} + 2x\frac{1}{6} \ldots = 3.5$. Now, $E(X^2)$ will simplye be $1^2x\frac{1}{6} + 2^2 + \frac{1}{6}\ldots 6^2x\frac{1}{6} = 15.17$. So the vrariance

$$\sigma^2 = E(X^2) - E(X)^2 = 2.92$$

Example: variance of a biased coin

If probability of heads is p

$$E(X) = 1 \cdot p + 0 \cdot (1-p) = p$$
and

$$E(X^2) = 1^2 p + 0^2(1-p) = p$$
thus

$$\sigma^2 = E(X^2) - E(X)^2 = p - p^2 = p(1-p)$$

Sample Variance

For a sample of size n , Variance

$$S^2 = \frac{\sum_{i-1}\left(X_i - \overline{X}\right)^2}{n-1}$$
Like sample means, *the sample variances also form a normal distribution around the populatoin variance.*

Discrete probability distributions: x can have only a finite number of values

Bernoulli distribution

Let's say that a certain event has only *two* outcomes, such as tossing a coin. It has two possible outcomes head (H) and tail (T). Let θ be the probability of head, $1-\theta$ be the probability of tails (for a *fair* coin, both are 1/2) . If I toss the coin only **once**, then what is the probability of the event X which denotes heads? Obviously, its just p . For any out come x

$$p(X = x) = \theta^x (1-\theta)^{1-x}$$

- The only 'expected' value of X is p, which is the E(X) or the theoretical mean
- The variance (σ^2) is $E(X^2) - [E(X)]^2 = p - p^2 = p \cdot (1-p) = pq$.

Binomial distribution

Now we do the tossing twice. The possible number of outcomes now become four (HH, HT, TH, TT). What is the probability of each of these occurences? Remeber that the probabilities of two independent events get multiplied if thet are to occur together. The outcomes of the two tosses are independent (i.e. the results of the first toss does, in no way, affect the second), so probabilities must be multiplied.

Outcome	**Probability**
HH	p×p = p^2
HT	p×q = pq
TH	q×p = pq
TT	q×q = q^2

Looking at the table, if we consider now, the possible values of the 'head' event as x after two tosses, x can have values 0, 1, 2 and 3. What are the probabilitie of these values?

Table 2. If we toss a coin twice, what is the probability distribution of heads?

Value of X	**Probability**
0	q^2
1	2pq
2	p^2

The set of possibilities of all possible outcomes of an event (such as 'heads' in a coin toss), is the *binomial distribution*. When tossing only twice ($n = 2$), the set of probabilities of an event 'heads' is [$p^2, 2pq, q^2$]. For tossing n times, we can generalise the formula by mathematical induction; it would be the elements in the expansion of

$(p+q)^n$
which results in the set (following Newton's binomial theorem; nCr denotes possible combinations of r things among n slots)

$[p^n, {}^nC_1 \cdot p^{n-1} \cdot q, {}^nC_2 \cdot p^{n-2} \cdot q^2, \ldots {}^nC_r \cdot p^{n-r} \cdot q^r, \ldots q^n]$
or, to put it concisely, the probability of X taking a value x (x < n) is

$P(X=x) = {}^nC_x \times p^x \cdot q^{n-x}$
where r is number of times we get a 'head' out of those n number of tosses.

Suppose the coin is biased, so that p = 0.6 and q = 0.4. Then, the probaility distribution of variable X (incidence of 'heads') becomes

x	0	1	2
p(x)	q^2 = 0.16	2pq = 0.48	p^2 = 0.36

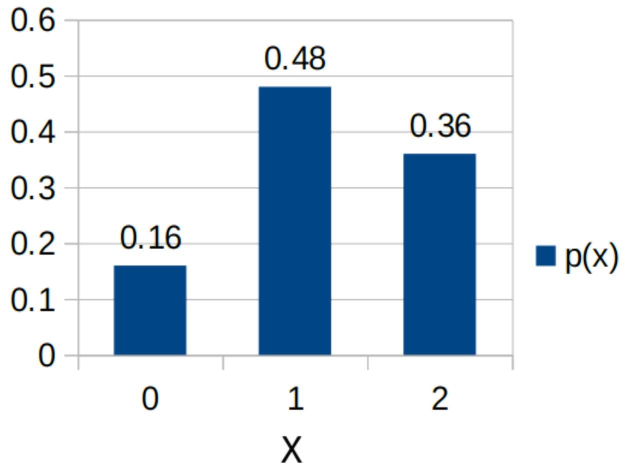


Figure 4. Plot of probability distribution of a biased coin

Expectance (theoretical mean) of the binomial distribution.

The expectance, in this case, is

$\mu = E(X) = \sum x \cdot p(x) = 1.2$
which, if you notice, is *not* a possible value of X (reason it is called the theoretical mean). However, as n increases, the average of X tends to E(X).

$\sigma^2 = E(X^2) - \left[E(X)^2\right] = 0.48$
When n is large enough (> 25), and p is close to 0.5, then the **binomial distribution begins to look like normal distribution**, so that a z score might (and a subsequent p value) be calculated, with a mean pn and SD of npq

Confidence interval of a binomial distribution

Suppose a random trial of a drug of 100 (n) people show 56 ($\hat{p}$) cures . Is it evidence enough it is an effective drug than placebo (i.e. cures more than 50% of the time? We know for a binomial distribution (cure or no cure), the variance $\sigma^2 = p(1-p)$, where p is the probability of cures. Thus the confidence interval for 'cure' is

$$\hat{p} \pm \sqrt{\frac{p(1-p)}{n}}$$

If p = 0.5, then this becomes $\hat{p} \pm \sqrt{0.5 \cdot \frac{0.5}{n}} = 0.56 \pm \frac{1}{\sqrt{100}} = [0.46, 0.56]$, which is the confidence of interval of curs. Note that this includes 0.50, thus the drug might not be very effective.

When n tends to infinite, and p is very small, the binomial distribution becomes the Poisson distribution

For rare events, the Binomial formula can be rewritten as

$P(X=x) = {}^nC_x \cdot p^x \cdot q^{n-x} = \frac{n!}{x!(n-x)!} \cdot p^x \cdot (1-p)^{n-x}$
Substituting $\lambda = np$ and limiting $n \to \infty$, this can be proved to be

$P(X=x) = \frac{\lambda^x e^{-\lambda}}{x!}$
where λ is the 'expectance' of the distribution, equal to np . You can then calculate a z score similar to binomial distribution.

A binomial distribution can be simulated in most programming languages

```
#Python
numpy.random.binomial(10, 0.4) # Flip a (biased) coin 10 times whose probability of heads is 0.4
```

```
>>> 4 # i.e. number of times 'heads' turned out
```

```
#R
binom.test(10,20,0.4) # Gives probability  of 10 'heads' in 20 flips, with a biased coin with 'head' probability
0.4
```

Continuous probability distributions

In such distributions, X can have any real value, so that P(X=x) for any real x is not defined, but P(a < X < b) is defined, i.e. probabilities come only for an *area*. Usually, p(X=x) is defined not by discrete values but a function f(x).

The normal distribution

If we could go on forever, and collect show size data of an *infinite* number of students, and if shoe sizes would vary *continuously* (that is, the class intervals, would be adjacent - there was no discrete jumps from size 6 to 6.5 but 6.1, 6.11 and so on), we would produce a normal (Gaussian) curve. It is a curve which has been sketched after infinite number of observations and with no gaps in between class intervals. It is a bell shaped, symmetrical curve with absolute continuity.

The equation of the normal curve is

$$P(X = x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

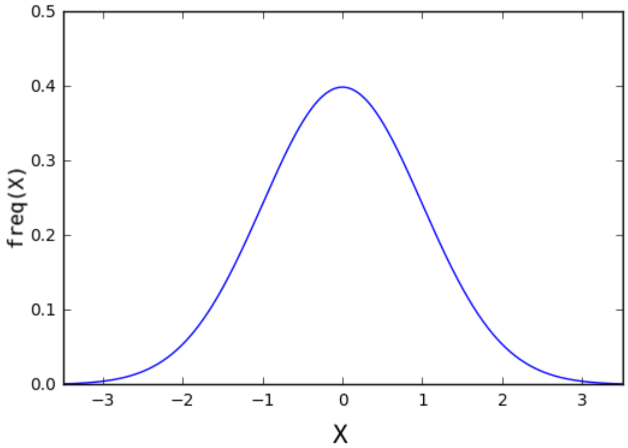


Figure 5. The normal curve

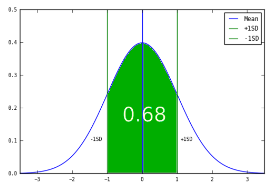
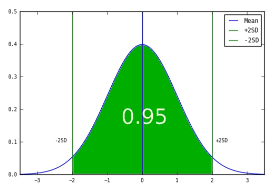
The *expectance* or **mean** of a normal distribution E(X) is the same as its median and mode.

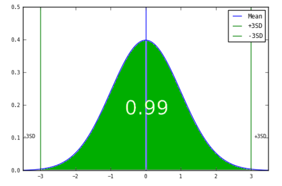
The standard normal curve

The standard normal curve is a member of the family of normal curves with μ = 0.0 and σ = 1.0. The value of 0.0 was selected because the normal curve is symmetrical around μ and the number system is symmetrical around 0.0. The value of 1.0 for σ is simply a unit value. The X-axis on a standard normal curve is often re labelled with multiples of σ and called Z scores (see later).

There are three areas on a standard normal curve that should become second nature.

Table 3. Three areas in the normal curve, denoted by distance from mean in terms of standard deviation: z = (x - μ) / σ

Z score	Area inside this Z score (one sided)	Area inside this Z score (two sided)	
1	0.34	0.68	
2 (approx) [2]	0.475	0.95	
3	0.495	0.99	



For the rest of this chapter, we will work with a population of children in a class of 101; we will assume a normal distribution of shoe sizea with mean $\mu = 7.8$ and $\sigma = 1.19$.

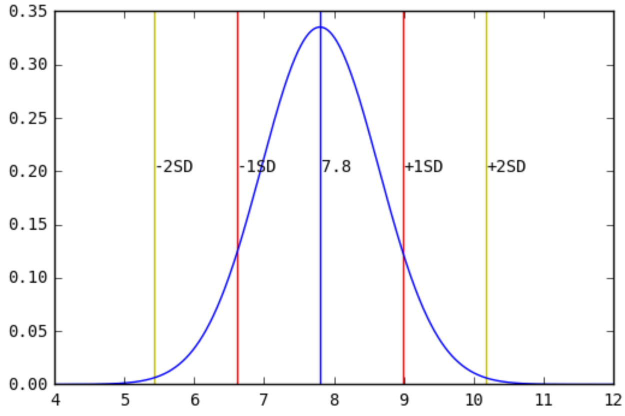


Figure 6. The normal distribution of shoe sizes

Conversion of a normal curve to a standard normal curve

Suppose a variable X has a mean μ and a standard deviation σ, and is normally distributed. It is easier, if we want to emphasise the variation rather than the actual values, to plot it in a standard normal curve by making the mean 0 and standard deviation 1.

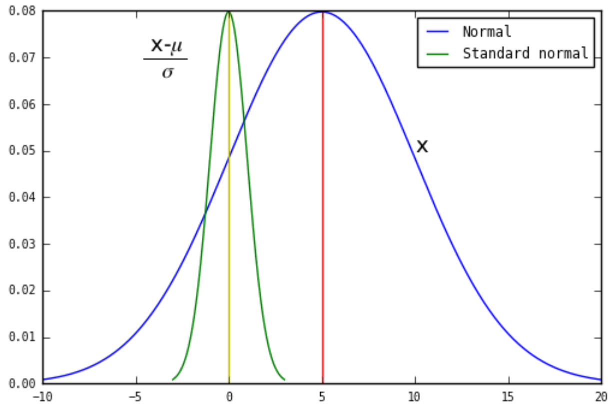


Figure 7. Making a standard normal curve from a normal curve

Think of a **relative deviate** z which is the reduced form of X for a standard normal curve. For any value X=x

$$z = \frac{X - \mu}{\sigma}$$

Now plot the curve of z. The curve of z is shifted parallel to x and is reduced in size, but the fractional areas under confidence intervals remain the same. In fact, we can prepare a table (by integrating the normal distribution function) to find the areas before and after a particular z-score. First, we find the area to the *left* of a particular score.

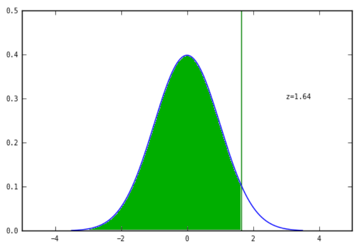


Table 4. The complete z table (area to the *left* of Z); to find a value z = 1.64, go to row 1.6 and column 0.04

z	+0.00	+0.01	+0.02	+0.03	+0.04	+0.05	+0.06	+0.07	+0.08	+0.09
0.0	0.50000	0.50399	0.50798	0.51197	0.51595	0.51994	0.52392	0.52790	0.53188	0.53586
0.1	0.53983	0.54380	0.54776	0.55172	0.55567	0.55966	0.56360	0.56749	0.57142	0.57535

0.2	0.57926	0.58317	0.58706	0.59095	0.59483	0.59871	0.60257	0.60642	0.61026	0.61409
0.3	0.61791	0.62172	0.62552	0.62930	0.63307	0.63683	0.64058	0.64431	0.64803	0.65173
0.4	0.65542	0.65910	0.66276	0.66640	0.67003	0.67364	0.67724	0.68082	0.68439	0.68793
0.5	0.69146	0.69497	0.69847	0.70194	0.70540	0.70884	0.71226	0.71566	0.71904	0.72240
0.6	0.72575	0.72907	0.73237	0.73565	0.73891	0.74215	0.74537	0.74857	0.75175	0.75490
0.7	0.75804	0.76115	0.76424	0.76730	0.77035	0.77337	0.77637	0.77935	0.78230	0.78524
0.8	0.78814	0.79103	0.79389	0.79673	0.79955	0.80234	0.80511	0.80785	0.81057	0.81327
0.9	0.81594	0.81859	0.82121	0.82381	0.82639	0.82894	0.83147	0.83398	0.83646	0.83891
1.0	0.84134	0.84375	0.84614	0.84849	0.85083	0.85314	0.85543	0.85769	0.85993	0.86214
1.1	0.86433	0.86650	0.86864	0.87076	0.87286	0.87493	0.87698	0.87900	0.88100	0.88298
1.2	0.88493	0.88686	0.88877	0.89065	0.89251	0.89435	0.89617	0.89796	0.89973	0.90147
1.3	0.90320	0.90490	0.90658	0.90824	0.90988	0.91149	0.91308	0.91466	0.91621	0.91774
1.4	0.91924	0.92073	0.92220	0.92364	0.92507	0.92647	0.92785	0.92922	0.93056	0.93189
1.5	0.93319	0.93448	0.93574	0.93699	0.93822	0.93943	0.94062	0.94179	0.94295	0.94408
1.6	0.94520	0.94630	0.94738	0.94845	0.94950	0.95053	0.95154	0.95254	0.95352	0.95449
1.7	0.95543	0.95637	0.95728	0.95818	0.95907	0.95994	0.96080	0.96164	0.96246	0.96327
1.8	0.96407	0.96485	0.96562	0.96638	0.96712	0.96784	0.96856	0.96926	0.96995	0.97062
1.9	0.97128	0.97193	0.97257	0.97320	0.97381	0.97441	0.97500	0.97558	0.97615	0.97670
2.0	0.97725	0.97778	0.97831	0.97882	0.97932	0.97982	0.98030	0.98077	0.98124	0.98169
2.1	0.98214	0.98257	0.98300	0.98341	0.98382	0.98422	0.98461	0.98500	0.98537	0.98574
2.2	0.98610	0.98645	0.98679	0.98713	0.98745	0.98778	0.98809	0.98840	0.98870	0.98899
2.3	0.98928	0.98956	0.98983	0.99010	0.99036	0.99061	0.99086	0.99111	0.99134	0.99158
2.4	0.99180	0.99202	0.99224	0.99245	0.99266	0.99286	0.99305	0.99324	0.99343	0.99361
2.5	0.99379	0.99396	0.99413	0.99430	0.99446	0.99461	0.99477	0.99492	0.99506	0.99520
2.6	0.99534	0.99547	0.99560	0.99573	0.99585	0.99598	0.99609	0.99621	0.99632	0.99643
2.7	0.99653	0.99664	0.99674	0.99683	0.99693	0.99702	0.99711	0.99720	0.99728	0.99736
2.8	0.99744	0.99752	0.99760	0.99767	0.99774	0.99781	0.99788	0.99795	0.99801	0.99807
2.9	0.99813	0.99819	0.99825	0.99831	0.99836	0.99841	0.99846	0.99851	0.99856	0.99861
3.0	0.99865	0.99869	0.99874	0.99878	0.99882	0.99886	0.99889	0.99893	0.99896	0.99900

Next, the area to the *right* of a z score

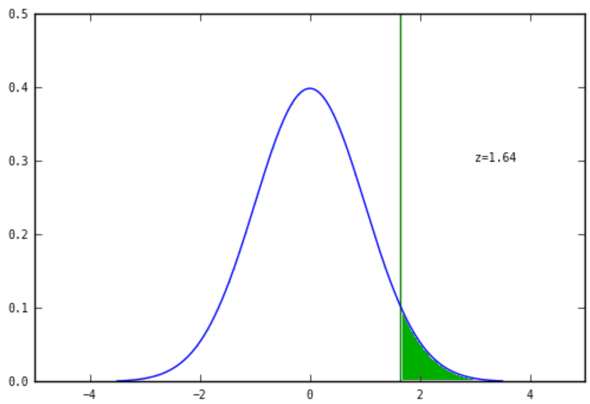


Table 5. The complete z table (area to the right of z)

z	+0.00	+0.01	+0.02	+0.03	+0.04	+0.05	+0.06	+0.07	+0.08	+0.09

0.0	0.50000	0.49601	0.49202	0.48803	0.48405	0.48006	0.47608	0.47210	0.46812	0.46414
0.1	0.46017	0.45620	0.45224	0.44828	0.44433	0.44034	0.43640	0.43251	0.42858	0.42465
0.2	0.42074	0.41683	0.41294	0.40905	0.40517	0.40129	0.39743	0.39358	0.38974	0.38591
0.3	0.38209	0.37828	0.37448	0.37070	0.36693	0.36317	0.35942	0.35569	0.35197	0.34827
0.4	0.34458	0.34090	0.33724	0.33360	0.32997	0.32636	0.32276	0.31918	0.31561	0.31207
0.5	0.30854	0.30503	0.30153	0.29806	0.29460	0.29116	0.28774	0.28434	0.28096	0.27760
0.6	0.27425	0.27093	0.26763	0.26435	0.26109	0.25785	0.25463	0.25143	0.24825	0.24510
0.7	0.24196	0.23885	0.23576	0.23270	0.22965	0.22663	0.22363	0.22065	0.21770	0.21476
0.8	0.21186	0.20897	0.20611	0.20327	0.20045	0.19766	0.19489	0.19215	0.18943	0.18673
0.9	0.18406	0.18141	0.17879	0.17619	0.17361	0.17106	0.16853	0.16602	0.16354	0.16109
1.0	0.15866	0.15625	0.15386	0.15151	0.14917	0.14686	0.14457	0.14231	0.14007	0.13786
1.1	0.13567	0.13350	0.13136	0.12924	0.12714	0.12507	0.12302	0.12100	0.11900	0.11702
1.2	0.11507	0.11314	0.11123	0.10935	0.10749	0.10565	0.10383	0.10204	0.10027	0.09853
1.3	0.09680	0.09510	0.09342	0.09176	0.09012	0.08851	0.08692	0.08534	0.08379	0.08226
1.4	0.08076	0.07927	0.07780	0.07636	0.07493	0.07353	0.07215	0.07078	0.06944	0.06811
1.5	0.06681	0.06552	0.06426	0.06301	0.06178	0.06057	0.05938	0.05821	0.05705	0.05592
1.6	0.05480	0.05370	0.05262	0.05155	0.05050	0.04947	0.04846	0.04746	0.04648	0.04551
1.7	0.04457	0.04363	0.04272	0.04182	0.04093	0.04006	0.03920	0.03836	0.03754	0.03673
1.8	0.03593	0.03515	0.03438	0.03362	0.03288	0.03216	0.03144	0.03074	0.03005	0.02938
1.9	0.02872	0.02807	0.02743	0.02680	0.02619	0.02559	0.02500	0.02442	0.02385	0.02330
2.0	0.02275	0.02222	0.02169	0.02118	0.02068	0.02018	0.01970	0.01923	0.01876	0.01831
2.1	0.01786	0.01743	0.01700	0.01659	0.01618	0.01578	0.01539	0.01500	0.01463	0.01426
2.2	0.01390	0.01355	0.01321	0.01287	0.01255	0.01222	0.01191	0.01160	0.01130	0.01101
2.3	0.01072	0.01044	0.01017	0.00990	0.00964	0.00939	0.00914	0.00889	0.00866	0.00842
2.4	0.00820	0.00798	0.00776	0.00755	0.00734	0.00714	0.00695	0.00676	0.00657	0.00639
2.5	0.00621	0.00604	0.00587	0.00570	0.00554	0.00539	0.00523	0.00508	0.00494	0.00480
2.6	0.00466	0.00453	0.00440	0.00427	0.00415	0.00402	0.00391	0.00379	0.00368	0.00357
2.7	0.00347	0.00336	0.00326	0.00317	0.00307	0.00298	0.00289	0.00280	0.00272	0.00264
2.8	0.00256	0.00248	0.00240	0.00233	0.00226	0.00219	0.00212	0.00205	0.00199	0.00193
2.9	0.00187	0.00181	0.00175	0.00169	0.00164	0.00159	0.00154	0.00149	0.00144	0.00139
3.0	0.00135	0.00131	0.00126	0.00122	0.00118	0.00114	0.00111	0.00107	0.00104	0.00100

See the Z score calculator

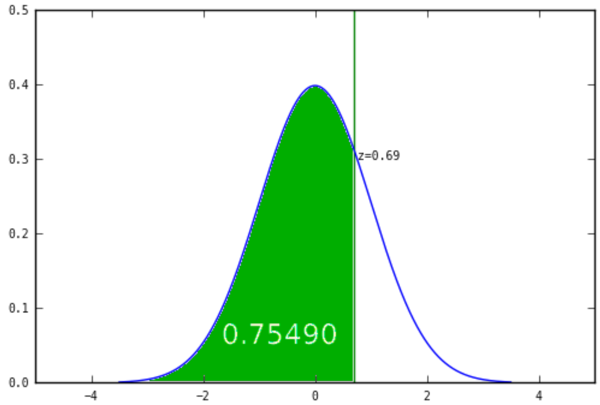


Figure 8. For example a Z score of of 0.69 gives this area 0.75490 to the left of Z

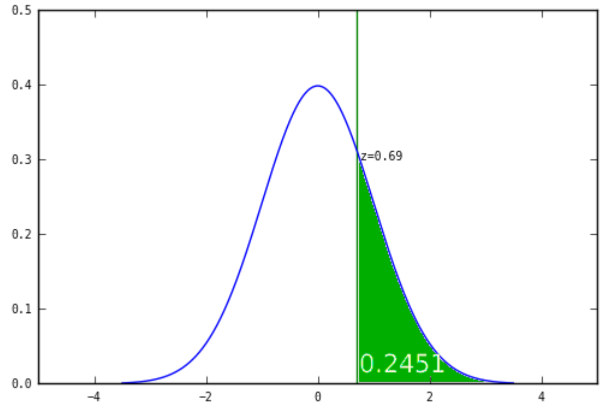


Figure 9. The same Z score gives an area 0.24510 to the right of Z

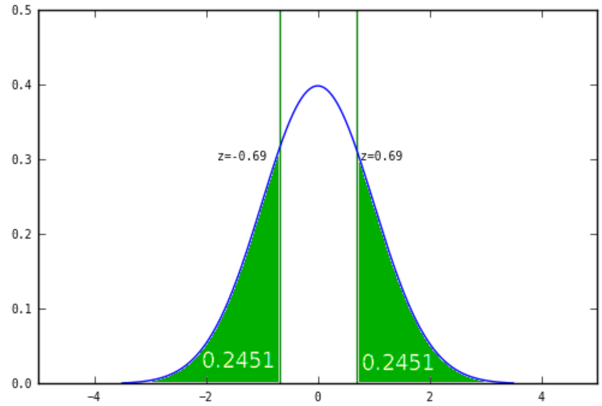


Figure 10. This is the same area to the left of z = -0.69

Skewed distributions

- positively skewed - mode < median < mean
- negatively skewed - mode > median > mean

Remember that mean is always dragged towards the tail of the distribution.

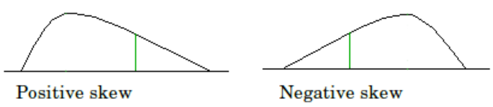


Figure 11. Skew

Probability and the normal curve

Each particular area bound between any two z-scores (any two vertical lines over the x axis) is associated with a certain degree of probability, and all such areas are called **confidence intervals** . In continuum with our example of shoe sizes, what of those students who have a size of 10.18 or more ? Could they be considered acromegalics, or perfectly 'normal' people? If we introduce a child with a shoe size of 10.18, he would fall more than two standard deviations away from the mean (7.8) - look at the normal distribution of shoe sizes again. The area inside two standard deviations in a normal curve, as I have already illustrated, is 0.95. Thus the area outside 2 standard deviations is obviously, 0.05. This means that the person with a shoe size of 10.18 has a 0.05 probability (or 5%) chance of being `normal' (or to put it more theoretically, a 5% chance of belonging to this class).

To be concise, the area of any interval of the normal curve, indicates the probability of a member from that interval being selected in a random sample. (And vice versa, i.e. if a random sample shows a member from this interval, the sample has only so much probablity of actuallly belonging to the population).

$$\sigma^2 = \frac{\sum (X - \mu)^2}{\eta}$$

where η is the size of the population.

Standard deviation

The positive squareroot of variance (σ); the `unit of confidence' in a normal distribution. It is a convenient method to desgnate distance of a member from the mean.

The central limit theorem

Suppose in the mean of a population is μ. Each sample from this population has a different mean ($\overline{X}$) value. If adequate number of samples (in fact, and infinite number of them) are collected, each of a significant size, then the sample means $\overline{X}$ – are found to be *normally distributed* around the universal mean μ. If we take any number of samples (each containing n members), then each sample will have its own mean $\overline{X}$. It is perfectly possible that we choose a sample from the lower end of the population, i.e. only the show sizes between 6-8, so that we get a sample mean = 7. It is also possible that we get, in our sample, only the largest shoe sizes, giving a sample mean = 11.

But if we go on taking random samples, chances are that we would encounter every shoe size in most of our samples. So the means of our samples could be any or all of 6, 6.5, 8. 8.5, 11.5 or any plausible value. If we go on taking infinite number of samples, we would, obviously, get an infinite number of sample means. The mean of these infinite number of means, as we will find out, will be equal or very close to the universal mean μ, and the sample means themselves will form a normal curve. This *normal distribution of the sample means* will, again, have the universal mean μ as its mean. This is the central limit theorem.

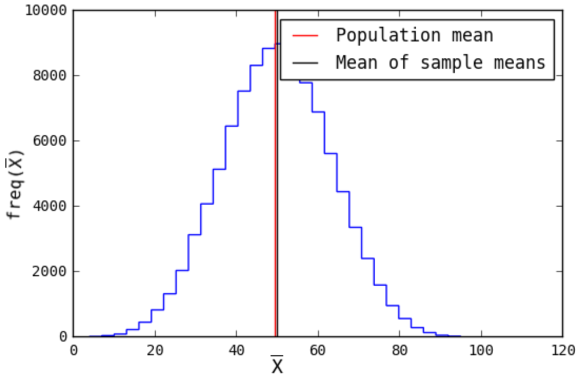


Figure 12. Central limit theorem; as number of sample increase, the mean of sample means form a normal distribution around population mean

Standard error of the mean

The standard deviation of this new normal distribution is called **standard error of the mean** (SEM) and has the value

$$\sigma_{\overline{X}} = \frac{\sigma}{\sqrt{n}}$$

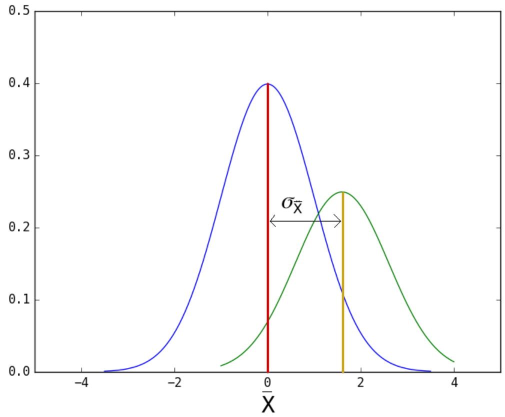
where *n* is the sample size. Note that the SEM no longer talks about the population variance; instead, *it shows the varaibaility in the means of samples (of size n) drawn from the population*.

The standard error of the mean provides a method to determine how much a sample of size *n*, drawn from a population η, is representative of the population. The z score, of a sample then, becomes

$$z = \frac{\overline{X} - \mu}{\sigma_{\overline{X}}}$$

Finding the population mean μ from a sample mean $\overline{X}$

Now that we have established that sample means form a normal distribution around the population mean, lets ponder what that means. **95% of the time, the sample mean will be within 2 standard errors of the population mean**. The converse is also true, i.e. **the population mean, will be within 2 standard error from the sample mean, about 95% of the time**, i.e. in 95 out of 100 samples.[3]



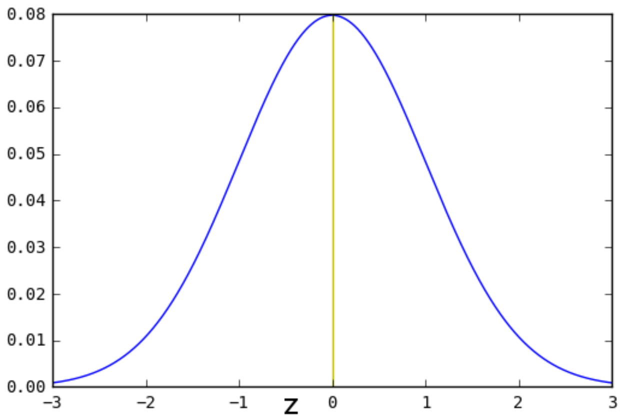
So, it can be said with 95% `confidence' that the population mean lies within 2 standard errors of sample mean. In general, for any z score, the **confidence limit** of the population mean is ($\overline{X} \pm z \cdot \sigma_{\overline{X}}$), i.e. we can say that population mean lies within $\overline{X} - z \cdot \sigma_{\overline{X}}$ and $\overline{X} + z \cdot \sigma_{\overline{X}}$.

To reduce this window, (i.e. to narrow down the range of confidence limit), the only way is to reduce $\sigma_{\overline{X}}$, which, if you will recall, is just $\frac{\sigma}{\sqrt{n}}$. Since, σ is not accessible, the only way to bring this down is to increase *n*, the sample size. Because it is *square root* of *n* at work, to halve the standard error, the sample size must be increased *fourfold*.

The **precision** of a sample in determining the population mean, is proportional to sample size (i.e., it reflects the width of the confidence limit). The wider a confidence limit, the less precise it is. **Accuracy** of a sample denotes the closeness of the sample mean to the population mean.

If Z has a *standard* normal distribution, then Z^2 has a χ^2 distribution

Consider a standard normal distribution



What is the distribution of Z^2 then? Consider all values of Z, their frequency, and try to find how Z^2 matches up. Obviously, Z=0 is the most frequent, followed by Z = -1 and +1 (with everything and between) and so on. Thus the probablity distribution of Z^2 becomes

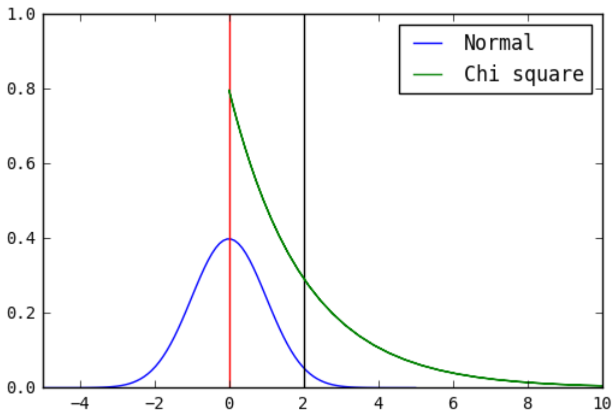


Figure 13. Chi square distribution

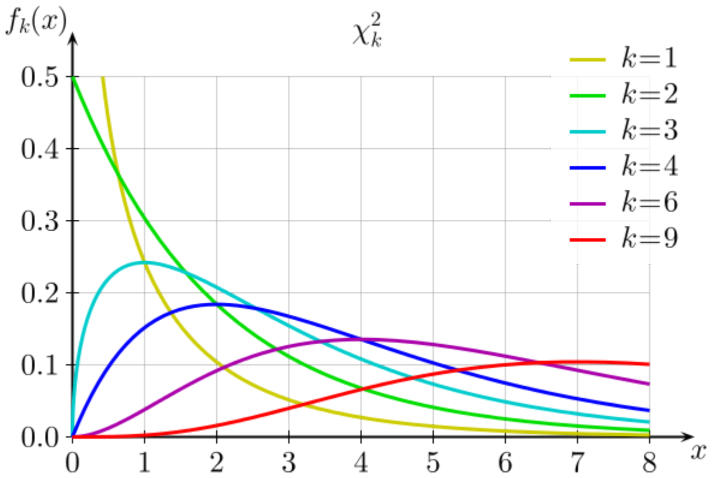


Figure 14. Chi square distribution over multiple degrees of freedom

In general, if k random variables $Z_1, Z_2, Z_3 ... Z_k$ have *standard* normal distribution, then the sum $\sum_{i=0}^{k} Z_i^2$ has a χ^2 (pronounced `chi squared') distribution with a single parameter, the **degree of freedom** = k . The distribution has a mean k .

```
np.random.chisquare(5, size=10000) # 5 degrees of freedom, 10000 Observations
```

NOTE

Some history

As you might have noticed, when sample size if sufficiently large, the binomial distribution approximates the normal distribution, with p = probability of head ('success'), n = number of tosses, m = observed number of heads ('successes'), q = 1-p; Lancaster, DeMoivre and Laplace showed that the binomial distribution could be written as

$\chi = \frac{m - np}{\sqrt{npq}}$ thus $\chi^2 = \frac{(m-np)^2}{npq}$ or $\chi^2 = \frac{(m-np)^2}{np(1-p)} = \frac{(m-np)^2}{np - np^2} = \frac{(m-np)^2}{np}$
(p being a fraction, p^2 can be safely ignored)

Of course, m is the observed incidince O of a 'success', np is the 'expected' incidence E , thus

$$\chi^2 = \frac{(O-E)^2}{E}$$

If more than one variable is being studuied (i.e. N varibles)

$$\chi^2 = \sum_{i=0}^{N} \frac{(O_i - E_i)^2}{E_i}$$

This is the form that the chi square statistic is usually written. However, remember that the mean of this distribution is still np and SD is $\sqrt{npq}$. So if the test statistics χ^2 is determined, then χ is a normally distributed variable with mean np and SD $\sqrt{npq}$. If χ^2 comes out to be 3.841, then χ is 1.96 (if degree of freedom is 1), and the corresponding area right of this Z score in a normal distribution is p = 0.05. This is how the χ^2 table has been made.

The estimated standard error and *t* distribution

The calculation of standard error of mean raises an obvious question: if we know the standard deviation of the population (σ) anyway, why bother about sampling at all? In fact, knowing σ is impossible; you can never survey the entire population. Hence caluculation of standard error of mean ($\sigma_{\overline{X}}$) is also impossible. Rather, we have to content ourselves with **estimated** standard error, or $s_{\overline{X}}$, derived solely from the sample at hand.

$$s_{\overline{X}} = \frac{s}{\sqrt{n-1}}$$

where, s is the SD of the sample at hand, and n its size.

In calculating the population mean from a sample then, we must devise a new variable called t [4], which is the same as z score, but with *estimated* standard error

$$t = \frac{\overline{X} - \mu}{s_{\overline{X}}} = \frac{\overline{X} - \mu}{\frac{s}{\sqrt{n-1}}}$$

With introduction of *t*, a variable derived from the sample at hand, we have committed ourselves to the mercy of the sample size.

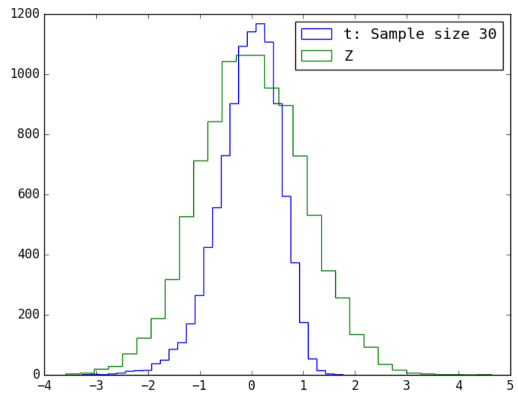


Figure 15. As sample size increases, *t* approaches *z* distribution

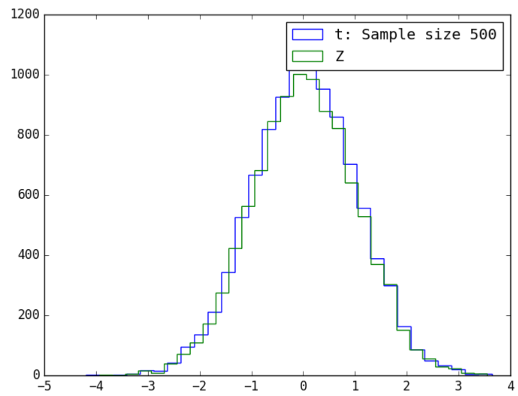


Table 6. Values of t for a given degree of freedom and α (α = 1 - confidence interval); for *t* for a given degree of freedom, find a value which is jus

	One-sided α											
	.25	.10	.05	.025	.01	.005	.0025	.001	.0005	.00025	.0001	.00005
	Two-sided α											
	.50	.20	.10	.05	.02	.01	.005	.002	.001	.0005	.0002	.0001

df												
1	1.00	3.08	6.31	12.71	31.82	63.66	127.32	318.31	636.62	1273.24	3183.10	6366.20
2	.82	1.89	2.92	4.30	6.96	9.22	14.09	22.33	31.60	44.70	70.70	99.99
3	.76	1.64	2.35	3.18	4.54	5.84	7.45	10.21	12.92	16.33	22.20	28.00
4	.74	1.53	2.13	2.78	3.75	4.60	5.60	7.17	8.61	10.31	13.03	15.54
5	.73	1.48	2.02	2.57	3.37	4.03	4.77	5.89	6.87	7.98	9.68	11.18
6	.72	1.44	1.94	2.45	3.14	3.71	4.32	5.21	5.96	6.79	8.02	9.08
7	.71	1.42	1.90	2.37	3.00	3.50	4.03	4.79	5.41	6.08	7.06	7.88
8	.71	1.40	1.86	2.31	2.90	3.36	3.83	4.50	5.04	5.62	6.44	7.12
9	.70	1.38	1.83	2.26	2.82	3.25	3.69	4.30	4.78	5.29	6.01	6.59
10	.70	1.37	1.81	2.23	2.76	3.17	3.58	4.14	4.59	5.05	5.69	6.21
11	.70	1.36	1.80	2.20	2.72	3.11	3.50	4.03	4.44	4.86	5.45	5.92
12	.70	1.36	1.78	2.18	2.68	3.06	3.43	3.93	4.32	4.72	5.26	5.69
13	.69	1.35	1.77	2.16	2.65	3.01	3.37	3.85	4.22	4.60	5.11	5.51
14	.69	1.35	1.76	2.15	2.63	2.98	3.33	3.79	4.14	4.50	4.99	5.36
15	.69	1.34	1.75	2.13	2.60	2.95	3.29	3.73	4.07	4.42	4.88	5.24
16	.69	1.34	1.75	2.12	2.58	2.92	3.25	3.69	4.02	4.35	4.79	5.13
17	.69	1.33	1.74	2.11	2.57	2.90	3.22	3.65	3.97	4.29	4.71	5.04
18	.69	1.33	1.73	2.10	2.55	2.88	3.20	3.61	3.92	4.23	4.65	4.97
19	.69	1.33	1.73	2.09	2.54	2.86	3.17	3.58	3.88	4.19	4.59	4.90
20	.69	1.33	1.73	2.09	2.53	2.85	3.15	3.55	3.85	4.15	4.54	4.84
21	.69	1.32	1.72	2.08	2.52	2.83	3.14	3.53	3.82	4.11	4.49	4.78
22	.69	1.32	1.72	2.07	2.51	2.82	3.12	3.51	3.79	4.08	4.45	4.74
23	.68	1.32	1.71	2.07	2.50	2.81	3.10	3.49	3.77	4.05	4.42	4.69
24	.68	1.32	1.71	2.06	2.49	2.80	3.09	3.47	3.75	4.02	4.38	4.65
25	.68	1.32	1.71	2.06	2.49	2.79	3.08	3.45	3.73	4.00	4.35	4.62
26	.68	1.32	1.71	2.06	2.48	2.78	3.07	3.44	3.71	3.97	4.32	4.59
27	.68	1.31	1.70	2.05	2.47	2.77	3.06	3.42	3.69	3.95	4.30	4.56
28	.68	1.31	1.70	2.05	2.47	2.76	3.05	3.41	3.67	3.94	4.28	4.53
29	.68	1.31	1.70	2.05	2.46	2.76	3.04	3.40	3.66	3.92	4.25	4.51
30	.68	1.31	1.70	2.04	2.46	2.75	3.03	3.39	3.65	3.90	4.23	4.48
35	.68	1.31	1.69	2.03	2.44	2.72	3.00	3.34	3.59	3.84	4.15	4.39
40	.68	1.30	1.68	2.02	2.42	2.70	2.97	3.31	3.55	3.79	4.09	4.32
45	.68	1.30	1.68	2.01	2.41	2.69	2.95	3.28	3.52	3.75	4.05	4.27
50	.68	1.30	1.68	2.01	2.40	2.68	2.94	3.26	3.50	3.72	4.01	4.23
55	.68	1.30	1.67	2.00	2.40	2.67	2.93	3.25	3.48	3.70	3.99	4.20
60	.68	1.30	1.67	2.00	2.39	2.66	2.91	3.23	3.46	3.68	3.96	4.17
65	.68	1.29	1.67	2.00	2.39	2.65	2.91	3.22	3.45	3.66	3.94	4.15
70	.68	1.29	1.67	1.99	2.38	2.65	2.90	3.21	3.44	3.65	3.93	4.13
75	.68	1.29	1.67	1.99	2.38	2.64	2.89	3.20	3.43	3.64	3.91	4.11
80	.68	1.29	1.66	1.99	2.37	2.64	2.89	3.20	3.42	3.63	3.90	4.10

85	.68	1.29	1.66	1.99	2.37	2.64	2.88	3.19	3.41	3.62	3.89	4.08
90	.68	1.29	1.66	1.99	2.37	2.63	2.88	3.18	3.40	3.61	3.88	4.07
95	.68	1.29	1.66	1.99	2.37	2.63	2.87	3.18	3.40	3.60	3.87	4.06
100	.68	1.29	1.66	1.98	2.36	2.63	2.87	3.17	3.39	3.60	3.86	4.05
200	.68	1.29	1.65	1.97	2.35	2.60	2.84	3.13	3.34	3.54	3.79	3.97
500	.68	1.28	1.65	1.97	2.33	2.59	2.82	3.11	3.31	3.50	3.75	3.92
∞	.67	1.28	1.65	1.96	2.33	2.58	2.81	3.10	3.30	3.49	3.73	3.91

For example, if sample size is 21, degree of freedom is 20, and t = -2.27, then the closest value more than t (for degree of freedom=20) is 2.53, which corresponds to an α=0.02 (two sided)

Once the sample size crosses about 100, the t and z distribution become almost the same.

NOTE

An example : how to estimate population mean from a sample using t score

Suppose from 101 students of a class, we select 10 and take their shoe size. This time, we don't make the foolish assumption that we know the mean and SD of the entire class. Instead, we find the mean of the sample to be 7.6 and SD 1.11. What does it say about the sample?

The estimated standard error

$$s_{\overline{X}} = \frac{s}{\sqrt{n-1}} = \frac{1.11}{3} = 0.37$$

The t score, is then

$$t = \frac{\overline{X} - \mu}{s_{\overline{X}}}$$

Of course, we know neither σ nor μ . So we have to find *t* from the table, which shows areas of *t* distribution for a particular degree of freedom (in this case, 9). The corresponding t-value for an area of 95% is 2.22 (two-tailed). The 95% confidence interval will be $\overline{X} \pm t \cdot s_{\overline{X}} = 7.6 \pm 2.22 \cdot 0.37 = (6.77, 8.42)$. Thus, **we are 95% sure that the mean shoe size of the population (the enitre class) lies between 6.77 to 8.42**.

Lets improve. We select a sample of 30, and mean 7.56, SD (s) 1.14, and estimated standard error $\frac{1.14}{\sqrt{29}} = 0.211$.

Calculating for a degree of freedom (30-1) = 29, t value for 95% confidence interval (two sided) is 2.05. Thus, the confidence interval

$$\overline{X} \pm t \cdot s_{\overline{X}} = 7.56 \pm 2.05 \cdot 0.211 = (7.12, 7.99)$$

With just an increase in sample size, our estimate has improved!

Testing for truth

Truth must ultimately be tested. The material sciences (physics, chemistry) usually provide us with the tools to conduct the tests, but it is statistics which tells how to interpret the test. Common to all tests is to find association between two events, i.e.

- to test whether the finding of bronchial sounds is diagnostic of pneumonia (a diagnostic test)
- to test whether smoking is associated with lung cancer (a study to discover risk factors)
- to test whether radiation is effective in lung cancer (a therapeutic test)

All tests must be

- **reproducible**, i.e. gives the same result over and over even if different samples are tested, by different observers with different skill levels
- **accurate**, i.e. yields result close to the GOLD STANDARD test, and reflects the true progression of the disease to that level which the test values suggests
- **valid**, i.e. can distinguish between a positive and a negative reult (i.e. between diseased and non diseased) to a satisfactory degree.

Every diagnosis or decision is based on a test, be it the history, a symptom or sign, or some lab routines, or the history of an exposure to a risk factor. Such a diagnostic test must bear a few accreditations if it has to qualify for being used in clinical reasoning.

Reproducibility

It is the ability of a test to yield the same results over and over, irrespective of variations in basis of test, method or skill. No test is wholly reproducible. Suppose you have diagnosed a man to have pulmonary tuberculosis by examining sputum smears. A fellow physician may wholly disagree with you, because, when he did the examination, either

- patient became sputum negative (variation in the basis of the test)
- the physician used a different stain (variation of method)
- the physician made an error in spotting the AFB (variation of skill)

Because no test is wholly reproducible, the whole medical business continues to run on uncertainty.

Accuracy

A test is accurate when it yields results equal, on the average, to a GOLD STANDARD test

Suppose you devise method X to determine blood glucose. To qualify as accurate, this test has to yield results consistent with that of the Glucose Oxidase reaction.

Validity

This is the challenge: to distinguish truth from just another chance finding.

Put simply, let's say you attend some kids with complaint of cough, fever and mid dyspnea. You did some auscultation (the test) and find bronchial sounds in some of these kids, and label them as pneumonia. Next, your boss carries out a culture on their lung aspirate (the Gold Standard test) and disproves your findings. The final scenario is this.

	Diseased (Culture +ve)	Non diseased (Culture –ve)
+ve test (Bronchial sounds)	a	b
-ve test (Vesicular sound)	c	d

The **sensitivity** of the test is the probability of diseased people yielding positive result, $\frac{a}{a+c}$. The **specificity** is the reverse, the probability of healthy people to give negative result, $\frac{d}{b+d}$.

A test which is very non specific will yield too many false positive results; on the other hand, an insensitive test gives too many false negative results. The importance we attach to a positive or negative result is thus a function of the cut off value of the test; i.e. after which level we consider the results positive. Selecting a low cut off reduces the specificity of the test, and a high cut off dampens sensitivity [5]. In fact, the curve of sensitivity vs specificity looks like this

sensitivity specificity
Figure 16. Sensitivity versus specificity curve

The perils of using non qualified tests are many. Too many false positive results are a burden on the health infrastructure, cause useless anxiety to the victim, and once labeled – it's hard to get rid of the stigma. Again, too many false negative results fail the entire purpose of screening.

Predictive value

This is the most important aspect of a test from a clinical viewpoint. A positive predictive value is the probability of someone testing positive actually having the disease, i.e. $\frac{a}{a+b}$. Similarly, a negative predictive value is the probability of *not* having the disease in someone testing negative = $\frac{d}{c+d}$.

The positive predictive value is affected by the

- *prevalence* of the disease - in areas of high prevalence of some disease, tests for the disease are more valid
- *specificity* of the test

The usual challenge: determine post test probability from pre test knowledge

Bayesian statistics states that the positive predictive value is much higher if the disease in question is very prevalent. In another words, the usefulness of a test, apart from an inherent quality of itself (the sensitivity and specificity), *is also dependant upon how common the disease is*. Suppose the prevalence of a disease in a certain area is *p* in a population of η; this means, the chance of any individual of that area of having the disease is p (the pretest probability). Now we do the test and get a positive result. Given the specificity and sensitivity of the test, what is the probability that the individual is truly diseased?

Table 7. Contingency table for a diagnostic test

	Diseased	Non diseased	Total
+ve test	a	b	a+b
-ve test	c	d	c+d
Total	a+c	b+d	

Now, obviously, the number of total diseased people $a+c=p\eta$ and non diseased people $b+d=(1-p)\eta$. Again, the positive predictive value is (number of diseased people who tested +ve/ total number of people who tested +ve) = $\frac{a}{a+b}$.

Given the sensitivity of the test is *sn* and specificity is *sp* , we know that

$sn=\frac{a}{a+c}$ and $sp=\frac{d}{b+d}$

From these equations, calculate your heart out for the value of poitive preditive value $\frac{a}{a+b}$; you will find it to be

$$ppv = \frac{p \times sn}{(p \times sn) + (1 - sp)(1 - p)}$$

This is the positive predictive value of a test if the sensitivity, specificity and prevalence is given. There is, however, a more subtle way to achieve the same result. The **odds** of an individual having the disease before the test is, obviously, $\frac{p}{1-p}$ (see definition of Odds). Now, Baysesian statistics states that the odds (r) of having the disease after a positive test is

$$r = \frac{p}{1-p} \times \frac{sn}{1-sp}$$

Suppose post test probability (the same as positive predictive value) is *ppv*; then by definition of odds

$$\frac{ppv}{1-ppv} = r \text{ or } , ppv = \frac{r}{1+r}$$

This *ppv* is the post test probability or the positive preditive value (do the actual calculation on a real problem and you will find the result from the two methods to be identical). The factor $\frac{sensitivity}{1 - spec \text{ if } icity}$ is called the *likelihood ratio* of the test.

Hypothesis testing

I mentioned earlier that inferential statistics allows you to predict both the probability of an event and the amount of error of that prediction. This section is to determine that amount of error.

The GOLD STANDARD of hypothesis testing is of course, census; i.e. study the entire population.

Hypothesise first

The null hypothesis (H_0)

There are several ways to state the null hypothesis

- two events are unrelated
- two samples have similar distribution and mean
- … and so on…

The alternate hypothesis (H_a).

It states that the two events are related, or that two populations differ. Obviously, both the hypotheses can not be true simultaneously.

Errors

Type I error (α)

The error that happens when null hypothesis is *rejected* in spite of it being true (i.e. you **wrongly diagnose an association** between travelling to Goa and ulcerative colitis, or something equally bizzare). The probability of a type I error happening in a test is called **p value or α limit** of the test.

Type II error (β)

The error that happens when the null hypothesis is accepted in spite of it being false (you miss a true association)

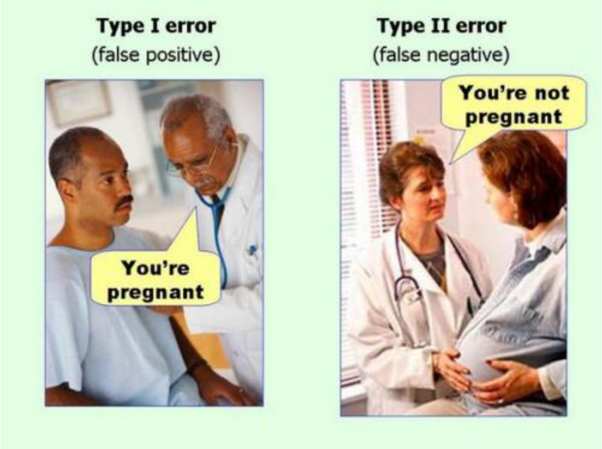


Figure 17. The two types of error (Image Courtesy: Wikipedia)

Power of a test

The power of a test, i.e. the probability that a test detects any difference that actually exist (avoids false negatives), is 1-β. It must be atleast 0.8 to qualify.

The power of a test (1-β) increases with

1. increasing α; setting a stricter (lower) α will reduce false positives, but increases false negatives (i.e. β)
2. if the difference between sample mean and population mean increases (i.e. the sample is more extreme)
3. reducing estimated standard error (thus increasing *t*, pushing it more to extremes towards rejection regions); the way to reduce standard error is, of course to increase sample size

Table 8. Relation between α and β

		Reality	
		H_0 true	H_0 false
Test result	H_0 accepted	CORRECT	β
	H_0 rejected	α	CORRECT

NOTE

How to determine power of a test

Let's exemplify these relations. Continuing with our example of shoe sizes

- mean show size of the class $\mu = 7.85$
- $\sigma = 1.19$.

We hypothesise (wrongly), that * $\mu_H = 8.5$. Thus the alternate hypothesis H_a is that * $\mu < 8.5$.

We have chosen α=0.05, which means that area to the left of z (one sided only) is 0.05; so critical value of z becomes -1.64 (one tailed, see the Z table).

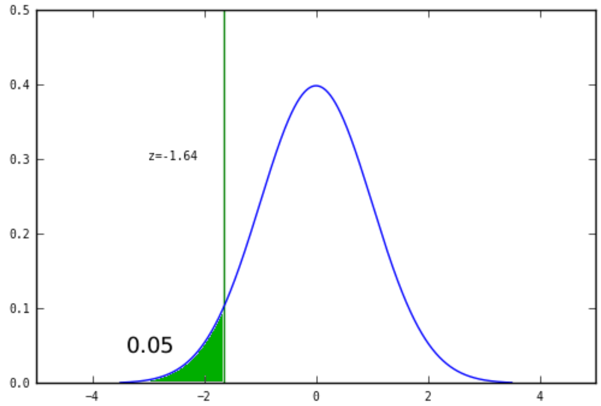


Figure 18. The area left of z=-1.64 is 0.05

Using central limit theorem, we find the relative deviate z of the distribution of $\overline{X}$ (i.e. the distribution of different sample means from the same population also makes a normal distribution). Now we sample 21 students. This distribution of sample means $\overline{X}$, has an standard error of mean = $\frac{\sigma}{\sqrt{n}}$, where n in sample size, and its mean is going to be approximately the population mean μ_H .

$$z = \frac{\overline{X} - \mu_H}{\frac{\sigma}{\sqrt{n}}}, \therefore \overline{X} = z \cdot \frac{\sigma}{\sqrt{n}} + \mu_H = -1.64 \cdot \frac{1.19}{\sqrt{21}} + 8.5 = 8.07$$

Translating to values of $\overline{X}$, if the mean of a representative sample is less than 8.07, the the null hypothesis is to be rejected, as it falls left to a z score of -1.64.

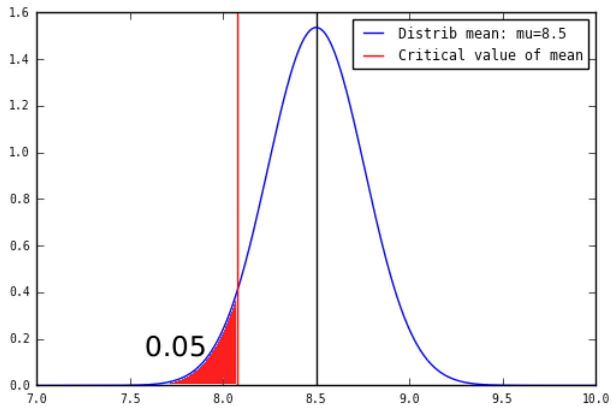


Figure 19. The probability of α (i.e. null hypothesis was rejected in spite of being true) is the area to the left of $\overline{X}$ = 8.07

However, the population mean mu = 7.8 (so the null hypothesis is actually false). If we are rejecting the null hypothesis only if $\overline{X}$ < 8.07, the interval 7.8 - 8.07 is in the rejection zone. But in the zone $\overline{X}$ > 8.07, **we will accept the null hypothesis in spite of it being false**.

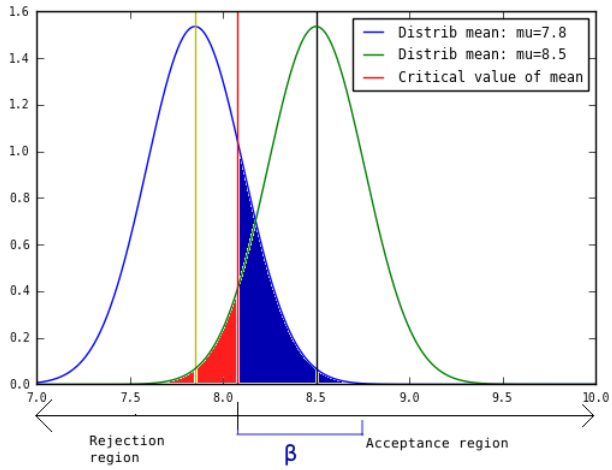


Figure 20. In the zone shaded in blue, the null hypothesis is *accepted* in spite of being false; thus its area is β

The critical value lies at z=0.049 of the blue curve, giving an area 0.48 to its right, which is the value of β.

Now increasing just the sample size, we can reduce β.

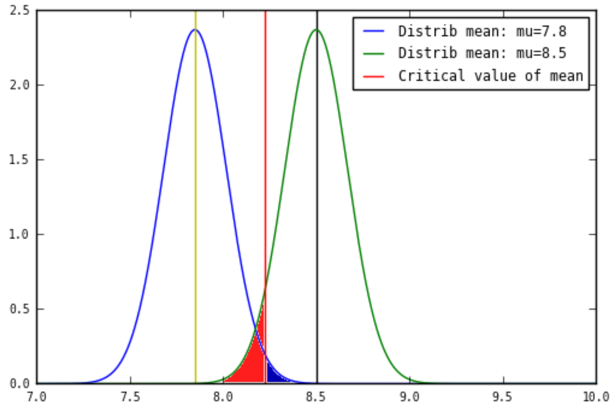


Figure 21. The plot with sample size = 50

Increasing α (i.e. making the test less stringent) will also reduce β.

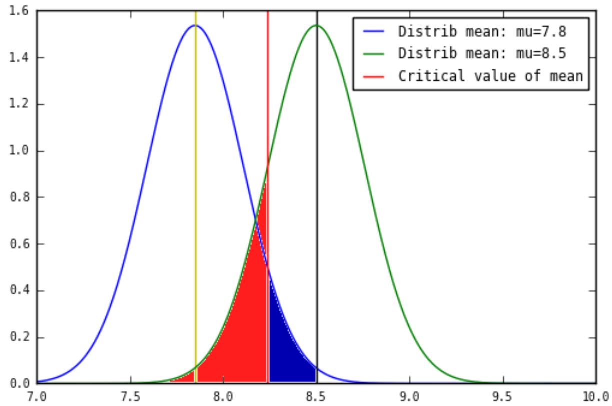


Figure 22. The same plot with α=0.15, and corresponding z=1.0, reduces β

β will also reduce if the difference in mean of the population and the sample mean is greater

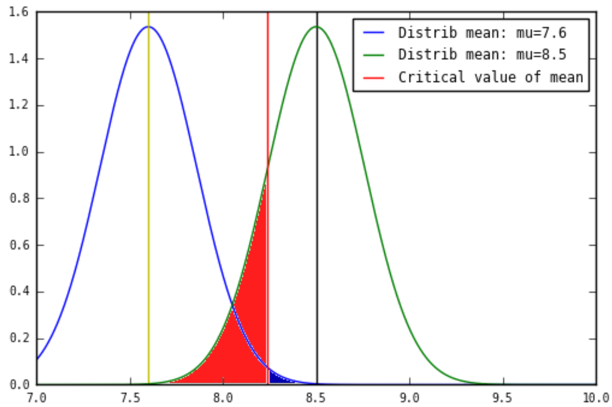


Figure 23. Plotting with population mean = 7.6

CAUTION

Why not choose a very low α?

A very low α makes it very difficult to reduce the null hypothesis, and β. Usually, in the fields of social sciences, we look forward to reduce α ('innocent until guilty'), even at the cost of rising β (acquitting criminals for lack of evidence).

Step two: Select decision criterion α

If the mean of our sample (or atleast, their *theoretical mean* or expectance) is far off from the population mean, we begin to suspect that the null hypothesis (i.e. mean of sample means = population mean, as per central limit theorem) might be false. If the probability that the sample was drawn from the population is less than a certain value α (usually 0.05) we reject the null hypothesis.

Recall that a sample which has a mean more than 2 standard deviations away from the population mean, has only 0.05 probability of belonging to the population. Thus is the the mean of our sample falls in this region, we begin to get uneasy, and tend to think that the population mean might be something else than the mean of sample means. However, that 5% chance lingers, and we can make a statement that **null hypothesis is false with 0.05 probability of α**, or simply, **null hypothesis rejected at p<0.05**

NOTE

Directional hypothesis and rejection region

We can always for a null hypothesis that $\mu = \mu_h$, in which case, we can disprove H_0 in either direction. Lets make it a little more tangible. Suppose, out of this population, we draw a sample and the sample mean turns out to be $\overline{X}$.

Assuming that this sample is representative of the population, we know that sample means form a normal distribution around the population mean. Thus, this particular sample mean is a member of a normal distribution, which is located at a certain distance $\overline{X} - \mu_h$ away from the mean μ_h . But this happens *if and only if* the population mean is actually the hypothesised μ_h . If the population mean is anything else (supposing $\mu_h + \varepsilon$), won't be normally distributed around it, but around $\mu_h + \varepsilon$. In fact, the probability that this sample actually belongs to the population is the height of the curve at $\overline{X}$. Samples with a mean *right* to this line have lesser chance (specifically, the red area beyond this line a) of belonging to this population; or to say the same in a roundabout manner, if a sample mean turns out to be at $\overline{X}$ or right, the null hypothesis (that $\mu = \mu_h$) has a probability a of being true.

But what if our sample turned out to have a mean $-\overline{X}$? We could argue that this time, the population mean is actually $\mu_h - \varepsilon$, and thus the sample with a mean $-\overline{X}$ is normally distributed around $\mu_h - \varepsilon$. Thus, we could reject the null hypothesis with a probability a , where *a* is the area to the *left* of $-\overline{X}$. (Of course, the rejection regions of both side are equal, since the normal distribution is symmetrical)

To summarise, in a **two sided test**, a sample mean $\overline{X}$ gives us *two areas of rejection*, to the right of $\overline{X}$, and to the left of $-\overline{X}$. If we have already selected an α, then the null hypothesis can be rejected only if $2a < \alpha$.

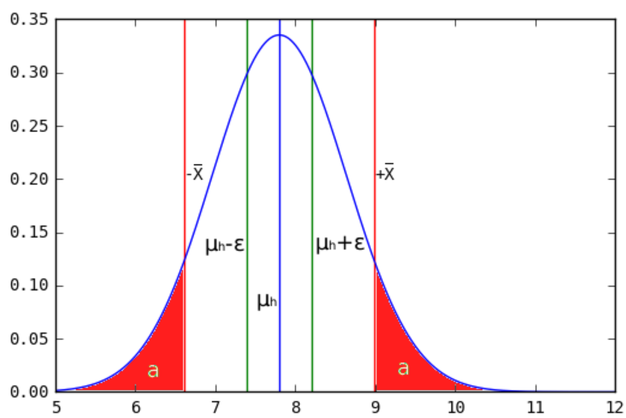


Figure 24. Two tailed rejection region: the combined area in both sides is *a + a = 2a*

Now, what if the null hypothesis was *one tailed*, i.e. $\mu \geq \mu_h$? In that case, H_a: $\mu < \mu_h$. Now the sample mean $-\overline{X}$ matters, because it is evidence that $\mu < \mu_h$, and can reject the null hypothesis provided it falls in the selected rejection region (defined by α). But the mean at the other end, $\overline{X}$, does not matter now? Why? A sample with mean $\overline{X}$ will only prove that the population mean might be $\mu > \mu_h$, which is *part of the null hypothesis*. Thus it is no use in disproving the null hypothesis.

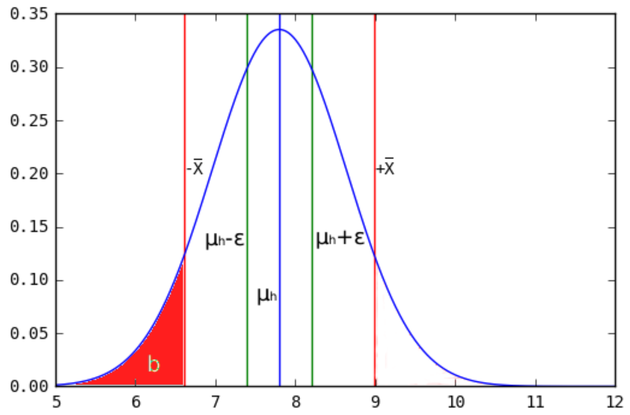


Figure 25. One tailed rejection region: the one tailed area *b*

If we have already selected an α, the area b alone must be less than α to reject the null hypothesis. Stated in another way, to prove that a sample mean differs significantly from the actual in one direction, it needs to be *really* far off. Using the same α=0.05, the area 0.05 in one side (to the left) corresponds to a z score of -1.5, while in two tailed score it is -2. Notice that the z-value is less extreme than two tailed score, thus **one tailed tests are more powerful than two tailed ones**. But on the converse, using one tailed tests, we would completely miss any action on the other side. If we are studying a prospective antihypertensive drug, using a one sided test, we would miss any effect of the drug that might *increase* blood pressure.

Step three: Select a test for statistical significance

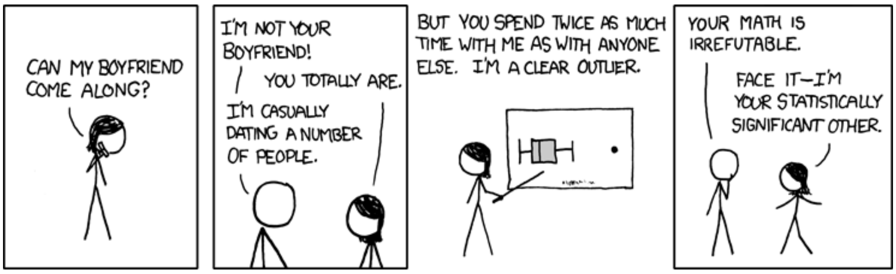


Figure 26. You can't deny mathematics[25]

The Z test

The Z test is useful only when

- the population is normally distributed
- the population mean and SD is known.

The crux of the matter is this: there exists a population with a hypothesised mean μ (null hypothesis) and σ (known), which is normally distributed. We pick a sample of size n with a mean $\overline{X}$ from this population, and define

$$z = \frac{\overline{X} - \mu}{\sigma_{\overline{X}}} = \frac{\overline{X} - \mu}{\frac{\sigma}{\sqrt{n}}}$$

Then, if and only if null hypothesis is true (i.e. the population mean is actually μ)

1. z will have a *standard* normal distribution
2. values of z outside 2 standard errors ($z < -2\sigma_{\overline{X}} \text{ or } z > 2\sigma_{\overline{X}}$) will be rare; specifically, probaility of such a value is 0.05

If $\overline{X}$ translates to a z score in this **rejection range**, we reject the null hypothesis.

Example 2. Testing null hypothesis with z test

Suppose from the class of students (mean 7.8, SD 1.19), we pick a sample of 20 with mean shoe size 8.0 and sample SD = 1.03. Is this proof enough (α=0.05) that the population mean is something else than 7.8?

Here

- $H_0 : \mu = 7.8$
- $H_a : \mu \neq 7.8$
- $\mu = 7.8$
- $\sigma = 1.19$
- n = 20
- s = 1.03

- $\overline{X} = 8.0$
- $\sigma_{\overline{X}} = \frac{\sigma}{\sqrt{n}} = 0.266$
- $\alpha = 0.05$

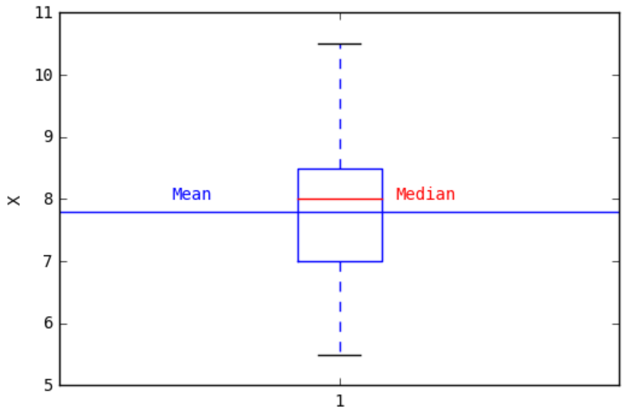


Figure 27. Box plot of population data

Thus, calculating z for the sample

$$z = \frac{\overline{X} - \mu}{\sigma_{\overline{X}}} = 0.75$$

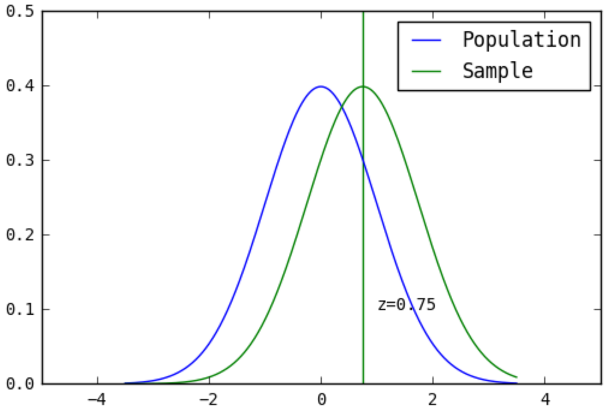


Figure 28. The sample is located at a Z score +0.75 from the population mean

The area beyond z-score 0.75 is 0.226. However, the alternate hypothesis is that population mean is *anything else* than 7.8. This is a two sided test, so the rejection region is in *both sides* of the mean = 0.226 * 2 = 0.452, which is much greater than α. Thus **null hypothesis can not be rejected at α=0.05**, i.e. this sample does not prove that the population mean is anything else than 7.8.

The t test

The t test is used when

- the population is normally distributed
  - if it is *not*, then the results will be distorted, but can be countered by increasing sample size
- mean and SD of the populatio are unknown

Hypothesis

- H_0 : The population mean is $\mu = 8.0$ (continuing with the shoe size example)

If this is true, then the variable t

$$t = \frac{\overline{X} - \mu_h}{\frac{s}{\sqrt{n}}}$$

(s = SD of a sample of size n)

will have the *t* distribution with degree of freedom (n-1). Lets say we choose 21 students from the class and get their shoe size.

CAUTION	Sample size for a t-test The t test is based on *sample* SD, thus does not work very well with sample sizes < 40. Over a sample size of 100, it becomes similar to z test.

Select critical levels for selected α

After you select α (say 0.05); select the t scores for the sample size you will be using, for a one tailed/ two tailed area (refer to t-table). For an α=0.05 and degree of freedom (21-1) = 20, the t value (two tailed) is 2.09.

Find the hypothetical population mean μ_h

If the null hypothesis is that the population mean is a certain μ_h , accept it for the time being. Continuing with our shoe size example, let us hypotehsise that the mean shoe size of the class is 8.

Sampling

Draw a random sample; calculate its SD s and estimated standard error $s_{\overline{X}}$. We draw a sample of 21 students, and find the mean $\overline{X}$ = 7.68 , SD s = 1.22, estimated standard error $s_{\overline{X}}$ = 0.28.

Calculate value of t

Let us find out where this sample lies among this population

$$t = \frac{\overline{X} - \mu}{s_{\overline{X}}} = \frac{7.38 - 8}{0.28} = -2.27$$

So the sample mean (7.38) lies 2.27 t-scores below the hypothesised population mean.

Compare the calculated and critical values of t

In the t distribution, an area outside -2.27 t-scores is 0.02 (two sided), which more than the selected α=0.05. So the null hypothesis must be accepted with a 0.02 *probability of error* (i.e. there is still a 2% chance that the null hypothesis population mean might actually be 8.0).

The paired t test

Suppose the mean shoe size in a class of 30 is 9.5. For a year, we apply growth hormone injections in each of the students and then measure their shoe sizes again. This time, we find the mean show size to be 10.3. Does this indicate a significant difference?

Like all statistical tests, we assume that there is, actually, no difference and the children grew up due to their natural growth spurt, not our hormone injections. To test this hypothesis, we must find the difference in shoe size of each individual student before and after injection, which we call d . Obviously, for 30 students, we will get 30 differnces ($d_1, d_2, d_3...d_{30}$). The summation of these differences ($\sum d$) divided by number of students (n), is the average difference or $\bar{d}$. The null hypothesis, states that the value of $\bar{d} = 0$ (i.e. there should no difference).

Now comes a crucial step. If these differences d_1, d_2 etc are plotted, they will form a distribution among themselves. Some students will have grown much more than others (high difference) and some not much (low difference). We could, in theory, deduce the *standard deviation of differences*, which is

$$s_d = \sqrt{\sum \frac{\left(d - \bar{d}\right)^2}{n-1}}$$

The t-value, in the paired t test is

$$t = \frac{\bar{d}}{\frac{s_d}{\sqrt{n-1}}}$$

This t-value is checked, in the standard t table, for a degree of freedom η - 1, and a p-value could be deduced. Note the central theme in paired t testing is that we use the mean and standard error of differences before and after intervention, rather than using actual values.

Example, if the heights of 10 students before and after are [10,12,14,11,13,12,15,11,10,9] and [14,13,16,15,12,10,17,15,16,15], then, their differences are [4,1,2,4,-1,-2,2,4,6,6], and mean difference 2.6, standard deviation

The unpaired (independent) t-test

While comparing variables of two categories

1. H^0 : We assume that there is no difference in shoe sizes at all between the two classes, i.e. $\mu_A = \mu_A$
2. DF : $n_1 - 1 + n_2 - 1 = 43$
3. Decision rule: Two sided alpha level 0.05, so one sided alpha 0.025, t = -2.0167 and 2.0167; if t is outside this range, difference is significant
4. Calculate t

$$\sigma = \frac{\sum_{i=1}^{n_1} \left(x_i - \bar{x}_1\right)^2 + \sum_{i=1}^{n_2} \left(x_i - \bar{x}_2\right)^2}{DF1 + DF2}$$

Because $\sigma_1^2 = \sum_{i=1}^{n_1} \frac{\left(x_i - \bar{x}_1\right)^2}{n_1}$, it can be rewritten as

$$\sigma = \frac{n_1 \sigma_1^{+} n_2 \sigma_2^2}{n_1 - 1 + n_2 - 1}$$

where n_1, n_2 are the number of students in two classes, respectively, and σ_1, σ_2 are the standard deviations of shoe sizes in those classes. The t-value, in the unpaired t test, is

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sigma \cdot \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

Analysis of variance

Let

1. Number of groups = k
2. Individual observaions = x_{ij}
3. Observations in each group = n_i
4. Overall observations = n
5. Mean of a particular group = $\overline{X}_i$
6. Overall mean = $\overline{X}$
7. SD of a group = s_i

Then, the Fischer Snedecor ratio F = variability between groups / vaiability within groups

(note that, F is a ratio of two chi square variables divided by their DF, where chi is a standard normal distribution)

$$F = \frac{\frac{\sum_{i=1}^{k} n_i \left(X_{ij} - \overline{X}_i\right)^2}{k-1}}{\sum_{i=1}^{k} \sum_{j=1}^{n_i} \frac{\left(X_{ij} - \overline{X}_i\right)^2}{n-k}}$$

The chi square test for independence

For a contingency table like this

	Acromegalics	Normal
Shoe size > 11	a	b
Shoe size < 11	c	d

The null hypothesis: We assume that shoe size is no indicator of acromegaly. Then the ones with small shoes are expected to have the same rate of acromegaly as those with large shoes (and that should be the prevalence of acromegaly in whole population in general).

The incidence of acromegaly in whole table is

$$\frac{a+c}{a+b+c+d}$$

Thus *expected* numbers in the four cells are calculated likewise, i.e. expected number in cell 'a' is total number of students with shoe size > 11 × incidence of acromegaly in whole population

$$(a+b) \times \frac{a+c}{a+b+c+d}$$

Similarly, expected number in cell b = Total number of students with shoe size < 11 × incidence of 'no acromegaly' (normal children)

$$(a+b) \times \frac{b+d}{a+b+c+d}$$

χ^2 for each cell = (observed number - expected number)^2 /expected number. The summation of values of χ^2 is calculated. Now the degree of freedom of a table is (rows-1)(columns-1). The probability that matches the χ^2 value we just got and the degree of freedom in the χ^2 table, and a p value is obtained.

Regression Models

For a dataset of two variable X and Y, the standard deviations

$$S_x = \sqrt{\frac{1}{n-1}\left(\sum_{i=1}^{n} \left(X_i - \overline{X}\right)\right)^2} \quad S_y = \sqrt{\frac{1}{n-1}\left(\sum_{i=1}^{n} \left(Y_i - \overline{Y}\right)\right)^2}$$

The covariance

$$Cov(X,Y) = \frac{1}{n-1}\sum_{i=1}^{n} \left(X_i - \overline{X}\right)\left(Y_i - \overline{Y}\right)$$

and the correlation

$$r(X,Y) = \frac{Cov(X,Y)}{S_x S_y}$$

This last quantity is a unitless variable between -1 and 1, denoting strength of relationship between X and Y. Now comes the fun part: for a line Y = mX + C that best fits through the XY plot (i.e. minimises the sum of square distances $\sum_{i=1}^{n} \left(Y_i - (m \cdot X_i + C)\right)^2$, the values of m and C are

$$m = r(Y,X)\frac{S_y}{S_x} \quad C = \overline{Y} - m\overline{X}$$

Obviously, because the data has been *normalized* by subtracting the means, this line passes through $\overline{Y}$ and $\overline{X}$. Also, note that if you reverse axis (i.e. X versus Y), you will have a new line.

Index

1. After Thomas Bayes
2. Actually, 1.96
3. Think about it. Possibly, this is the most important statement of inferential statistics
4. A term coined by 'Student', a pen-name taken by W A Gossett
5. If while screening for diabetes, you select a fasting sugar cut off of 80, of course you will detect all diabetics, but in addition, so many normal people who range over 80 mg/dL will be caught delinquent (loss of specificity). Think yourself what may happen if you select a cut off 160 mg/dL.

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