p-values, Power and Sample Size

JH Notes: Inference about a Population Mean (μ)

Sahir Bhatnagar and James Hanley

EPIB 607
Department of Epidemiology, Biostatistics, and Occupational Health
McGill University

sahir.bhatnagar@mcgill.ca
https://sahirbhatnagar.com/EPIB607/

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p-values

p-values and statistical tests

Definition 1 (p-value)

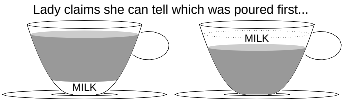
*A **probability concerning the observed data**, calculated under a **Null Hypothesis** assumption, i.e., assuming that the only factor operating is sampling or measurement variation.*

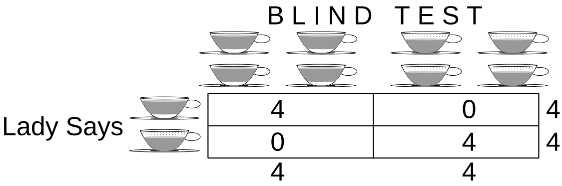
Use: To assess the evidence provided by the sample data in relation to a pre-specified claim or 'hypothesis' concerning some parameter(s) or data-generating process.

Basis: As with a confidence interval, it makes use of the concept of a *distribution*.

Caution: A p-value is NOT the probability that the null 'hypothesis' is true

Example 1 – from *Design of Experiments*, by R.A. Fisher





Null Hypothesis (H_{null}): she can not tell them apart, i.e., just guessing.

Alternative Hypothesis (H_{alt}): she can.

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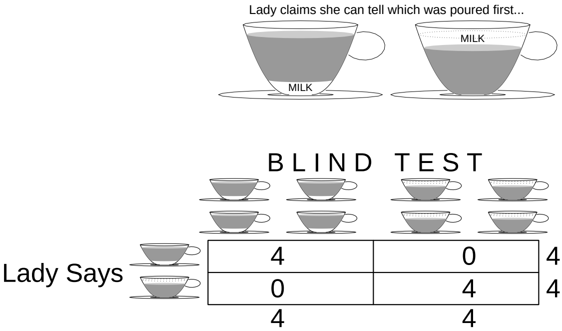

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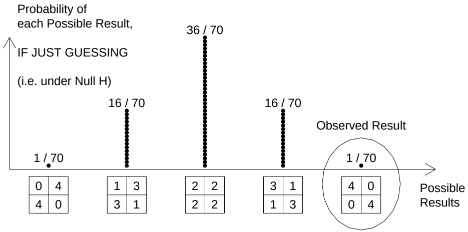
The evidence provided by the test

- Rank possible test results by degree of evidence against H_{null}.
- "*p*-value" is the probability, calculated under null hypothesis, of observing a result as extreme as, or more extreme than, the one that was obtained/observed.



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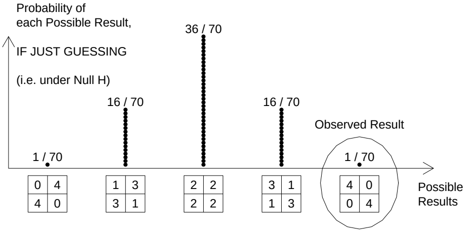

In this example, observed result is the most extreme, so

$$P_{value} = \text{Prob[correctly identifying all 4, IF merely guessing]} = 1/70 = 0.014.$$

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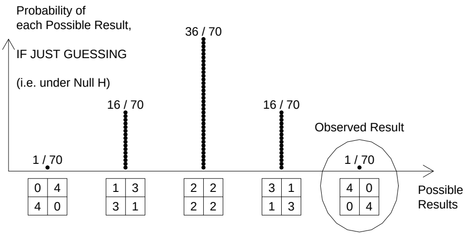

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$P_{value} = \text{Prob[correctly identifying all 4, IF merely guessing]} = 1/70 = 0.014.$

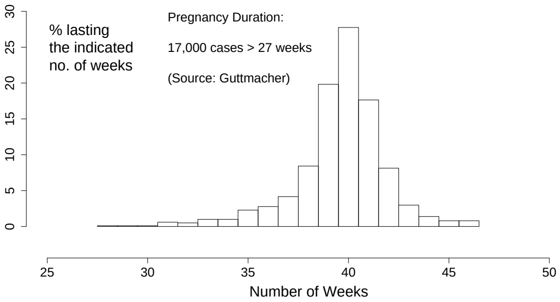
- Interpretation of such data often rather simplistic, as if these *data alone* should *decide*: i.e. if $P_{value} < 0.05$, we ~~'reject' H~~$_{null}$; if $P_{value} > 0.05$, we don't (or worse, we ~~'accept' H~~$_{null}$). Avoid such simplistic 'conclusions'.

Example 2 – Preston-Jones vs. Preston-Jones, English House of Lords, 1949

Divorce case:

- Sole evidence of adultery was that a baby was born almost 50 weeks after husband had gone abroad on military service. The appeal failed.
- To quote the court:
  - *"The appeal judges agreed that the limit of credibility had to be drawn somewhere, but on medical evidence 349 (days) while improbable, was scientifically possible."*

Example 2 – data collected from the 1970s



- *p*-value, calculated under “Null” assumption that husband was father, = ‘tail area’ or probability corresponding to an observation of ‘50 or more weeks’ in above distribution
- Same system used to report how extreme a lab value is – are told where value is located in distribution of values from healthy (reference) population.

p-value via the Normal (Gaussian) distribution.

- When judging extremeness of a sample mean or proportion (or difference between 2 sample means or proportions) calculated from an amount of information that is sufficient for the Central Limit Theorem to apply, one can use Gaussian distribution to readily obtain the p-value.
- Calculate how many standard errors of the statistic, $SE_{statistic}$, the statistic is from where null hypothesis states true value should be. This "number of SE's" is in this situation referred to as a 'Z_{value}.'

  $$Z_{value} = \frac{statistic - \text{its expected value under } H_{null}}{SE_{statistic}}.$$

  p-value can then be obtained by determining what % of values in a Normal distribution are as extreme or more extreme than this Z_{value}.
- If n is small enough that value of $SE_{statistic}$, is itself subject to some uncertainty, one would instead refer the "number of SE's" to a more appropriate reference distribution, such as Student's t- distribution.

More about the p-value

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$$
\begin{aligned}
p_{value} &= P(\text{this or more extreme data}|H_0) \\
&\neq P(H_0|\text{this or more extreme data}).
\end{aligned}
$$

- Statistical tests are often coded as statistically significant or not according to whether results are extreme or not with respect to a reference (null) distribution. But a test result is just one piece of data, and needs to be considered *along with rest of evidence* before coming to a 'conclusion.'
- **Likewise with statistical 'tests': the p-value is just one more piece of *evidence*, hardly enough to 'conclude' anything**.

The prosecutor's fallacy [1]

- A criminal leaves fifty thousand blood cells at the scene of a crime which is just barely enough to stain a handkerchief.
- A forensic scientist extracts DNA from the sample to create a 'DNA fingerprint'.
- Its pattern resembles that of a suspect.
- The scientist calculates that the chance of a match between the sample and a random member of the public is one in a million. How incriminating is this evidence?

[1] Who's the DNA fingerprinting pointing at? New Scientist, 1994.01.29, 51-52.

The prosecutor’s fallacy

- Statistician Peter Donnelly opened a new area of debate, remarking that
  - Forensic evidence answers the question: “What is the probability that the defendant’s DNA profile matches that of the crime sample, assuming that the defendant is innocent?”
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  - While the jury must try to answer the question: "What is the probability that the defendant is innocent, assuming that the DNA profiles of the defendant and the crime sample match?"
- The error in mixing up these two probabilities is called "**the prosecutor's fallacy**," and it is suggested that newspapers regularly make this error.
- Donnelly's testimony convinced the judges that the case before them involved an example of this and they ordered a retrial.

The prosecutor's fallacy in a game of poker

- Imagine the judges were playing a game of poker with the Archbishop of Canterbury.
- If the Archbishop were to deal a royal flush on the first hand, one might suspect him of cheating.
- The probability of the Archbishop dealing a royal flush on any one hand, assuming he is an honest card player, is about 1 in 70 000.
- But if the judges were asked whether the Archbishop was honest, given that he had just dealt a royal flush, they would be likely to quote a probability greater than 1 in 70 000.

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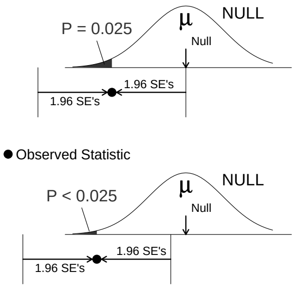
- But if the judges were asked whether the Archbishop was honest, given that he had just dealt a royal flush, they would be likely to quote a probability greater than 1 in 70 000.
- The first probability is analogous to the answer of the forensic scientist’s question, and the second probability analogous to the answer of the jury’s question.

(Intimate) Relationship between p-value and CI



- (Upper graph) If upper limit of 95% CI *just touches* null value, then the 2 sided p-value is 0.05 (or 1 sided p-value is 0.025).

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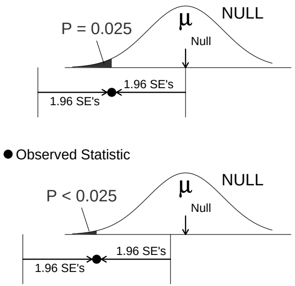

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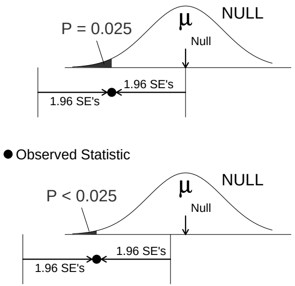


- (Upper graph) If upper limit of 95% CI *just touches* null value, then the 2 sided *p*-value is 0.05 (or 1 sided *p*-value is 0.025).
- (Lower graph) If upper limit *excludes* null value, then the 2 sided *p*-value is less than 0.05 (or 1 sided *p*-value is less than 0.025).
- (Graph not shown) If CI *includes* null value, then the 2-sided *p*-value is greater than (the conventional) 0.05, and thus observed statistic is “not statistically significantly different” from hypothesized null value.

Don't be overly-impressed by *p*-values

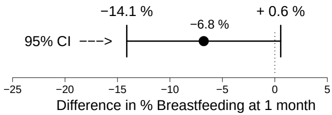
- *p*-values and 'significance tests' widely misunderstood and misused.
- Very large or very small *n*'s can influence what is or is not 'statistically significant.'
- Use CI's instead.
- *Pre study* power calculations (the chance that results will be 'statistically significant', as a function of the true underlying difference) of some help.
- *post-study* (i.e., *after the data have 'spoken'*), a CI is much more relevant, as it focuses on magnitude & precision, not on a probability calculated under H_{null}.

Applications

Do infant formula samples ↓ dur$^{n.}$ of breastfeeding?[2]

Randomized Clinical Trial (RCT) which withheld free formula samples [given by baby-food companies to breast-feeding mothers leaving Montreal General Hospital with their newborn infants] from a random half of those studied.

At 1 month	Mothers given sample	not given sample	Total	**Conclusion...**
Still Breast feeding	175 (*77%*)	182 (*84%*)	357 (80.4%)	P=0.07. So, ... the difference is "Not Statistically Significant" at 0.05 level
Not Breast feeding	52	35	87	
Total	227	217	444	



[2]Bergevin Y, Dougherty C, Kramer MS. Lancet. 1983 1(8334):1148-51

Messages

- no matter whether the *p*-value is “statistically significant” or not, always look at the location and width of the confidence interval. it gives you a better and more complete indication of the magnitude of the effect and of the precision with which it was measured.
- this is an example of an **inconclusive negative** study, since it has **insufficient precision** (“resolving power”) **to distinguish** between two important possibilities – **no harm**, and what authoroties would consider a **substantial harm: a reduction of 10 percentage points** in breastfeeding rates .
- “**statistically** significant“ and “**clinically**-” (or “**public health**-”) significant are different concepts.
- (message from 1st author:) plan to have **enough statistical power**. his study had only 50% power to detect a difference of 10 percentage points)

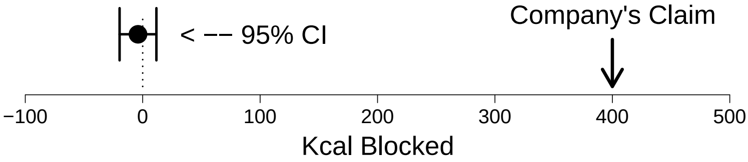
Do starch blockers really block calorie absorption?

Starch blockers – their effect on calorie absorption from a high-starch meal. Bo-Linn GW. et al New Eng J Med. 307(23):1413-6, 1982 Dec 2

- Known for more than 25 years that certain plant foods, e.g., kidney beans & wheat, contain a substance that inhibits activity of salivary and pancreatic amylase.
- More recently, this antiamylase has been purified and marketed for use in weight control under generic name "starch blockers."
- Although this approach to weight control is highly popular, it has never been shown whether starch-blocker tablets actually reduce absorption of calories from starch.
- Using a one-day calorie-balance technique and a high starch (100 g) meal (spaghetti, tomato sauce, and bread), we measured excretion of fecal calories after $n = 5$ normal subjects in a cross-over trial had taken either placebo or starch-blocker tablets.
- If the starch-blocker tablets had prevented the digestion of starch, fecal calorie excretion should have increased by 400 kcal.

Do starch blockers really block calorie absorption?

- However, fecal calorie excretion was same on the 2 test days (mean $\pm$ S.E.M., 80 $\pm$ 4 as compared with 78 $\pm$ 2).



- We conclude that starch blocker tablets do not inhibit the digestion and absorption of starch calories in human beings.
- EFFECT IS MINISCULE (AND ESTIMATE QUITE PRECISE) AND VERY FAR FROM COMPANY'S CLAIM !!!
- A '**DEFINITIVELY NEGATIVE**' STUDY.

Summary

SUMMARY - 1

- Confidence intervals preferable to *p*-values, since they are expressed in terms of (comparative) parameter of interest; they allow us to judge magnitude and its precision, and help us in ‘ruling in / out’ certain parameter values.
- A ‘statistically significant’ difference does not necessarily imply a clinically important difference.
- A ‘not-statistically-significant’ difference does not necessarily imply that we have ruled out a clinically important difference.

SUMMARY - 2

- Precise estimates distinguish b/w that which – if it were true – would be important and that which – if it were true – would not. 'n' an important determinant of precision.
- A lab value in upper 1% of reference distribution (of values derived from people without known diseases/conditions) does not mean that there is a 1% chance that person in whom it was measured is healthy; i.e., it doesn't mean that there's a 99% chance that the person in whom it was measured does have some disease/condition.
- Likewise, p-value $\neq$ probability that null hypothesis is true.
- The fact that

$$\textit{Prob}[\textit{the data} \mid \textit{Healthy}] \text{ is small [or large]}$$

does not necessarily mean that

$$\textit{Prob}[\textit{Healthy} \mid \textit{the data}] \text{ is small [or large]}$$

SUMMARY - 3

- Ultimately, *p*-values, CI's and other evidence from a study need to be combined with other information bearing on parameter or process.
- Don't treat any one study as last word on the topic.

Power and Sample Size

Is this milk watered down?[3]

- A cheese maker buys milk from several suppliers. It suspects that some suppliers are adding water to their milk to increase their profits.
- Excess water can be detected by measuring the freezing point of the liquid.

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- Excess water can be detected by measuring the freezing point of the liquid.
- The freezing temperature of natural milk varies according to a Gaussian distribution, with mean $\mu = -0.540°$ Celsius (C) and standard deviation $\sigma = 0.008°$C.
- Added water raises the freezing temperature toward $0°$C, the freezing point of water.

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- The laboratory manager measures the freezing temperature of five consecutive lots of 'milk' from one supplier. The mean of these 5 measurements is -0.533°C.
- Question: Is this good evidence that the producer is adding water to the milk?

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  - $H_a : \mu > -0.540$°C
- Which test should we use and why?

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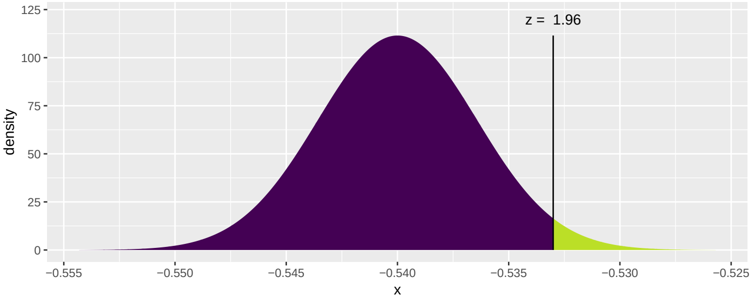
  - $H_0 : \mu = -0.540°\text{C}$
  - $H_a : \mu > -0.540°\text{C}$

- Which test should we use and why?

```
mosaic::xpnorm(q = -0.533, mean = -0.540, sd = 0.008/sqrt(5))
##
## If X ~ N(-0.54, 0.003578), then
## P(X <= -0.533) = P(Z <= 1.957) = 0.9748
## P(X >  -0.533) = P(Z >  1.957) = 0.0252
##
```



Testing using the p-value

Appropriate wordings to accompany $p = 0.0252$:

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- If we test samples of pure milk, only 2.6% of test results would be this high or higher.

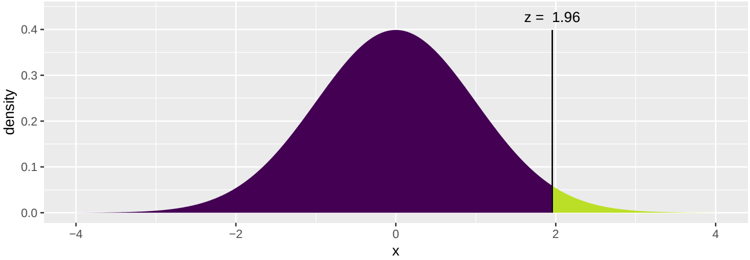
- IF the only factor operating here were sampling variation, only 2.6% of test results on pure milk would be this high or higher.

Test using a Z statistic

- $H_0 : \mu = -0.540°\text{C}$ $\qquad$ $H_a : \mu > -0.540°\text{C}$
- We can also standardize our observed mean and calculate the p-value under a $\mathcal{N}(0, 1)$

```
SEM <- 0.008/sqrt(5)
z_stat <- (-0.533 - (-0.540)) / SEM
mosaic::xpnorm(q = z_stat, mean = 0, sd = 1)
```

```
##
## If X ~ N(0, 1), then
## P(X <= 1.957) = P(Z <= 1.957) = 0.9748
## P(X >  1.957) = P(Z >  1.957) = 0.0252
##
```

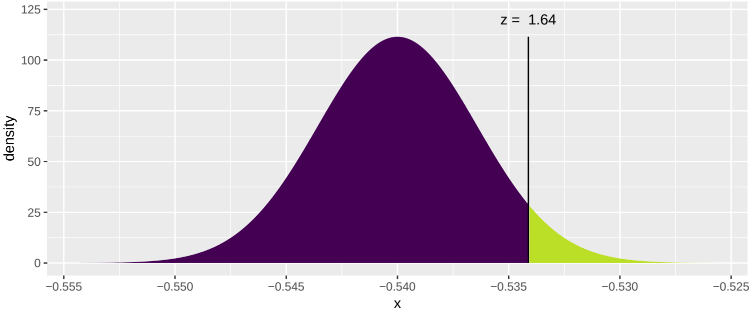


Test using critical values

- An observed mean freezing temperature greater than -0.5341 rejects the null hypothesis:

```
mosaic::xqnorm(p = 0.95, mean = -0.540, sd = 0.008/sqrt(5))
```

```
##
## If X ~ N(-0.54, 0.003577709), then
## P(X <= -0.5341152) = 0.95
## P(X >  -0.5341152) = 0.05
##
```




```
## [1] -0.5341152
```

Test using critical values

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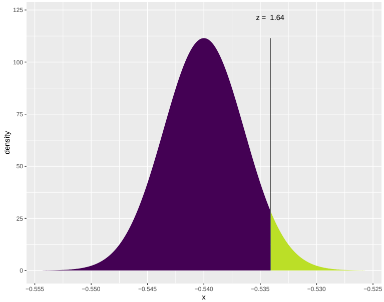

Fig.: critical value under the null distribution

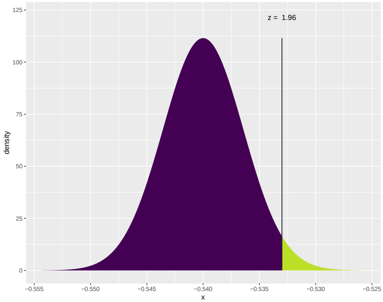

Fig.: test statistic under the null distribution

Thus we reject H_0 at $\alpha = 0.05$.

Type I and II errors

What does it mean to reject H_0 at level α?

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- It means that, if H_0 were true and the procedure (sampling data, performing the significance test) were repeated many times, the testing procedure would reject H_0 $\alpha 100\%$ of the time.

		Truth about the population	
		H_0 true	H_a true
Decision based on sample	Reject H_0	Type I error	Correct decision
	Accept H_0	Correct decision	Type II error

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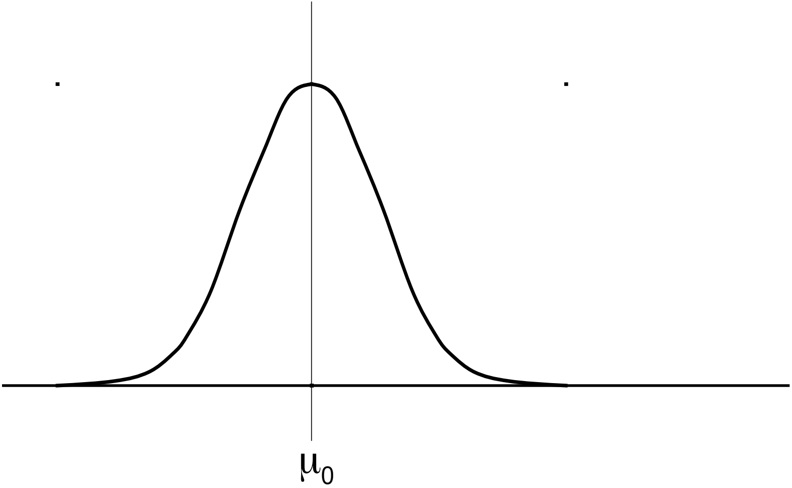
The Type I error is the significance level of the test, α, which is often set to 0.05.

As we will see in a moment, the Type II error, β, is determined by the sample size and the chosen Type I error rate/significance level. (Therefore, with α fixed at, say 0.05, the only way to reduce β is to increase n or decrease s.)

Type I and II errors

Distribution of $\overline{y}$ under
the null hypothesis:



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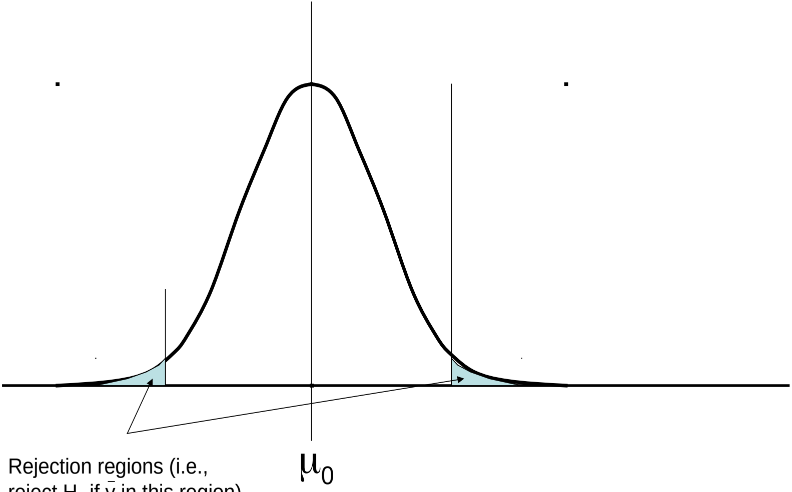
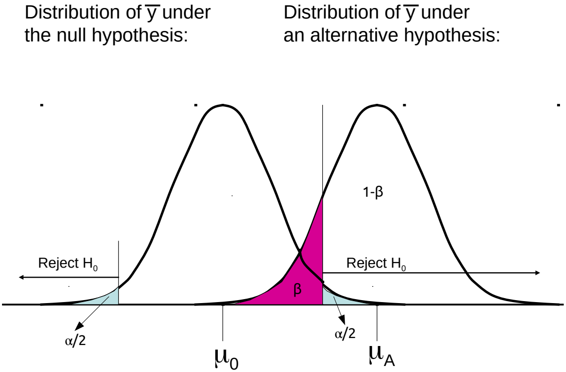


Rejection regions (i.e., reject H_0 if $\bar{y}$ in this region)
Each tail is equal to $\alpha/2$

Type I and II errors



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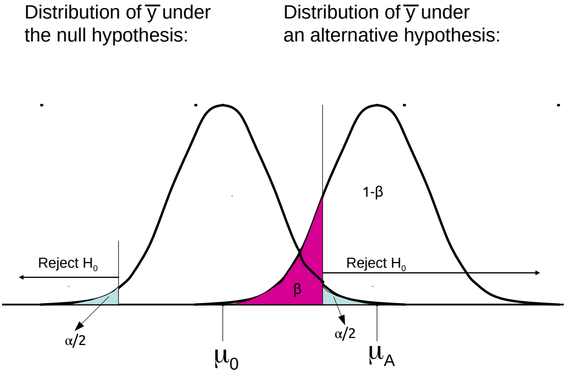
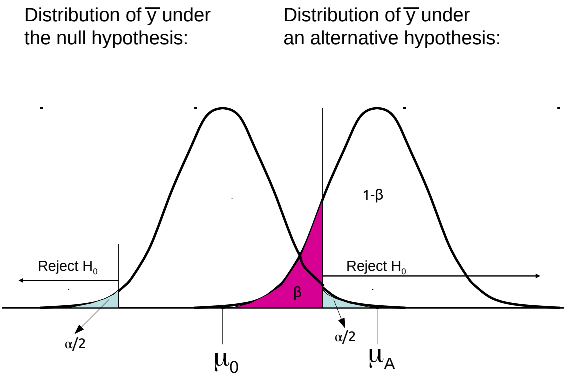
- The blue area represents the Type I error – the probability of rejecting H_0 **if H_0 is true**.



Type I and II errors

- The blue area represents the Type I error – the probability of rejecting H_0 **if** H_0 **is true**.
- The purple area represents the Type II error – the probability of *not* rejecting H_0 **if** H_A **is in fact true** (and therefore H_0 should be rejected).



Type I and II errors

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Type I and II errors

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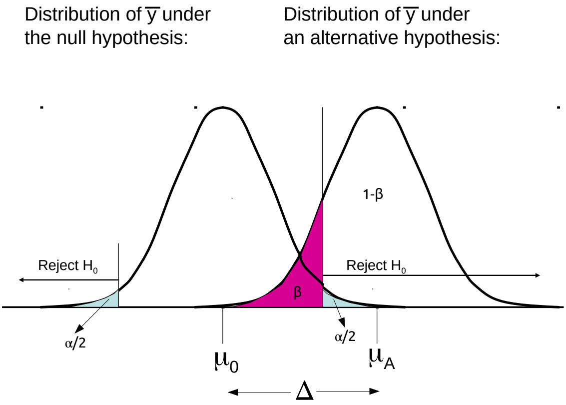
- The distance between μ_0 and the true value of μ (in our previous slide we called this μ_A) will affect the Type II error. This distance is denoted as Δ.



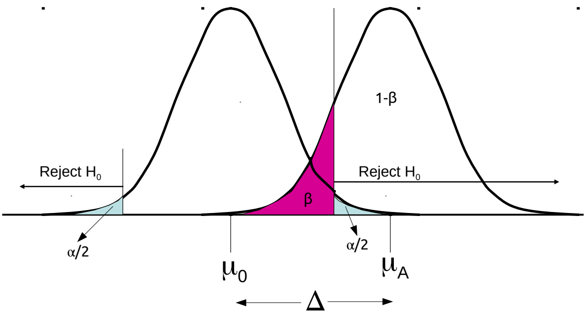
Power = $1 - \beta$

Definition 2 (Power = $1 - \beta$)

The probability that a fixed level α significance test will reject H_0 when a particular alternative value of the parameter is true is called the ***power*** *of the test to detect the alternative.*

Distribution of $\overline{y}$ under the null hypothesis:

Distribution of $\overline{y}$ under an alternative hypothesis:



Power and Sample Size: 3 questions

1. How much water a supplier could add to the milk before they have a 10% , 50%, 80% chance of getting caught, i.e., of the buyer detecting the cheating ?

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Power and Sample Size: 3 questions

1. How much water a supplier could add to the milk before they have a 10% , 50%, 80% chance of getting caught, i.e., of the buyer detecting the cheating ?
2. Assume a 99:1 mix of milk and water. What are the chances of detecting cheating if the buyer uses samples n=10, 15 or 20 rather than just 5 measurements?
3. At what n does the chance of detecting cheating reach 80%? (*a commonly used, but arbitrary, criterion used in sample-size planning by investigators seeking funding for their proposed research*)

How much water a supplier could add to the milk before they have a 10% , 50%, 80% chance of getting caught, i.e., of the buyer detecting the cheating ?

Statistical Power: the chance of getting caught

- We want to know how much water a farmer could add to the milk before they have a 10% , 50%, 80% chance of getting caught (of the buyer detecting the cheating).

- Assume the buyer continues to use an $n = 5$, and the same $\sigma = 0.008$°C, and bases the boundary for rejecting/accepting the product on a $\alpha = 0.05$, and a 1-sided test which translates to the buyer setting the cutoff at

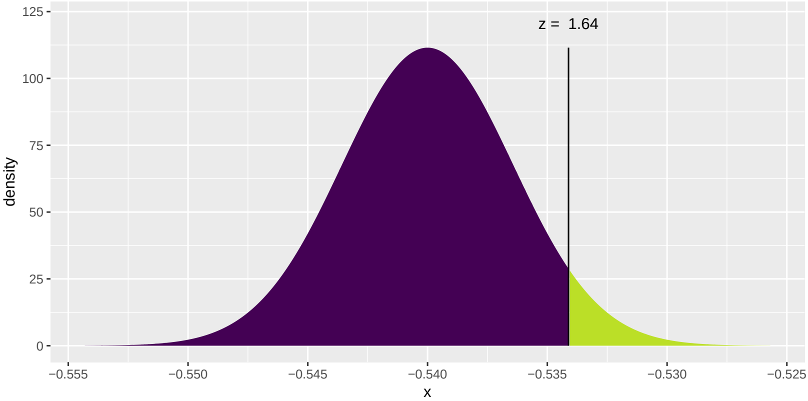
$$-0.540 + 1.645 \times 0.008/\sqrt{5} = -0.534°\mathrm{C}.$$

- This is equivalent to `qnorm(p = 0.95, mean = -0.540, sd = 0.008/sqrt(5))`

The cutoff at $\alpha = 0.05$

- $-0.540 + 1.645 \times 0.008/\sqrt{5} = -0.534°\mathrm{C}.$

```
mosaic::xqnorm(p = 0.95, mean = -0.540, sd = 0.008/sqrt(5))
```




```
## [1] -0.5341152
```

Statistical Power

- Assume that mixtures of M% milk and W% water would freeze at a mean of

$$\mu_{mixture} = (M/100) \times -0.545^{\circ}C + (W/100) \times 0^{\circ}C$$

and that the σ would remain unchanged.

Statistical Power

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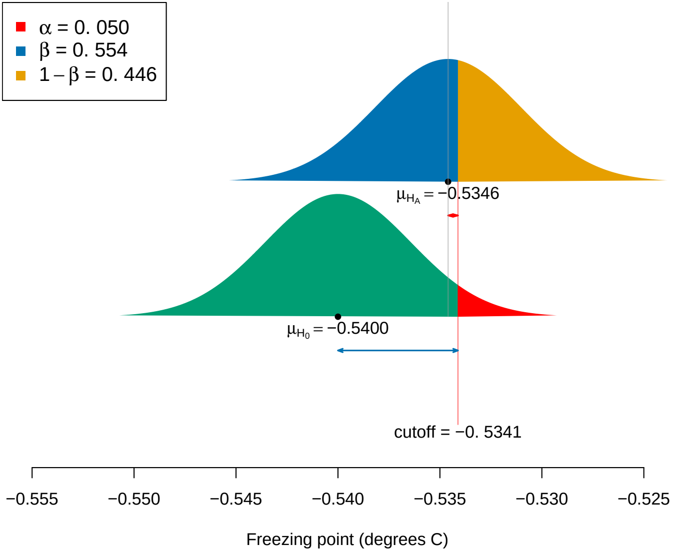
$$\mu_{mixture} = (M/100) \times -0.545°C + (W/100) \times 0°C$$

  and that the σ would remain unchanged.

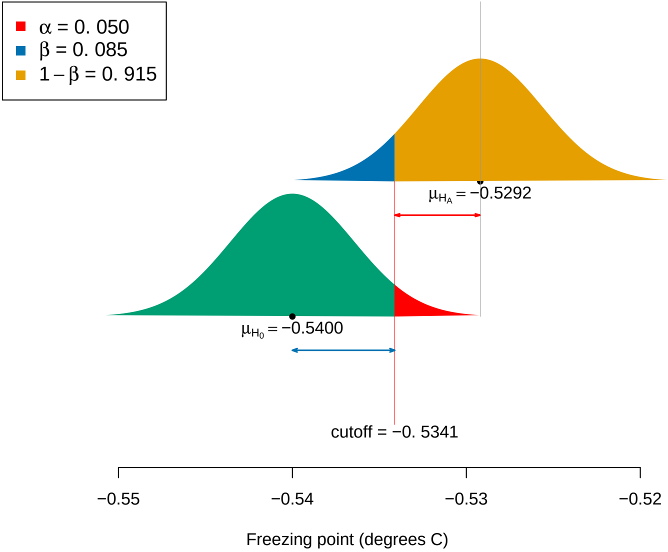
- Thus, mixtures of 99% milk and 1% water would freeze at a mean of $\mu = (99/100) \times -0.540°C + (1/100) \times 0°C = -0.5346°C$.

% milk	% water	mean (μ)
99	1	-0.5346°C
98	2	-0.5292°C
97	3	-0.5238°C

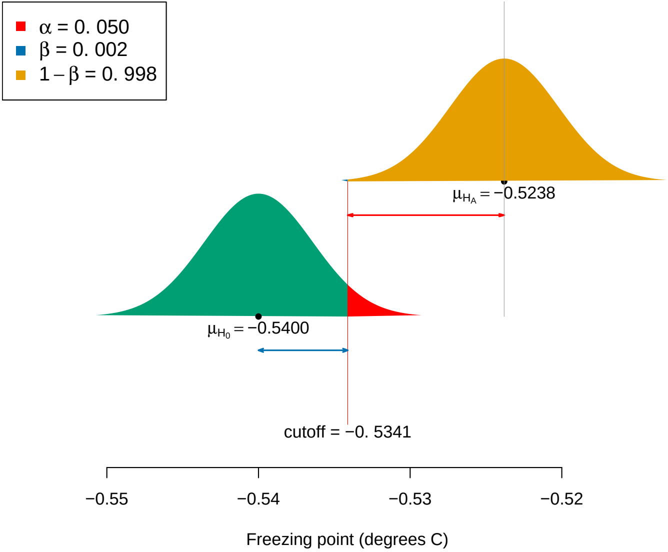
If the supplier added 1% water to the milk

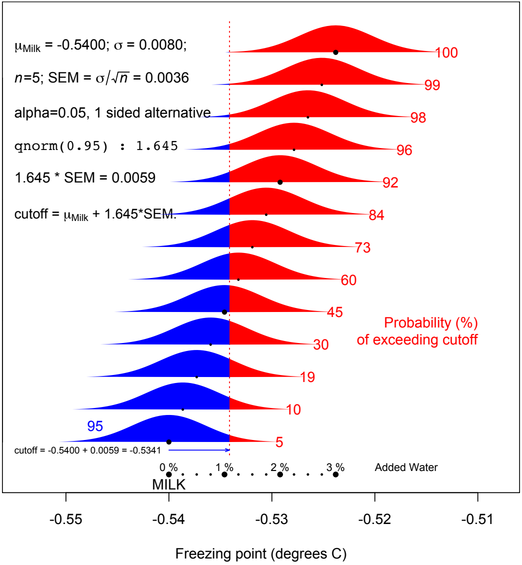


If the supplier added 2% water to the milk



If the supplier added 3% water to the milk





The probabilities in red were calculated using the formula:

```
stats::pnorm(cutoff, mean = mu.mixture, sd = SEM,
lower.tail=FALSE)
```

Statistical Power: the chance of getting caught

- The calculations shown at the left in the figure on the previous slide are used to set the cutoff; it is based on the null distribution shown at the bottom.

Statistical Power: the chance of getting caught

- The calculations shown at the left in the figure on the previous slide are used to set the cutoff; it is based on the <u>null</u> distribution shown at the bottom.
- Clearly the bigger the signal (the 'Δ') the more chance the test will 'raise the red flag.' It is 92% when it is a 98:2, and virtually 100% when it is a 97:3 mix.

Assume a 99:1 mix of milk and water. What are the chances of detecting cheating if the buyer uses samples n=10, 15 or 20 rather than just 5 measurements?

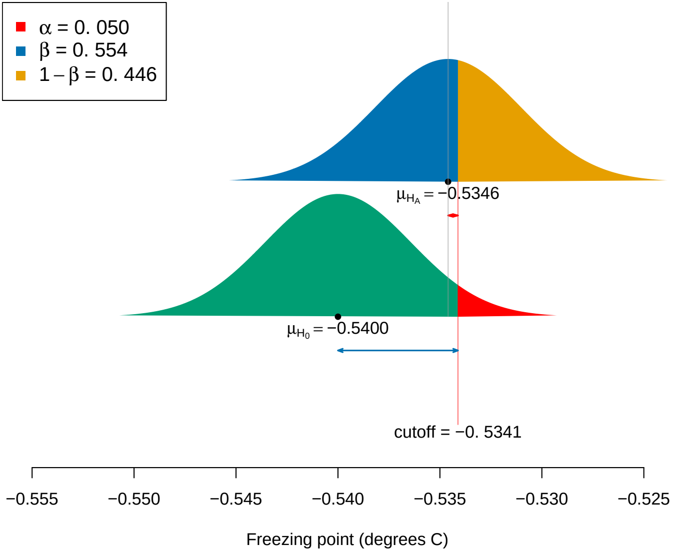
Power as a function of sample size

- Suppose even a 1% added water is serious, and worth detecting.
- Clearly, from the previous Figure, and again at the bottom row of the following Figure, one has only a 45% chance of detecting it: there is a **large overlap between the sampling distributions under the null (100% Milk) and the mixture (99% milk, 1% water) scenarios**.

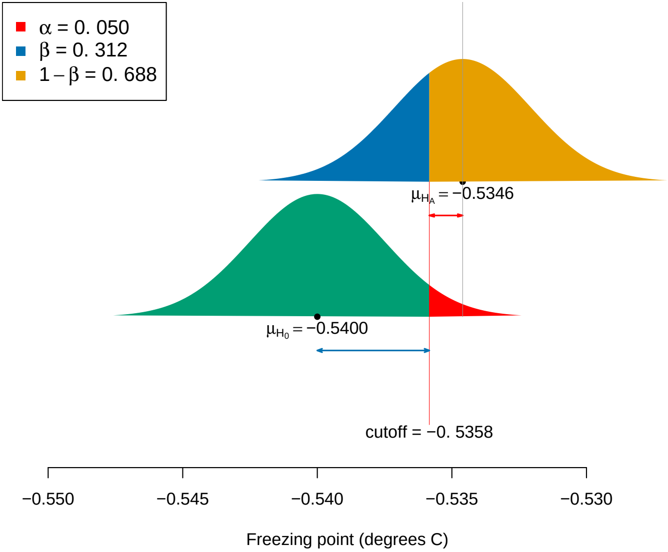
Power as a function of sample size

- Suppose even a 1% added water is serious, and worth detecting.
- Clearly, from the previous Figure, and again at the bottom row of the following Figure, one has only a 45% chance of detecting it: there is a **large overlap between the sampling distributions under the null (100% Milk) and the mixture (99% milk, 1% water) scenarios**.
- So, to better discriminate, one needs to make a bigger resting effort, and measure more lots, i.e., increase the n.

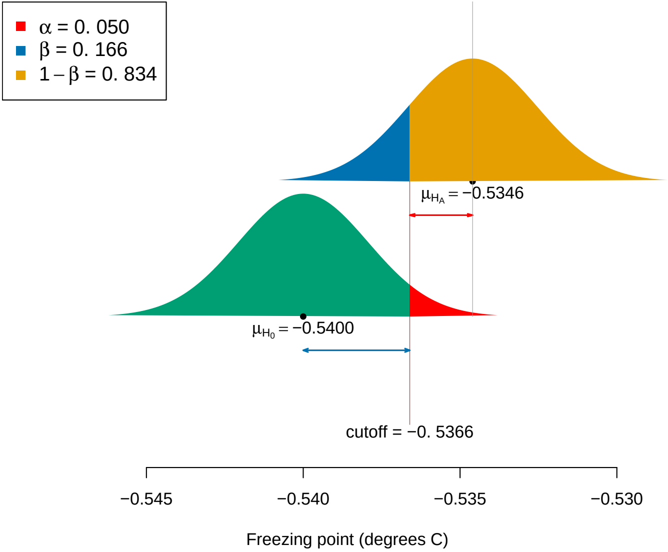
When the buyer uses samples of size 5

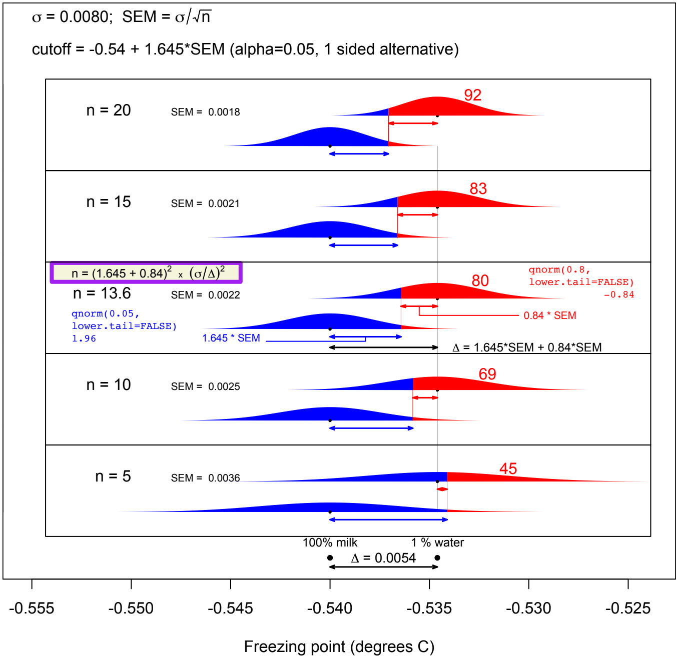


When the buyer uses samples of size 10



When the buyer uses samples of size 15




σ = 0.0080; SEM = σ/√n
cutoff = -0.54 + 1.645*SEM (alpha=0.05, 1 sided alternative)
n = 20
SEM = 0.0018
92
n = 15
SEM = 0.0021
83
n = (1.645 + 0.84)² x (σ/Δ)²
n = 13.6
SEM = 0.0022
80
qnorm(0.8, lower.tail=FALSE) -0.84
0.84 * SEM
qnorm(0.05, lower.tail=FALSE) 1.96
1.645 * SEM
Δ = 1.645*SEM + 0.84*SEM
n = 10
SEM = 0.0025
69
n = 5
SEM = 0.0036
45
100% milk
1 % water
Δ = 0.0054
-0.555
-0.550
-0.545
-0.540
-0.535
-0.530
-0.525
Freezing point (degrees C)

Increasing n leads to increased power

- The larger n narrows and concentrates the sampling distribution. The width is governed by the SD of the sampling distribution of the mean of n measurements, i.e., by the Standard Error of the Mean, or SEM = $\sigma/\sqrt{n}$.

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- Indeed, under the alternative (i.e., cheating) scenario the probability of exceeding the threshold is almost 70% when $n = 10$, 82% when $n = 15$ and 92% when n=20.

Increasing *n* leads to increased power

- The larger *n* narrows and concentrates the sampling distribution. The width is governed by the SD of the sampling distribution of the mean of *n* measurements, i.e., by the Standard Error of the Mean, or SEM = $\sigma/\sqrt{n}$.
- Because the null sampling distribution narrows, the cutoff is brought closer to the null. And under the alternative (non-null) scenario, a greater portion of its sampling distribution is to the right of (i.e., exceeds) the cutoff.
- Indeed, under the alternative (i.e., cheating) scenario the probability of exceeding the threshold is almost 70% when $n = 10$, 82% when $n = 15$ and 92% when n=20.
- You can check these for yourself in R using this expression:

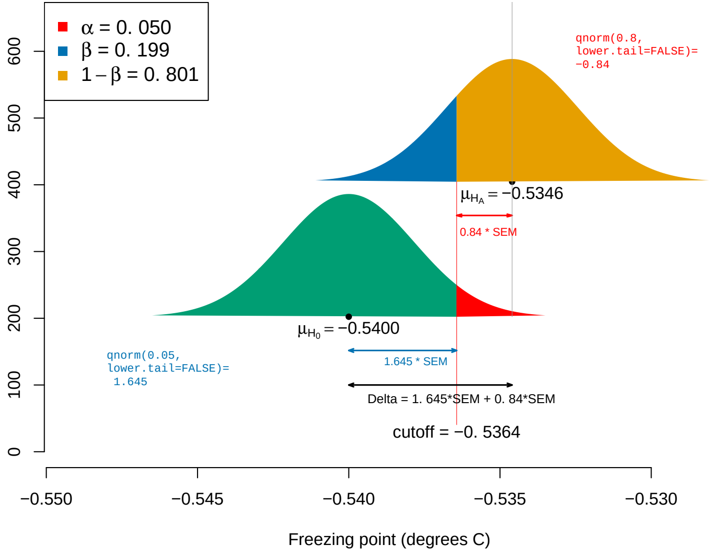
```
  stats::pnorm(cutoff, mean = mu.mixture, sd =
sigma/sqrt(n), lower.tail=FALSE)
```

At what n does the chance of detecting cheating reach 80%?

What sample size needed?

- We can come up with a closed form formula that (a) allows you to compute the sample size ‘by hand’ and (b) shows you, more explicitly than the diagram or R code can, what drives the n.

The balancing formula



What sample size needed?

- The 'balancing formula', in SEM terms, is simply the n where

$$1.645 \times SEM + 0.84 \times SEM = \Delta.$$

Replacing each of the SEMs (assumed equal, because we assumed the variability is approx. the same under both scenarios) by $\sigma/\sqrt{n}$, i.e.,

$$1.645 \times \sigma/\sqrt{n} + 0.84 \times \sigma/\sqrt{n} = \Delta.$$

and solving for n, one gets

$$n = (1.645 + 0.84)^2 \times \left\{ \frac{\sigma}{\Delta} \right\}^2 = (1.645 + 0.84)^2 \times \left\{ \frac{Noise}{Signal} \right\}^2.$$

What sample size needed?

- Notice the structure of the formula. The *first* component has to do with the operating characteristics or performance of the test, i.e., the type I error probability α and the desired power (the complement of the type II error probability, β).

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- Notice the structure of the formula. The *first* component has to do with the operating characteristics or performance of the test, i.e., the type I error probability α and the desired power (the complement of the type II error probability, β).

- The *second* has to do with the context in which it is applied, i..e, the size of the noise relative to the signal.

- In our example, where the Noise-to-Signal Ratio is $\frac{\sigma=0.0080}{\Delta=0.0054}$ = 1.48, so that its square is 1.48^2 or approx 2.2, and $(1.645 + 0.84)^2 = 2.485^2$ = approx 6.2,

$$n = 6.2 \times 2.2 = 13.6, \text{approx, or, rounded up, } n = 14.$$

Code for null and alternative distribution plots

```
source("https://raw.githubusercontent.com/sahirbhatnagar/EPIB607/
master/assignments/a6/plot_null_alt.R")

mu0 <- -0.540 # mean under the null
mha <- 0.99*-0.540 # mean under the alternative
s <- 0.0080 # sample/population SD
n <- 5 # sample size
cutoff <- mu0 + qnorm(0.95) * s / sqrt(n)

power_plot(n = n,
        s = s,
        mu0 = mu0,
        mha = mha,
        cutoff = cutoff,
        alternative = "greater",
        xlab = "Freezing point (degrees C)")
```

Code for power as a function of sample size and noise

```
source("https://raw.githubusercontent.com/sahirbhatnagar/EPIB607/
master/assignments/a6/plot_null_alt.R")

pacman::p_load(manipulate) # or library(manipulate)

mu0 <- -0.540 # mean under the null
mha <- 0.99*-0.540 # mean under the alternative
s <- 0.0080
n <- 5
cutoff <- mu0 + qnorm(0.95) * s / sqrt(n)

manipulate::manipulate(
power_plot(n = sample_size, s = sample_sd,
        mu0 = mu0, mha = mha,
        cutoff = cutoff,
        alternative = "greater",
        xlab = "Freezing point (degrees C)"),
        sample_size = manipulate::slider(5, 100),
        sample_sd = manipulate::slider(0.001, 0.01, initial = 0.008))
```

Interpreting p-values from statistical tests

- In the milk example, an $n = 5$ gives an SEM of $\sigma/\sqrt{5}$ = 0.0080/2236 = 0.0036. So the cutoff for a 1 sided test with α = 0.05 is $1.645 \times 0.0036 = 0.0059$ above -0.5400, i.e,. at - 0.5341.

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- The 1 sided alternative is that we are testing a 'less than 100%, more than 0%' mix, where the mean is above (to right of) -0.540, i.e., on the (upper) 'added water' side of the null.

- Formally, these two hypotheses are

$$\mathrm{H}_0 : \mu = -0.540;\ H_{alt} : \mu > -0.540.$$

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- Formally, these two hypotheses are

$$\mathrm{H}_0 : \mu = -0.540; \; H_{alt} : \mu > -0.540.$$

- Since the mean of the 5 measurements, namely -0.533°C, is to the right of (**exceeds**) this threshold, it would be considered 'statistically significant at the 0.05 level.' The actual p-value is `pnorm(-0.533, mean=-0.54, sd = 0.0036, lower.tail=FALSE)` = 0.026.

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- In particular, it would not be appropriate – or accurate – to say that you are 1 - 0.026 = 0.974 = 97.4% certain that the supplier is cheating.
- Remember that a p-value is a probability concerning the data, **conditional** on (i.e., computed under the assumption that) H_0 being (is) true. In other words, the p-value has to do with P(data | ‘innocence’), whereas at issue is the reverse, P(‘innocence’ | data).

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- As to this latter probability (of being innocent), there are a lot of other factors to consider first, before accusing the supplier of cheating.

Other factors to consider before accusing the supplier

- First, did you (re-)check the calculations? How recently was the instrument calibrated? etc.

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- JH calls these **Type III errors**: the data were wrong, or the instrument was wrong, or the technician mis-calculated something.
- It should remind us that, in the *real* world, there are *many* alternative hypotheses, not just the one.
- Second, why did you chose to test **this** supplier?
  - Is it someone that the manager suspected based on previous data, or based on knowing that he is behind in his loan payments to the bank?
  - Or maybe the laboratory manager merely asked a technician to start randomly testing, and the first supplier (blindly) chosen was the manager's brother-in-law?

Are all *p*-values created equal?

- So, you can see that, just as in medical tests, there are **many other pieces of evidence** or information, or circumstances, besides the *p*-value, that bear on the probability of innocence or guilt.
- This is very nicely brought out in the article 'Are all p-values created equal?' which you can here: `http://www.biostat.mcgill.ca/hanley/BionanoWorkshop/AreAllSigPValuesCreatedEqual.pdf`
- Sadly, the mixing up of P(data | hypothesis) and P(data | data) – often referred to as 'The Prosecutor's Fallacy' – is common, and can lead to serious harm.

When does the p-value work well?

- The use of p-values works well in Quality Control, where the aim is to detect (the few) deviations ('bad' ones) from the desired specifications, to stop and fix the offending machine, or to flag defective batches.

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- The use of *p*-values works well in Quality Control, where the aim is to detect (the few) deviations ('bad' ones) from the desired specifications, to stop and fix the offending machine, or to flag defective batches.
- It is not clear that it is equally effective at identifying the (few) truly active ('good) compounds via the mass testing of lots of compounds, most of which are expected to be inactive – and then investing all one's effort in these few 'good' ones at the next stage of development.

Another example on power: Lake Wobegon

Power: Lake Wobegon

- It is claimed that the children of Lake Wobegon are above average. Take a simple random sample of 9 children from Lake Wobegon, and measure their IQ to obtain a sample mean of 112.8.
- IQ scores are scaled to be Normally distributed with mean 100 and standard deviation 15.
- Does this sample provide evidence to reject the null hypothesis of no difference between children of Lake Wobegon and the general population?

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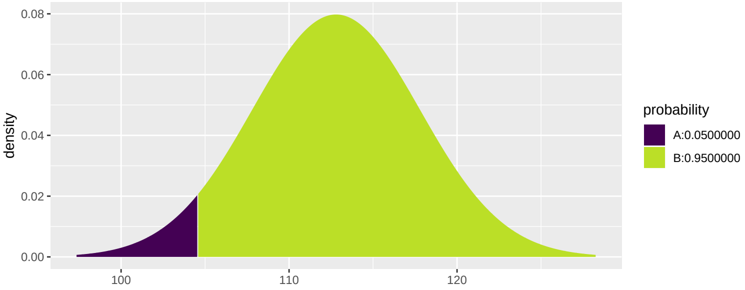
- IQ scores are scaled to be Normally distributed with mean 100 and standard deviation 15.
- Does this sample provide evidence to reject the null hypothesis of no difference between children of Lake Wobegon and the general population?

1. Null and alternative hypotheses: The claim made is that the population of children Lake Wobegon have higher than average intellidence. Thus the null hypothesis is that the population has average intelligence, or a score of 100. Therefore $H_0 : \mu = 100$, and the (one-sided) alternative is $H_A : \mu > 100$.

Lower limit of 95% CI

1. Hypotheses. $H_0 : \mu = 100$, $H_A : \mu > 100$.
2. Calculate 95% CI.

```
mosaic::xqnorm(p = c(0.05,1), 112.8, 15/sqrt(9))
```




```
## [1] 104.5757      Inf
```

Lower limit of 95% CI

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2. Calculate 95% CI.

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mosaic::xqnorm(p = c(0.05,1), 112.8, 15/sqrt(9))
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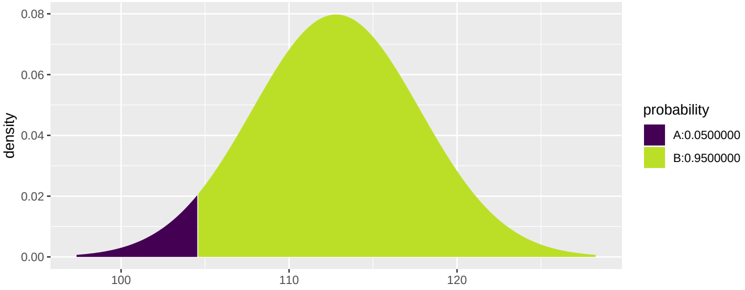


```
## [1] 104.5757      Inf
```

3. Statement. The lower limit of the CI excludes $\mu_0 = 100$, and so there is evidence to suggest that the children at Lake Wobegon are brighter than other children at the $\alpha = 0.05$ level.

Power

Steps to finding power:

1. State null hypothesis, H_0, and state a specific alternative, H_A, as the minimum (clinical/substantive) departure from the null hypothesis that would be of interest.

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3. Calculate the probability of observing the values found in (2) when the alternative is true.

Power

Example: Lake Wobegon
Suppose you hope to use a **one-sided** test to show that the children from Lake Wobegon are at least 10 points higher than average on the IQ test. What power do you have to detect this with the sample of 9 children if using a 0.05-level test?

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1. Hypotheses. $H_0 : \mu = 100$, $H_A : \mu > 110$.

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Suppose you hope to use a **one-sided** test to show that the children from Lake Wobegon are at least 10 points higher than average on the IQ test. What power do you have to detect this with the sample of 9 children if using a 0.05-level test?

1. Hypotheses. $H_0 : \mu = 100$, $H_A : \mu > 110$.

2. Find values of the sample mean that reject the null.

   The test will reject H_0 at the 0.05 level whenever

$$z = \frac{\bar{y} - \mu_0}{\sigma/\sqrt{n}} = \frac{\bar{y} - 100}{15/\sqrt{9}} \geq 1.645.$$

   Now we must translate this back to values of $\bar{y}$...

Power

Example: Lake Wobegon

2. Values of the sample mean that reject H_0 (con't)

   The test will reject H_0 at the 0.05 level whenever

   $$\frac{\bar{y} - 100}{15/\sqrt{9}} \geq 1.645,$$

   which means we reject H_0 whenever

   $$\bar{y} \geq 1.645 \times 15/\sqrt{9} + 100 = 108.2$$

   If H_0 is true, the probability of seeing an IQ score as big as 108.2 or bigger is 5%.

Power

Example: Lake Wobegon

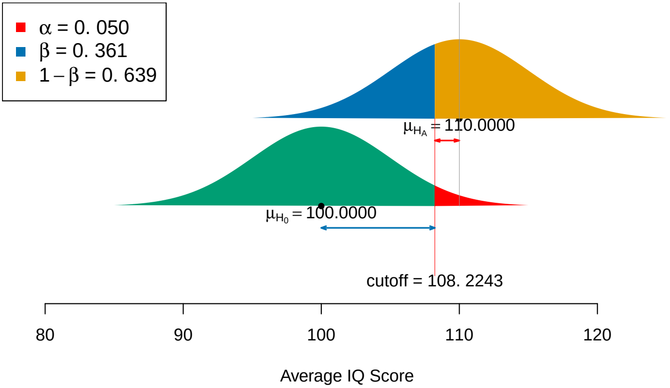
3. Find the probability of rejecting H_0 if $\mu = \mu_A = 110$.

$$
\begin{aligned}
P(\bar{y} > 108.2 | \mu = \mu_A = 110) \\
&= P\left(\frac{\bar{y} - \mu_A}{\sigma/\sqrt{n}} > \frac{108.2 - 110}{15/\sqrt{9}} \middle| \mu = \mu_A = 110\right) \\
&= P\left(z > -0.36\right) \\
&= 0.64
\end{aligned}
$$

So there is approximately a 2/3 chance of detecting a difference of 10 points on the IQ scale at the 0.05 level of significance with a sample size of 9.

Null and alternative distribution plots

```
power_plot(n = 9, s = 15, mu0 = 100, mha = 110,
       cutoff = 100 + qnorm(0.95) * 15 / sqrt(9),
       alternative = "greater", xlab = "Average IQ Score")
```



Power

Example: Lake Wobegon

If you hoped to use a two-sided test to show that the children from Lake Wobegon are at least 10 points higher than average on the IQ test, what power do you have with the sample size of 9 and a 0.05-level test?

Power

Example: Lake Wobegon

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1. Hypotheses. $H_0 : \mu = 100$, $H_A : \mu = 110$.

Power

Example: Lake Wobegon

If you hoped to use a two-sided test to show that the children from Lake Wobegon are at least 10 points higher than average on the IQ test, what power do you have with the sample size of 9 and a 0.05-level test?

1. Hypotheses. $H_0 : \mu = 100$, $H_A : \mu = 110$.

2. Find values of the sample mean that reject the null.

   The test will reject H_0 at the 0.05 level whenever

$$z = \frac{\bar{y} - \mu_0}{\sigma/\sqrt{n}} = \frac{\bar{y} - 100}{15/\sqrt{9}} \geq 1.96 \qquad \textbf{OR when}$$

$$z = \frac{\bar{y} - \mu_0}{\sigma/\sqrt{n}} = \frac{\bar{y} - 100}{15/\sqrt{9}} \leq -1.96$$

   since we are performing a two-sided test.

Power

Thus we reject H_0 if $\bar{y} \geq 1.96 \times 5 + 100 = 109.8$ **OR** if $\bar{y} \leq -1.96 \times 5 + 100 = 90.2$

3. Find the probability of rejecting H_0 if $\mu = \mu_A = 110$.

$$P(\bar{y} > 109.8 \text{ OR } \bar{y} < 90.2 | \mu = \mu_A = 110)$$

$$\begin{aligned} &= P(\bar{y} > 109.8 | \mu_A = 110) + P(\bar{y} < 90.2 | \mu_A = 110) \\ &= P\left(\frac{\bar{y} - \mu_A}{\sigma/\sqrt{n}} > \frac{109.8 - 110}{15/\sqrt{9}} \middle| \mu_A = 110 \right) \\ &\quad + P\left(\frac{\bar{y} - \mu_A}{\sigma/\sqrt{n}} < \frac{90.2 - 110}{15/\sqrt{9}} \middle| \mu_A = 110 \right) \\ &= P\left(z > -0.04\right) + P\left(z < -3.96\right) \\ &= 0.52 + 3.7 \times 10^{-5} \approx 0.52 \end{aligned}$$

There is about a 1/2 chance of detecting a difference of 10 pts on the IQ scale at the 0.05 level of significance with $n = 9$ using a two-sided alternative hypothesis.

Power

- Steps 1 and 2 used to find the power of a one-sided test to detect a difference of x points above (or below) the population mean are similar to the steps for finding the power of a two-sided test to detect a difference of x points on either side of the population mean.
- However for a two-sided test, there will be two sets of values of $\bar{y}$ that lead us to reject H_0 (also, z_α for one-sided and $z_{\alpha/2}$ for two-sided).
- **However**, there is one critical difference in the third step: we need to calculate the probability of seeing $\bar{y}$ in either of the two tails (rejection regions) of the null distribution under the assumption that the true distribution has mean μ_A. So there will be two probabilities to calculate in the third step.

Power

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- Note: If we felt that the minimum significant departure from μ_0 was different above and below (e.g., we are interested in increases of blood pressure of at least 3.5mmHg and decreases of blood pressure of at least 2mmHg), we perform the calculations as though we were interested in the minimum of the two values (Why?).

Power

Exercises: Lake Wobegon

Find the power of the following tests, assuming two-sided alternative hypotheses:

1. A 0.05-level test to detect a difference of 15 points on the IQ scale using the 9 children.
2. A 0.05-level test to detect a difference of 5 points on the IQ scale using the 9 children.
3. A 0.05-level test to detect a difference of 10 points on the IQ scale using 25 children.
4. A 0.01-level test to detect a difference of 10 points on the IQ scale using the 9 children.