Statistical Inference Course Notes

Xing Su

Contents

Overview

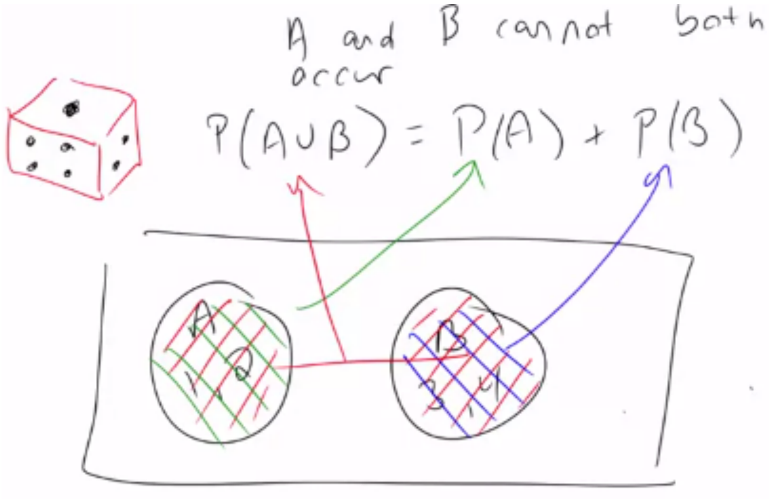
- **Statistical Inference** = generating conclusions about a population from a noisy sample
- Goal = extend beyond data to population
- Statistical Inference = only formal system of inference we have
- many different modes, but **two** broad flavors of inference (inferential paradigms): ***Bayesian*** vs ***Frequencist***
  - **Frequencist** –> uses long run proportion of times an event occurs independent identically distributed repetitions
    - frequentist is what this class is focused on
    - believes if an experiment is repeated many many times, the resultant percentage of success/something happening defines that population parameter
  - **Bayesian** –> probability estimate for a hypothesis is updated as additional evidence is acquired
- **statistic** = number computed from a sample of data
  - statistics are used to infer information about a population
- **random variable** = outcome from an experiment
  - deterministic processes (variance/means) produce additional random variables when applied to random variables, and they have their own distributions

Probability

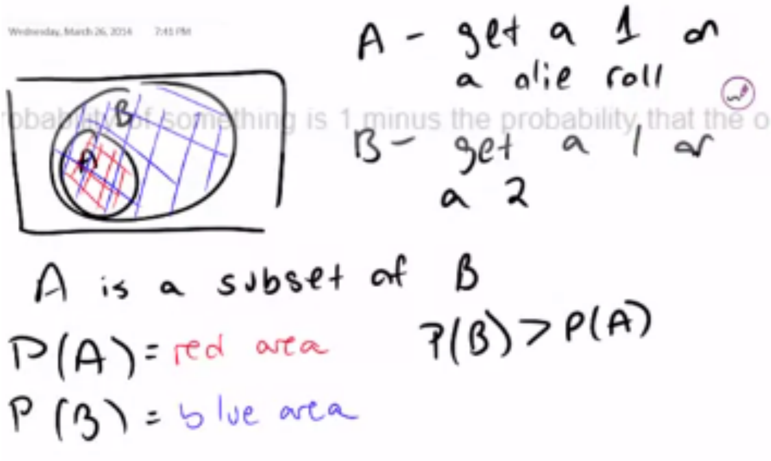
- **Probability** = the study of quantifying the likelihood of particular events occurring
  - given a random experiment, ***probability*** = population quantity that summarizes the randomness
    - not in the data at hand, but a conceptual quantity that exist in the population that we want to estimate

General Probability Rules

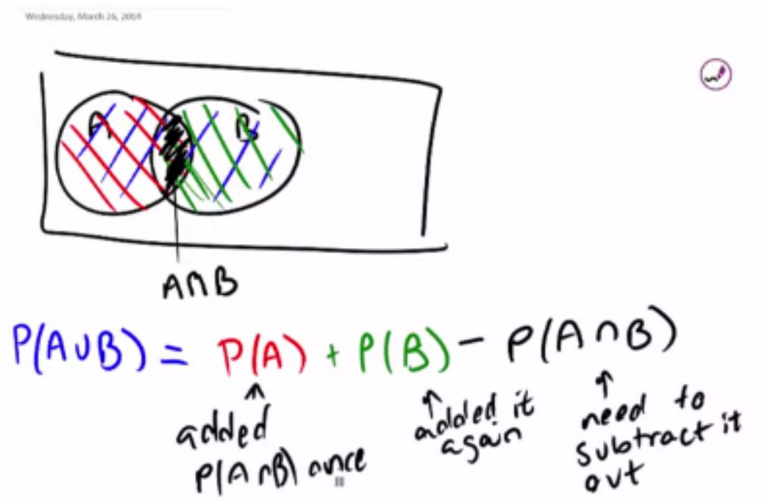
- discovered by Russian mathematician Kolmogorov, also known as "Probability Calculus"
- probability = function of any set of outcomes and assigns it a number between 0 and 1
  - $0 \leq P(E) \leq 1$, where E = event
- probability that nothing occurs = 0 (impossible, have to roll dice to create outcome), that something occurs is 1 (certain)
- probability of outcome or event E, ***P(E)*** = ratio of ways that E could occur to number of all possible outcomes or events
- probability of something = 1 - probability of the opposite occurring
- probability of the **union** of any two sets of outcomes that have nothing in common (mutually exclusive) = sum of respective probabilities



- if A implies occurrence of B, then P(A) occurring < P(B) occurring


Wednesday, March 26, 2014 7:41 PM
B
A
A - get a 1 on a die roll
B - get a 1 or a 2
probability of something is 1 minus the probability that the o
A is a subset of B
P(A) = red area
P(B) = blue area
P(B) > P(A)

- for any two events, probability of at least one occurs = the sum of their probabilities - their intersection (in other words, probabilities can not be added simply if they have non-trivial intersection)



- for independent events A and B, $P(A \cup B) = P(A) \times P(B)$
- for outcomes that can occur with different combination of events and these combinations are mutually exclusive, the $P(E_{total}) = \sum P(E_{part})$

Conditional Probability

- let B = an event so that $P(B) > 0$
- **conditional probability** of an event A, given B is defined as the probability that BOTH A and B occurring divided by the probability of B occurring

$$P(A \mid B) = \frac{P(A \cap B)}{P(B)}$$

- if A and B are ***independent***, then

$$P(A \mid B) = \frac{P(A)P(B)}{P(A)} = P(A)$$

- ***example***
  - for die roll, $A = \{1\}$, $B = \{1, 3, 5\}$, then

$$P(1 \mid Odd) = P(A \mid B) = \frac{P(A \cap B)}{P(B)} = \frac{P(A)}{P(B)} = \frac{1/6}{3/6} = \frac{1}{3}$$

Baye's Rule

- definition

$$P(B \mid A) = \frac{P(A \mid B)P(B)}{P(A \mid B)P(B) + P(A \mid B^c)P(B^c)}$$

where B^c = corresponding probability of event B, $P(B^c) = 1 - P(B)$

Random Variables

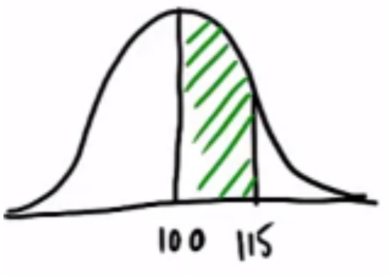
- **random variable** = numeric outcome of experiment
- **discrete** (what you can count/categories) = assign probabilities to every number/value the variable can take
  - coin flip, rolling a die, web traffic in a day
- **continuous** (any number within a continuum) = assign probabilities to the range the variable can take
  - BMI index, intelligence quotients
  - ***Note**: limitations of precision in taking the measurements may imply that the values are discrete, but we in fact consider them continuous*
- `rbinom()`, `rnorm()`, `rgamma()`, `rpois()`, `runif()` = functions to generate random variables from the binomial, normal, Gamma, Poisson, and uniform distributions
- density and mass functions (population quantities, not what occurs in data) for random variables = best starting point to model/think about probabilities for numeric outcome of experiments (variables)
  - use data to estimate properties of population –> linking sample to population

Probability Mass Function (PMF)

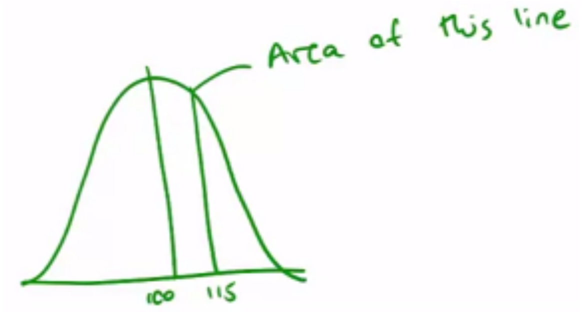
- evaluates the probability that the **discrete random variable** takes on a specific value
  - measures the chance of a particular outcome happening
  - always ≥ 0 for every possible outcome
  - $\sum$ possible values that the variable can take = 1
- ***Bernoulli distribution example***
  - X = 0 –> tails, X = 1 –> heads
    - X here represents potential outcome
  - $p(X = x) = (\frac{1}{2})^x(\frac{1}{2})^{1-x}$ for $X = 0, 1$
    - x here represents a value we can plug into the PMF
    - general form –> $p(x) = (\theta)^x(1-\theta)^{1-x}$
- `dbinom(k, n, p)` = return the probability of getting `k` successes out of `n` trials, given probability of success is `p`

Probability Density Function (PDF)

- evaluates the probability that the **continuous random variable** takes on a specific value
  - always $\geq$ everywhere
  - total area under the must = 1
- **areas under PDFs** correspond to the probabilities for that random variable taking on that range of values (PMF)



- but the probability of the variable taking a specific value = 0 (area of a line is 0)



- ***Note**: the above is true because it is modeling random variables as if they have infinite precision, when in reality they do not*
- `dnorm()`, `dgamma()`, `dpois()`, `dunif()` = return probability of a certain value from the normal, Gamma, Poisson, and uniform distributions

Cumulative Distribution Function (CDF)

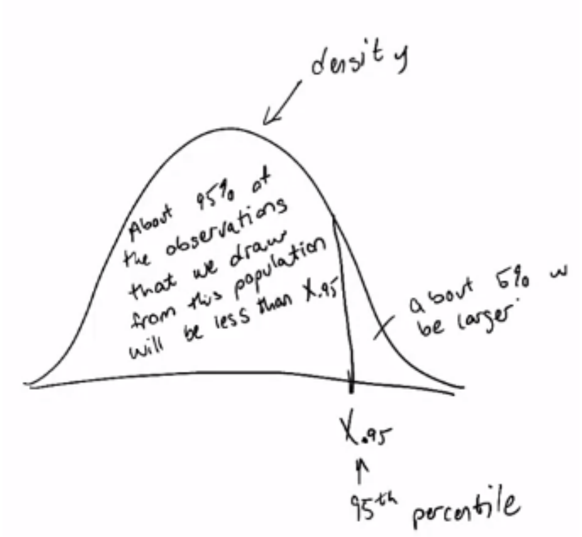
- CDF of a random variable X = probability that the random variable is $\leq$ value x
  - $F(x) = P(X \leq x)$ <- applies when X is discrete/continuous
- PDF = derivative of CDF
  - integrate PDF –> CDF
    - `integrate(function, lower=0, upper=1)` –> can be used to evaluate integrals for a specified range
- `pbinom()`, `pnorm()`, `pgamma()`, `ppois()`, `punif()` = returns the cumulative probabilities from 0 up to a specified value from the binomial, normal, Gamma, Poisson, and uniform distributions

Survival Function

- survival function of a random variable X = probability the random variable > x, complement of CDF
  - $S(x) = P(X > x) = 1 - F(x)$, where $F(x)$ = CDF

Quantile

- the α^{th} quantile of a distribution with distribution function F = point x_α
  - $F(x_\alpha) = \alpha$
  - percentile = quantile with α expressed as a percent
  - median = 50th percentile
  - α% of the possible outcomes lie below it


density
About 95% of the observations that we draw from this population will be less than X.95
about 5% w be larger
X.95
95th percentile

- `qbeta(quantileInDecimals, 2, 1)` = returns quantiles for beta distribution
  - works for `qnorm()`, `qbinom()`, `qgamma()`, `qpois()`, etc.
- median estimated in this fashion = a population median
- probability model connects data to population using assumptions
  - population median = ***estimand***, sample median = ***estimator***

Independence

- two events A and B are ***independent*** if the following is true
  - $P(A \cap B) = P(A)P(B)$
  - $P(A \mid B) = P(A)$
- two random variables X and Y are ***independent***, if for any two sets, **A** and **B**, the following is true
  - $P([X \in A] \cap [Y \in B]) = P(X \in A)P(Y \in B)$
- **independence** = statistically unrelated from one another
- if A is ***independent*** of B, then the following are true
  - A^c is independent of B
  - A is independent of B^c
  - A^c is independent of B^c

IID Random Variables

- random variables are said to be **IID** if they are ***independent and identically distributed***
  - **independent** = statistically unrelated from each other
  - **identically distributed** = all having been drawn from the same population distribution
- IID random variables = default model for random samples = default starting point of inference

Diagnostic Test

- Let $+$ and $-$ be the results, positive and negative respectively, of a diagnostic test
- Let D = subject of the test has the disease, D^c = subject does not
- **sensitivity** $= P(+ \mid D)$ = probability that the test is positive given that the subject has the disease (the higher the better)
- **specificity** $= P(- \mid D^c)$ = probability that the test is negative given that the subject does not have the disease (the higher the better)
- **positive predictive value** $= P(D \mid +)$ = probability that that subject has the disease given that the test is positive
- **negative predictive value** $= P(D^c \mid -)$ = probability that the subject does not have the disease given the test is negative
- **prevalence of disease** $= P(D)$ = marginal probability of disease

Example

- specificity of 98.5%, sensitivity = 99.7%, prevalence of disease = .1%

$$\begin{aligned} P(D \mid +) &= \frac{P(+ \mid D)P(D)}{P(+ \mid D)P(D) + P(+ \mid D^c)P(D^c)} \\ &= \frac{P(+ \mid D)P(D)}{P(+ \mid D)P(D) + \{1 - P(- \mid D^c)\}\{1 - P(D)\}} \\ &= \frac{.997 \times .001}{.997 \times .001 + .015 \times .999} \\ &= .062 \end{aligned}$$

- low positive predictive value –> due to low prevalence of disease and somewhat modest specificity
  - suppose it was know that the subject uses drugs and has regular intercourse with an HIV infect partner (his probability of being + is higher than suspected)
  - evidence implied by a positive test result

Likelihood Ratios

- from Baye's Rules, we can derive the *positive predictive value* and *false positive value*

$$P(D \mid +) = \frac{P(+ \mid D)P(D)}{P(+ \mid D)P(D) + P(+ \mid D^c)P(D^c)}$$

$$P(D^c \mid +) = \frac{P(+ \mid D^c)P(D^c)}{P(+ \mid D)P(D) + P(+ \mid D^c)P(D^c)}$$

- if we divide the about quantities over each other (same denominator), we get the following

$$\frac{P(D \mid +)}{P(D^c \mid +)} = \frac{P(+ \mid D)}{P(+ \mid D^c)} \times \frac{P(D)}{P(D^c)}$$

- **odds** $= p/(1-p)$
  - $\frac{P(D)}{P(D^c)}$ = odds of disease in absence of test
  - $\frac{P(D \mid +)}{P(+ \mid D^c)}$ = odds of disease given a positive test result
- **Diagnostic Likelihood Ratio** of a positive test result is defined as

$$DLR_+ = \frac{P(+ \mid D)}{P(Dc \mid +)}$$

  - in previous example, $DLR_+ = .997/(1 - .985) = 66$
  - $DLR_- = (1 - .997)/.985 = 0.003$

- **post-test odds of D** $= DLR_+ \times$ **pre-test odds of D**
  - $DLR_+ =$ the factor by which you multiply your odds in the presence of a positive test to obtain your post-test odds

Expected Values/Mean

- useful for characterizing a distribution (properties of distributions)
- **mean** = characterization of the center of the distribution = *expected value*
- expected value operation = ***linear*** –> $E(aX + bY) = aE(X) + bE(Y)$
- **variance/standard deviation** = characterization of how spread out the distribution is
- sample expected values for sample mean and variance will estimate the population counterparts
- **population mean**
  - expected value/mean of a random variable = center of its distribution (center of mass)
  - ***discrete variables***
    - for X with PMF $p(x)$, the population mean is defined a: $E[X] = \sum_x xp(x)$ where the ***sum*** is taken over all possible values of x
    - $E[X]$ = center of mass of a collection of location and weights $x, p(x)$
    - *coin example*
      - $E[X] = 0 \times (1 - p) + 1 \times p = p$

  - ***continuous variable***
    - for X with density $f(x)$, the expected value = the center of mass of the density
    - instead of summing over discrete values, the expectation ***integrates*** over a continuous function
      - pdf = $f(x)$
      - $\int xf(x)$ = area under the curve = mean/expected value of X
- **sample mean**
  - sample mean estimates the population mean
    - sample mean = center of mass of observed data = empirical mean

$$\bar{X} = \sum_{x}^{n} x_i p(x_i)$$

      where $p(x_i) = 1/n$

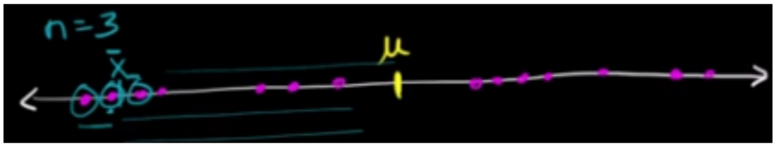
- average of random variables = a random variable and its distribution has an expected value that is the **same** as the original distribution (centers are the same)
  - the mean of the averages = average of the original data –> estimates average of the population
  - E[sample mean] = population mean <- this estimator is **unbiased**
    - derivation
      - let X_1, X_2, X_3, . . . X_n be a collection of n samples from the population with mean μ
      - mean of this sample = $\frac{X_1+X_2+X_3+.+X_n}{n}$
      - since $E(aX) = aE(X)$, the expected value of the mean, $E[\frac{X_1+X_2+X_3+...+X_n}{n}] = \frac{1}{n} \times [E(X_1) + E(X_2) + E(X_3) + ... + E(X_n)]$
      - since each of the $E(X_i)$ is drawn from the population with mean μ, we expect that the $E(X_i) = \mu$
      - so $\frac{1}{n} \times [E(X_1) + E(X_2) + E(X_3) + ... + E(X_n)] = \frac{1}{n} \times n \times \mu = \mu$
- ***Note:****the more data that goes into the sample mean, the more concentrated its density/mass functions are around the population mean*

Variance

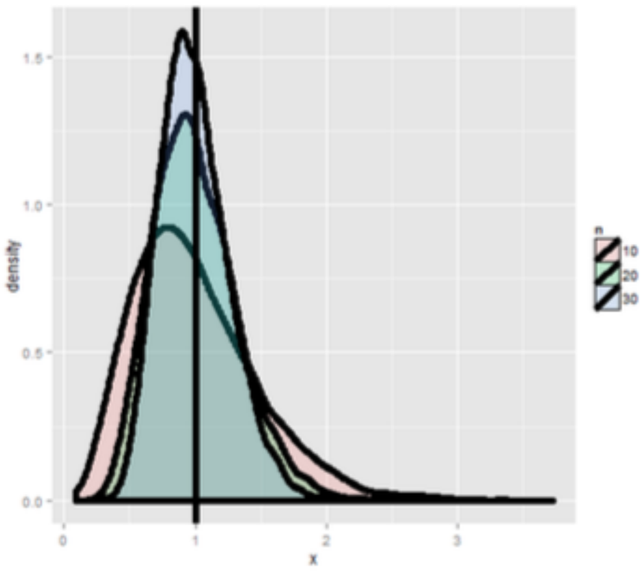
- **variance** = measure of spread, the square of expected distance from the mean (expressed in X's units^2)
  - $Var(X) = E[(X - \mu)^2] = E[X^2] - E[X]^2$
  - higher variances –> more spread, lower –> smaller spread
  - **standard deviation** = $\sqrt{var(X)}$ –> has same units as X
  - ***example***
    - for die roll, $E[X] = 3.5$
    - $E[X^2] = 12 \times 1/6 + 22 \times 1/6 + 32 \times 1/6 + . + 62 \times 1/6 = 15.17$
    - $Var(X) = E[X^2] - E[X]^2 \approx 2.92$
  - ***example***
    - for coin flip, $E[X] = p$
    - $E[X^2] = 0^2 \times (1 - p) + 1^2 \times p = p$
    - $Var(X) = E[X^2] - E[X]^2 = p - p^2 = p(1 - p)$

Sample Variance

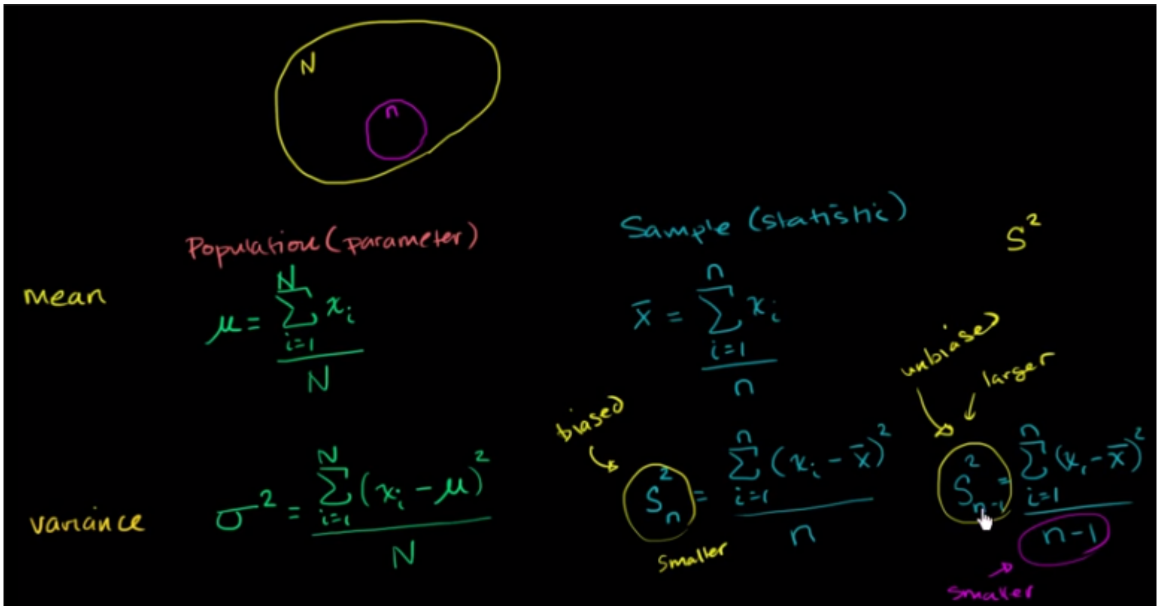
- $S^2 = \frac{\sum_{i=1}(X_i - \bar{X})^2}{n-1}$
  - ***Note****: samples are much more likely to have variances lower than the population –> why S^2 is calculated by dividing by n - 1*



- on the above line, any subset of data will most likely have a variance that is ***lower than*** the population variance
- dividing by n - 1 will make the variance estimator ***larger*** to adjust for this fact –> leads to more accurate estimation
  - random variable, and thus has an associate population distribution
    - $E[S^2]$ = population variance, where S = sample standard deviation
    - with more data, its distribution gets more concentrated around population variance



- ***Note:*** *for any variable, properties of the population = parameter, estimates of properties for samples = statistic*


N
n
Population (parameter)
Sample (statistic)
S^2
Mean
$\mu = \frac{\sum_{i=1}^{N} x_i}{N}$
$\bar{x} = \frac{\sum_{i=1}^{n} x_i}{n}$
unbiased
larger
biased
variance
$\sigma^2 = \frac{\sum_{i=1}^{N} (x_i - \mu)^2}{N}$
$S_n^2 = \frac{\sum_{i=1}^{n} (x_i - \bar{x})^2}{n}$
$S_{n-1}^2 = \frac{\sum_{i=1}^{n} (x_i - \bar{x})^2}{n-1}$
Smaller
Smaller

- **distribution for mean of random samples**
  - expected value of the mean of this distribution = expected value of the sample = population mean
    - $E[\bar{X}] = \mu$
  - expected value of the variance of this distribution
    - $Var(\bar{X}) = \sigma^2/n$
    - as **n** becomes larger, the mean of random sample –> more concentrated around the population mean –> variance approaches 0
  - ***Note:*** *normally we only have 1 sample mean (from collected sample) and can estimate the variance* σ^2 *= so we know a lot about the distribution of the means from the data observed*

- **Standard Error (SE)**
    - SE of the mean $= \sigma/\sqrt{n}$ –> effectively the standard deviation of the distribution of a statistic (i.e. mean)
        - represents variability of means

Entire Estimator-Estimation Relationship

- Start with a sample
- S^2 = sample variance
    - estimates how variable the population is
    - estimates population variance σ^2
    - S^2 = a random variable and has its own distribution centered around σ^2
        - more concentrated around σ^2 as n increases
- $\bar X$ = sample mean
    - estimates population mean μ
    - $\bar X$ = a random variable and has its own distribution centered around μ
        - more concentrated around μ as n increases
        - variance of distribution of $\bar X = \sigma^2/n$
        - estimate of variance $= S^2/n$
        - estimate of standard error $= S/\sqrt{n}$ –> "sample standard error of the mean"
        - estimates how variable sample means (n size) from the population are

Example - Standard Normal

- variance = 1
- means of **n** standard normals (sample) have standard deviation $= 1/\sqrt{n}$

```r
# specify number of simulations with 10 as number of observations per sample
nosim <- 1000; n <-10
sd(apply(matrix(rnorm(nosim * n), nosim), 1, mean))
```

```
## [1] 0.3208222
```

- `rnorm()` –> generate samples from the standard normal
- `matrix()` –> puts all samples into a nosim by n matrix, so that each row represents a simulation with `nosim` observations
- `apply()` –> calculates the mean of the n samples
- `sd()` –> returns standard deviation
- ***Note:*** *standard uniform –> triangle straight line distribution –> mean = 1/2 and variance = 1/12*

Binomial Distribution

- **binomial random variable** = sum of **n** Bernoulli variables = $\sum X_i$ where $X_i = Bernoulli(p)$
  - PMF –> $P(X = x) = \binom{n}{x} p^x (1-p)^{n-x}$
    - * $\binom{n}{x}$ = counts the number of ways selecting x items out of n options without replacement or regard to order
      - · $\binom{n}{x} = \frac{n!}{x!(n-x)!}$
      - · $\binom{n}{x}, \binom{n}{x} = 1$
- **Bernoulli distribution** –> binary outcome
  - only possible outcomes
    - * 1 = “success” with probability of p
    - * 0 = “failure” with probability of $1 - p$
  - PMF –> $P(X = x) = p^x (1-p)^{1-x}$
  - mean = p, variance = $p(1-p)$

Example

- of 8 children, whats the probability of 7 or more girls (50/50 chance)?
- $\binom{8}{7}.5^7(1-.5)^1 + \binom{8}{8}.5^8(1-.5)^0 \approx 0.04$
- `choose(8, 7)` –> R function to calculate n choose x
- `pbinom(6, size=8, prob =0.5, lower.tail=F)` –> probability of 6 or less out of 8 samples with probability of 0.5
  - `lower.tail = F` returns the complement

Normal Distribution

- normal/Gaussian distribution = random variable X
  - mean = μ, variance = σ^2
  - PMF –> $(2\pi\sigma^2)^{-1/2} e^{-(x-\mu)^2/2\sigma^2}$
  - notation –> $X \sim N(\mu, \sigma^2)$
- $X \sim N(0, 1)$ = **standard normal distribution** (standard normal RVs often labeled Z)
  - ~68% of data/normal density –> between ± 1 standard deviation from μ
  - ~95% of data/normal density –> between ± 2 standard deviation from μ
  - ~99% of data/normal density –> between ± 3 standard deviation from μ
  - ± 1.28 standard deviations from μ –> 10^{th} (-) and 90^{th} (+) percentiles
  - ± 1.645 standard deviations from μ –> 5^{th} (-) and 95^{th} (+) percentiles
  - ± 1.96 standard deviations from μ –> 2.5^{th} (-) and 97.5^{th} (+) percentiles
  - ± 2.33 standard deviations from μ –> 1^{st} (-) and 99^{th} (+) percentiles
- for any $X \sim N(\mu, \sigma^2)$, calculating the number of standard deviation from the mean ***converts the random variable to a standard normal***

$$Z = \frac{X - \mu}{\sigma} \sim N(0, 1)$$

- conversely, ***a standard normal can then be converted to any normal distribution*** by multiplying by standard deviation and adding the mean

$$X = \mu + \sigma Z \sim N(\mu, \sigma^2)$$

- R Commands:
  - nth percentiles –> `qnorm(n, mean = mu, sd = sd)`
  - probability larger than x –> `pnorm(x, mean = mu, sd = sd, lower.tail = F)`

Poisson Distribution

- used to model counts
  - PMF–>
$$P(X = x; \lambda) = \frac{\lambda^x e^{-\lambda}}{x!}$$
    where $X = 0, 1, 2, ...\infty$
  - mean = λ, variance = λ
- modeling uses for Poisson distribution
  - count data
  - event-time/survival –> cancer trials, some patients never develop and some do, dealing with the data for both ("censoring"")
  - contingency tables –> record results for different characteristic measurements
  - approximating binomials –> instances where **n** is large and **p** is small (i.e. pollution on lung disease)
    - $X \sim Binomial(n, p)$
    - $\lambda = np$
  - rates –> $X \sim Poisson(\lambda t)$
    - $\lambda = E[X/t]$ –> expected count per unit of time
    - t = total monitoring time
    - example: `ppois(n, lambda = lambda * t)` –> returns probability of n or fewer events happening given the rate and time

Asymptotics

- **asymptotics** = behavior of statistics as sample size –> ∞
- useful for simple statistical inference/approximations
- form basis for frequency interpretation of probabilities ("Law of Large Numbers")
- **Law of Large Numbers (LLN)** = IID sample statistic becomes population statistic to what it estimates as **n** increases (sample mean –> population mean)
- ***Note****: an estimator is* ***consistent*** *if it converges to what it is estimating*
  - sample mean, variance, standard deviation are all consistent for their population counterparts
- **Central Limit Theorem**
  - distribution of means of IID variables –> standard normal as **n** increases
  - for large values of **n**

$$\frac{\bar X_n - \mu}{\sigma/\sqrt{n}} = \frac{\sqrt{n}(\bar X_n - \mu)}{\sigma} = \frac{\text{Estimate} - \text{Mean of estimate}}{\text{Std. Err. of estimate}} \longrightarrow N(0, 1)$$

  - this translates to the distribution of the sample mean $\bar{X}$ is approximately $N(\mu, \sigma^2/n)$
  - ***Note**: speed at which the normalized coin flips converge to normal distribution depends on how biased the coin is (value of p)*
  - ***Note**: does not guarantee that the normal distribution will be a good approximation, but just that eventually it will be a good approximation as n –> ∞*

Confidence Intervals - Z (using Central Limit Theorem)

- Z confidence interval
$$Estimate \pm ZQ \times SE_{Estimate}$$
  - ZQ = quantile from the standard normal distribution
- sample mean = $\bar{X} \sim N(\mu, \sigma^2/n)$, with mean = μ and standard deviation = σ^2/n
- **95% confidence interval for** $\mu = \bar{X} \pm 2\sigma^2/n$ (1.96 to be more accurate)
  - probability that $\bar{X}$ is larger than $\mu + 2\sigma^2/n$ or smaller than $\mu - 2\sigma^2/n = 5\%$
  - interpretation: if we were to repeated samples of size n from the population and construct this confidence interval for each case, approximately 95% of the intervals will contain μ
- ***Note**: Poisson and binomial distributions have exact intervals that don't require CLT*
- **Wald confidence interval**
  - for Bernoulli distributions, confidence interval takes the form
$$\hat{p} \pm z_{1-\alpha/2}\sqrt{\frac{p(1-p)}{n}}$$
  - p = unknown, so use $\hat{p} = X/n$ to replace
  - $p(1-p)$ –> largest when $p = 1/2$, confidence interval becomes $\hat{p} \pm \frac{1}{\sqrt{n}}$
  - this is useful in ***roughly estimating confidence intervals***
    - generally need n = 100 for 1 decimal place, 10,000 for 2, and 1,000,000 for 3
- `binom.test(success, n)` = returns confidence interval
- **Agresti/Coull interval** (binomial distribution)
  - for smaller values of **n**, when **n** is not large enough for CLT
  - take number of successes, X, add 2
  - take number of failure, add 2
  - $\hat{p} = \frac{X+2}{n+4}$, use this to construct confidence interval (tend to be ***conservative***)
- **Poisson Interval**
  - $X \sim Poisson(\lambda t)$
    - estimate rate $\hat{\lambda} = X/t$
    - $var(\hat{\lambda}) = \lambda/t$
    - variance estimate = $\hat{\lambda}/t$
  - for small values of λ (few events larger time interval), should not use the asymptotic interval estimated here
  - as $t \to \infty$, the interval becomes the true 95% interval

Confidence Intervals - T (small samples)

- **t** Confidence Interval
$$Estimate \pm TQ \times SE_{Estimate} = \bar{X} \pm \frac{t_{n-1}S}{\sqrt{n}}$$

    - TQ = quantile from T distribution
    - t_{n-1} = relevant quantile = `qt(0.975, df = n-1)`
    - t interval assumes data is IID normal
    - works well with data distributions that are roughly symmetric/mound shaped, and ***does not*** work with skewed distributions
        - skewed distribution –> meaningless to center interval around the mean $\bar X$
        - logs/median can be used instead
    - paired observations (multiple measurements from same subjects) can be analyzed by t interval of differences
    - as more data collected (large degrees of freedom), t interval –> z interval

- William Gosset's **t** Distribution ("Student's T distribution")
    - test = Gosset's pseudoname which he published under
    - indexed/defined by ***degrees of freedom***, and becomes more like standard normal as degrees of freedom gets larger
    - thicker tails centered around 0, thus confidence interval = ***wider*** than Z interval (more mass concentrated away from the center)
    - for ***small*** sample size (value of n), normalizing the distribution by $\frac{\bar X - \mu}{S/\sqrt{n}}$ –> t distribution, ***not*** the standard normal distribution
        - S = standard deviation may be inaccurate, as the std of the data sample may not be truly representative of the population std
        - using the Z interval here thus may produce an interval that is too ***narrow***

- Independent Group **t** Intervals - Same Variance
    - compare two groups in randomized trial ("A/B Testing")
        - cannot use the paired t test because the groups are independent and may have different sample sizes
    - perform randomization to balance unobserved covariance that may otherwise affect the result
    - Confidence Interval for $\mu_y - \mu_x$

$$\bar Y - \bar X \pm t_{n_x+n_y-2,1-\alpha/2} S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}$$

        - $t_{n_x+n_y-2,1-\alpha/2}$ = relevant quantile
        - $n_x + n_y - 2$ = degrees of freedom
        - $S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}$ = standard error
        - $S_p^2 = \{(n_x - 1)S_x^2 + (n_y - 1)S_y^2\}/(n_x + n_y - 2)$ = pooled variance estimator
            - This is effectively a weighted average between the two variances, such that different sample sizes are taken in to account
        - ***Note:*** *this interval assumes* ***constant variance*** *across two groups; if variance is different, use the next interval*

- Independent Group **t** Intervals - Different Variance
    - Confidence Interval for $\mu_y - \mu_x$

$$\bar Y - \bar X \pm t_{df} \times \left(\frac{s_x^2}{n_x} + \frac{s_y^2}{n_y}\right)^{1/2}$$

        - t_{df} = relevant quantile with df as defined below
        - ***Note:*** *normalized statistic does not follow t distribution but can be approximated through the formula with df defined below*

- $$df = \frac{\left(S_x^2/n_x + S_y^2/n_y\right)^2}{\left(\frac{S_x^2}{n_x}\right)^2/(n_x-1) + \left(\frac{S_y^2}{n_y}\right)^2/(n_y-1)}$$
- $\left(\frac{s_x^2}{n_x} + \frac{s_y^2}{n_y}\right)^{1/2}$ = standard error

- Comparing other kinds of data
  - binomial –> relative risk, risk difference, odds ratio
  - binomial –> Chi-squared test, normal approximations, exact tests
  - count –> Chi-squared test, exact tests
- R commands
  - t Confidence Intervals
    - `mean + c(-1, 1) * qt(0.975, n - 1) * std / sqrt(n)`
      - ***c(-1, 1)*** = plus and minus, ±
  - Difference Intervals (all equivalent)
    - `mean2 - mean1 + c(-1, 1) * qt(0.975, n - 1) * std / sqrt(n)`
      - ***n*** = number of paired observations
      - ***qt(0.975, n - 1)*** = relevant quantile for paired
      - ***qt(0.975, n_x + n_y - 2)*** = relevant quantile for independent
    - `t.test(mean2 - mean1)`
    - `t.test(data2, data1, paired = TRUE, var.equal = TRUE)`
      - ***paired*** = whether or not the two sets of data are paired (same subjects different observations for treatment) <– `TRUE` for paired, `FALSE` for independent
      - ***var.equal*** = whether or not the variance of the datasets should be treated as equal <– `TRUE` for same variance, `FALSE` for unequal variances
    - `t.test(extra ~ I(relevel(group, 2)), paired = TRUE, data = sleep)`
      - ***relevel(factor, ref)*** = reorders the levels in the factor so that "ref" is changed to the first level –> doing this here is so that the second set of measurements come first (1, 2 –> 2, 1) in order to perform mean$_2$ - mean$_1$
      - ***I(object)*** = prepend the class "AsIs" to the object
      - ***Note***: *I(relevel(group, 2)) = explanatory variable, must be* ***factor*** *and have* ***two levels***

Hypothesis Testing

- Hypothesis testing = making decisions using data
    - **null** hypothesis ($\mathbf{H}_0$) = status quo
    - assumed to be ***true*** –> statistical evidence required to reject it for **alternative** or "research" hypothesis ($\mathbf{H}_a$)
        - alternative hypothesis typically take form of >, < or ≠
    - Results

Truth	Decide	Result
H_0	H_0	Correctly accept null
H_0	H_a	Type I error
H_a	H_a	Correctly reject null
H_a	H_0	Type II error

- α = Type I error rate
    - probability of ***rejecting*** the null hypothesis when the hypothesis is ***correct***
    - $\alpha = 0.5$ –> standard for hypothesis testing
    - ***Note***: *as Type I error rate increases, Type II error rate decreases and vice versa*
- for large samples (large n), use the **Z Test** for $H_0 : \mu = \mu_0$
    - H_a**:**
        - $H_1 : \mu < \mu_0$
        - $H_2 : \mu \neq \mu_0$
        - $H_3 : \mu > \mu_0$
    - Test statistic $TS = \frac{\bar X - \mu_0}{S/\sqrt{n}}$
    - Reject the null hypothesis H_0 when
        - $H_1 : TS \leq Z_\alpha$ OR $-Z_{1-\alpha}$
        - $H_2 : |TS| \geq Z_{1-\alpha/2}$
        - $H_3 : TS \geq Z_{1-\alpha}$
    - ***Note***: *In case of $\alpha = 0.5$ (most common), $Z_{1-\alpha} = 1.645$ (95 percentile)*
    - α = low, so that when H_0 is rejected, original model –> wrong or made an error (low probability)
- For small samples (small n), use the **T Test** for $H_0 : \mu = \mu_0$
    - H_a**:**
        - $H_1 : \mu < \mu_0$
        - $H_2 : \mu \neq \mu_0$
        - $H_3 : \mu > \mu_0$
    - Test statistic $TS = \frac{\bar X - \mu_0}{S/\sqrt{n}}$
    - Reject the null hypothesis H_0 when
        - $H_1 : TS \leq T_\alpha$ OR $-T_{1-\alpha}$
        - $H_2 : |TS| \geq T_{1-\alpha/2}$
        - $H_3 : TS \geq T_{1-\alpha}$
    - ***Note***: *In case of $\alpha = 0.5$ (most common), $T_{1-\alpha}$ =* `qt(.95, df = n-1)`
    - R commands for T test:

        - `t.test(vector1 - vector2)`
        - `t.test(vector1, vector2, paired = TRUE)`
            - `alternative` argument can be used to specify one-sided tests: `less` or `greater`
            - `alternative` default = `two-sided`
        - prints test statistic (`t`), degrees of freedom (`df`), `p-value`, 95% confidence interval, and mean of sample
            - confidence interval in units of data, and can be used to intepret the practical significance of the results

- **rejection region** = region of TS values for which you reject H_0
- **power** = probability of rejecting H_0
    - power is used to calculate sample size for experiments
- **two-sided tests** –> $H_a : \mu \neq \mu_0$
    - reject H_0 only if test statistic is too larger/small
    - for $\alpha = 0.5$, split equally to 2.5% for upper and 2.5% for lower tails
        - equivalent to $|TS| \geq T_{1-\alpha/2}$
        - example: for T test, `qt(.975, df)` and `qt(.025, df)`
    - ***Note**: failing to reject one-sided test = fail to reject two-sided*
- **tests vs confidence intervals**
    - $(1 - \alpha)$% confidence interval for μ = set of all possible values that fail to reject H_0
    - if $(1 - \alpha)$% confidence interval contains μ_0, fail to reject H_0
- **two-group intervals/test**
    - Rejection rules the same
    - Test H_0: $\mu_1 = \mu_2$ –> $\mu_1 - \mu_2 = 0$
    - Test statistic:
    $$\frac{Estimate - H_0 Value}{SE_{Estimate}} = \frac{\bar X_1 - \bar X_2 - 0}{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}}$$
    - R Command
        - `t.test(values ~ factor, paired = FALSE, var.equal = TRUE, data = data)`
            - `paired = FALSE` –> independent values
            - `factor` argument must have only two levels
- **p values**
    - most common measure of statistical significance
    - **p-value** = probability under the null hypothesis of obtaining evidence as extreme or more than that of the obtained
        - Given that H_0 is true, how likely is it to obtain the result (test statistic)?
    - **attained significance level** = smallest value for α for which H_0 is rejected –> equivalent to p-value
        - if p-value $< \alpha$, reject H_0
        - for two-sided tests, double the p-values
    - if p-value is small, either H_0 is true AND the obeserved is a rare event **OR** H_0 is false
    - R Command
        - p-value = `pt(statistic, df, lower.tail = FALSE)`
            - `lower.tail = FALSE` = returns the probability of getting a value from the t distribution that is larger than the test statistic

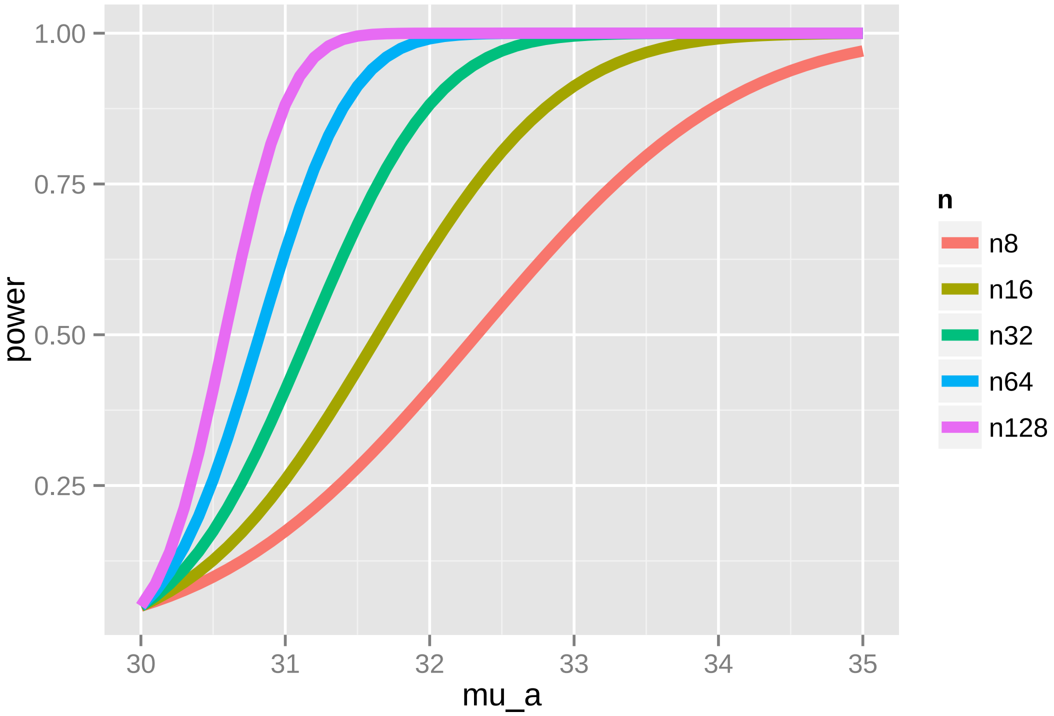
- ∗ Binomial (coin flips)
  - · probability of getting x results out of n trials and event probability of p = `pbinom(x, size = n, prob = p, lower.tail = FALSE)`

  - · two-sided interval (testing for ≠): find the smaller of two one-sided intervals (X < value, X > value), and double the result
  - · ***Note**: `lower.tail = FALSE` = strictly greater*
- ∗ Poisson
  - · probability of getting x results given the rate r = `ppois(x - 1, r, lower.tail = FALSE)`
  - · `x - 1` is used here because the upper tail includes the specified number (since we want greater than x, we start at x - 1)
  - · `r` = events that should occur given the rate (multiplied by 100 to yield an integer)
  - · ***Note**: `lower.tail = FALSE` = strictly greater*

Power

- **Power** = probability of rejecting the null hypothesis when it is false (the more power the better)
  - most often used in designing studies so that there's a reasonable chance to detect the alternative hypothesis if the alternative hypothesis is true
- β = probability of type II error = failing to reject the null hypothesis when it's false
- power = $1 - \beta$
- ***example***
  - $H_0 : \mu = 30 \to \bar{X} \sim N(\mu_0, \sigma^2/n)$
  - $H_a : \mu > 30 \to \bar{X} \sim N(\mu_a, \sigma^2/n)$
  - Power:
$$Power = P\left(\frac{\bar{X} - 30}{s/\sqrt{n}} > t_{1-\alpha,n-1} \; ; \; \mu = \mu_a\right)$$
    - ***Note:*** *the above function depends on value of* μ_a
    - ***Note:*** *as* μ_a *approaches 30, power approaches* α
  - assuming the sample mean is normally distributed, H_0 is rejected when $\frac{\bar{X}-30}{\sigma/\sqrt{n}} > Z_{1-\alpha}$
  - or, $\bar{X} > 30 + Z_{1-\alpha}\frac{\sigma}{\sqrt{n}}$
- R commands:
  - `alpha = 0.05; z = qnorm(1-alpha)` –> calculates $Z_{1-\alpha}$
  - `pnorm(mu0 + z * sigma/sqrt(n), mean = mua, sd = sigma/sqrt(n), lower.tail = FALSE)` –> calculates the probability of getting a sample mean that is larger than $Z_{1-\alpha}\frac{\sigma}{\sqrt{n}}$ given that the population mean is μ_a
    - ***Note:*** *using* `mean = mu0` *in the function would = alpha*
  - Power curve behavior
    - Power increases as mu_a increases –> we are more likely to detect the difference in mu_a and mu_0
    - Power increases as **n** increases –> with more data, more likely to detect any alternative mu_a

```r
library(ggplot2)
mu0 = 30; mua = 32; sigma = 4; n = 16
alpha = 0.05
z = qnorm(1 - alpha)
nseq = c(8, 16, 32, 64, 128)
mu_a = seq(30, 35, by = 0.1)
power = sapply(nseq, function(n)
    pnorm(mu0 + z * sigma / sqrt(n), mean = mu_a, sd = sigma / sqrt(n),
          lower.tail = FALSE)
    )
colnames(power) <- paste("n", nseq, sep = "")
d <- data.frame(mu_a, power)
library(reshape2)
d2 <- melt(d, id.vars = "mu_a")
names(d2) <- c("mu_a", "n", "power")
g <- ggplot(d2,
            aes(x = mu_a, y = power, col = n)) + geom_line(size = 2)
g
```



- **Solving for Power**
  - When testing $H_a : \mu > \mu_0$ (or $<$ or $\neq$)

    $$Power = 1 - \beta = P\left(\bar{X} > \mu_0 + Z_{1-\alpha}\frac{\sigma}{\sqrt{n}}; \mu = \mu_a\right)$$

    where $\bar{X} \sim N(\mu_a, \sigma^2/n)$
  - Unknowns = μ_a, σ, n, β
  - Knowns = μ_0, α
  - Specify any 3 of the unknowns and you can solve for the remainder; most common are two cases
    1. Given power desired, mean to detect, variance that we can tolerate, find the **n** to produce desired power (designing experiment/trial)
    2. Given the size **n** of the sample, find the power that is achievable (finding the utility of experiment)
  - ***Note**: for $H_a : \mu \neq mu_0$, calculated one-sided power using $z_{1-\alpha/2}$; however, the power calculation here exclusdes the probability of getting a large TS in the opposite direction of the truth, but this is only applicable when μ_a and μ_0 are close together*
- **Power Behavior**
  - Power increases as α becomes larger
  - Power of one-sided test $>$ power of associated two-sided test
  - Power increases as μ_a gets further away from μ_0
  - Power increases as **n** increases (sample mean has less variability)
  - Power increases as σ decreases (again less variability)
  - Power usually depends only $\frac{\sqrt{n}(\mu_a - \mu_0)}{\sigma}$, and not μ_a, σ, and n
    - **effect size** = $\frac{\mu_a - \mu_0}{\sigma}$ –> unit free, can be interpretted across settings
- **T-test Power**

- for Gossett's T test,

$$Power = P\left(\frac{\bar{X} - \mu_0}{S/\sqrt{n}} > t_{1-\alpha,n-1}; \mu = \mu_a\right)$$

  - $\frac{\bar{X}-\mu_0}{S/\sqrt{n}}$ does not follow a t distribution if the true mean is μ_a and NOT μ_0 –> follows a non-central t distribution instead
- `power.t.test` –> evaluates the non-central t distribution and solves for a parameter given all others are specified
  - `power.t.test(n = 16, delta = 0.5, sd = 1, type = "one.sample", alt = "one.sided")$power` –> calculates power with inputs of n, difference in means, and standard deviation
    - `delta` = argument for difference in means
    - ***Note**: since effect size = `delta/sd`, as `n`, `type`, and `alt` are held constant, any distribution with the same effect size will have the same power*
  - `power.t.test(power = 0.8, delta = 0.5, sd = 1, type = "one.sample", alt = "one.sided")$n` –> calculates size n with inputs of power, difference in means, and standard deviation
    - ***Note**: n should always be rounded up (ceiling)*

Multiple Testing

- Hypothesis testing/significant analysis commonly overused
- correct for multiple testing to avoid false positives/conclusions (two key components)
    1. error measure
    2. correction
- multiple testing is needed because of the increase in ubiquitous data collection technology and analysis
    - DNA sequencing machines
    - imaging patients in clinical studies
    - electronic medical records
    - individualized movement data (fitbit)

Type of Errors

```
|                  | Actual $H_0$ = True | Actual $H_a$ = True |  Total
```

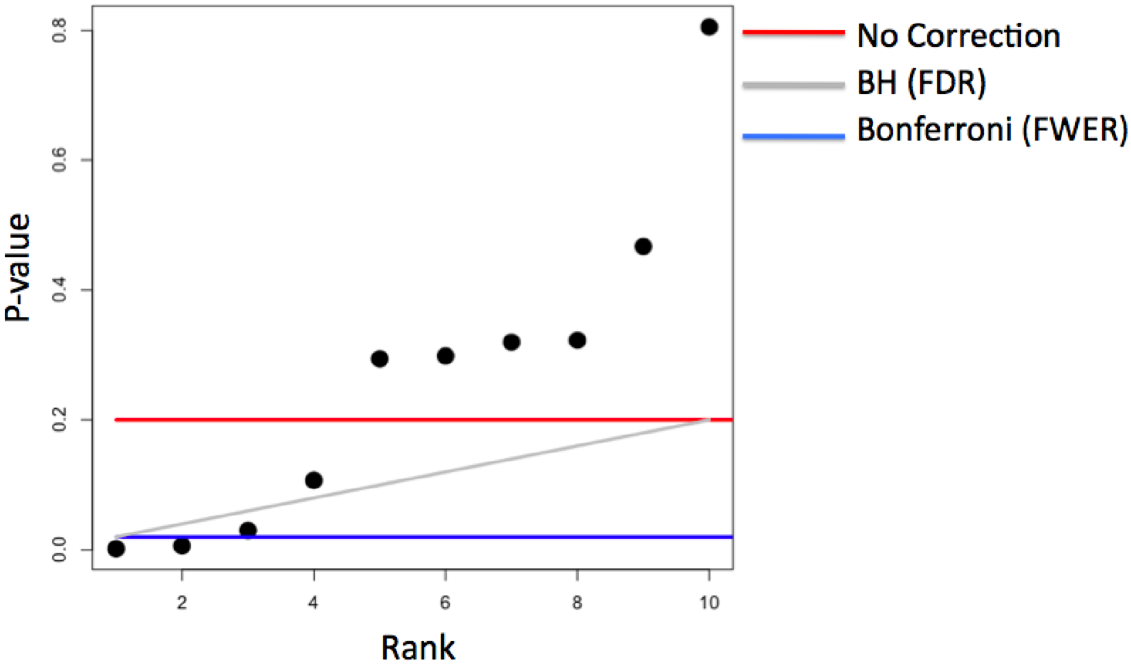
——————-|————|————|——— Conclude $H_0$ = True (non-significant) | U | T | $m-R$ Conclude $H_a$ = True (significant) | V | S | R **Total** | m_0 | $m-m_0$ | m

- m_0 = number of true null hypotheses, or cases where $H_0$ = actually true (unknown)
- $m-m_0$ = number of true alternative hypotheses, or cases where $H_a$ = actually true (unknown)
- R = number of null hypotheses rejected, or cases where $H_a$ = concluded to be true (measurable)
- $m-R$ = number of null hypotheses that failed to be rejected, or cases where $H_0$ = concluded to be true (measurable)
- V = Type I Error / false positives, concludes $H_a$ = True when $H_0$ = actually True
- T = Type II Error / false negatives, concludes $H_0$ = True when $H_a$ = actually True
- S = true positives, concludes $H_a$ = True when $H_a$ = actually True
- U = true negatives, concludes $H_0$ = True when $H_0$ = actually True

Error Rates

- ***false positive rate*** = rate at which false results are called significant $E[\frac{V}{m_0}]$ –> average fraction of times that $H_a$ is claimed to be true when $H_0$ is actually true
    - ***Note****: mathematically equal to type I error rate –> false positive rate is associated with a post-prior result, which is the expected number of false positives divided by the total number of hypotheses under the real combination of true and non-true null hypotheses (disregarding the "global null" hypothesis). Since the false positive rate is a parameter that is not controlled by the researcher, it cannot be identified with the significance level, which is what determines the type I error rate.*
- ***family wise error rate (FWER)*** = probabilit of at least one false positive $Pr(V \geq 1)$
- ***false discovery rate (FDR)*** = rate at which claims of significance are false $E[\frac{V}{R}]$
- **controlling error rates (adjusting α)**
    - false positive rate
        - if we call all $P < \alpha$ significant (reject $H_0$), we are expected to get $\alpha \times m$ false positives, where m = total number of hypothesis test performed
        - with high values of m, false positive rate is very large as well

- family-wise error rate (FWER)
    - controlling FWER = controlling the probability of even one false positive
    - *bonferroni* correction (oldest multiple testing correction)
        - for m tests, we want $Pr(V \geq 1) < \alpha$
        - calculate P-values normally, and deem them significant if and only if $P < \alpha_{fewer} = \alpha/m$
    - easy to calculate, but tend to be very ***conservative***
- false discovery rate (FDR)
    - most popular correction = controlling FDR
    - for m tests, we want $E[\frac{V}{R}] \leq \alpha$
    - calculate P-values normally and sort some from smallest to largest $->$ $P_{(1)}, P_{(1)}, ..., P_{(m)}$
    - deem the P-values significant if $P_{(i)} \leq \alpha \times \frac{i}{m}$
    - easy to calculate, less conservative, but allows for more false positives and may behave strangely under dependence (related hypothesis tests/regression with different variables)
- ***example***
    - 10 P-values with $\alpha = 0.20$



- **adjusting for p-values**
    - ***Note**: changing P-values will fundamentally change their properties but they can be used directly without adjusting /alpha*
    - *bonferroni* (FWER)
        - $P_i^{fewer} = max(mP_i, 1)$ $->$ since p cannot exceed value of 1
        - deem P-values significant if $P_i^{fewer} < \alpha$
        - similar to controlling FWER

Example

```
set.seed(1010093)
pValues <- rep(NA,1000)
for(i in 1:1000){
  x <- rnorm(20)
  # First 500 beta=0, last 500 beta=2
  if(i <= 500){y <- rnorm(20)}else{ y <- rnorm(20,mean=2*x)}
  # calculating p-values by using linear model; the [2, 4] coeff in result = pvalue
  pValues[i] <- summary(lm(y ~ x))$coeff[2,4]
}
# Controls false positive rate
trueStatus <- rep(c("zero","not zero"),each=500)
table(pValues < 0.05, trueStatus)
```

```
##        trueStatus
##         not zero zero
##   FALSE        0  476
##   TRUE       500   24
```

```
# Controls FWER
table(p.adjust(pValues,method="bonferroni") < 0.05,trueStatus)
```

```
##        trueStatus
##         not zero zero
##   FALSE       23  500
##   TRUE       477    0
```

```
# Controls FDR (Benjamin Hochberg)
table(p.adjust(pValues,method="BH") < 0.05,trueStatus)
```

```
##        trueStatus
##         not zero zero
##   FALSE        0  487
##   TRUE       500   13
```

Resample Inference

- **Bootstrap** = useful tool for constructing confidence intervals and caclulating standard errors for difficult statistics
  - ***principle*** = if a statistic's (i.e. median) sampling distribution is unknown, then use distribution defined by the data to approximate it
  - ***procedures***
    1. simulate n observations **with replacement** from the observed data –> results in 1 simulated complete data set
    2. calculate desired statistic (i.e. median) for each simulated data set
    3. repeat the above steps B times, resulting in B simulated statistics
    4. these statistics are approximately drawn from the sampling distribution of the true statistic of n observations
    5. perform one of the following
       - plot a histogram
       - calculate standard deviation of the statistic to estimate its standard error
       - take quantiles (2.5th and 97.5th) as a confidence interval for the statistic ("*bootstrap CI*")
  - ***example***
    - Bootstrap procedure for calculating confidence interval for the median from a data set of n observations –> approximate sampling distribution

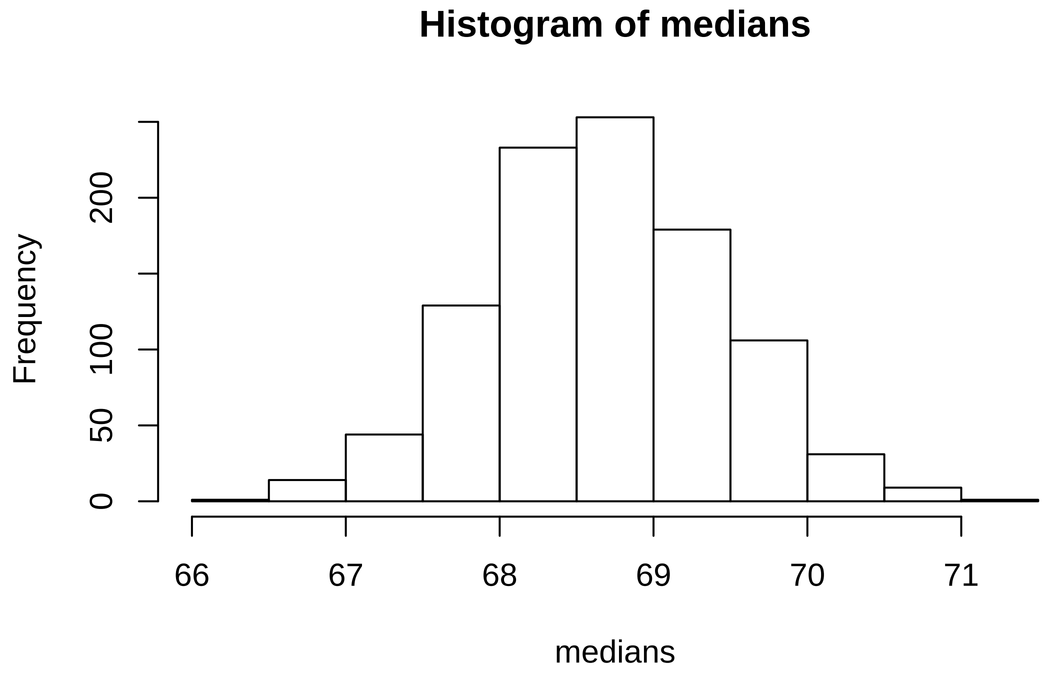
```r
# load data
library(UsingR); data(father.son)
# observed dataset
x <- father.son$sheight
# number of simulated statistic
B <- 1000
# generate samples
resamples <- matrix(
    sample(x,               # sample to draw frome
           n * B,           # draw B datasets with n observations each
           replace = TRUE), # cannot draw n*B elements from x (has n elements) without replacement
    B, n)                   # arrange results into n x B matrix
                            # (every row = bootstrap sample with n observations)
# take median for each row/generated sample
medians <- apply(resamples, 1, median)
# estimated standard error of median
sd(medians)
```

```
## [1] 0.76595
```

```r
# confidence interval of median
quantile(medians, c(.025, .975))
```

```
##     2.5%    97.5%
## 67.18292 70.16488
```

```r
# histogram of bootstraped samples
hist(medians)
```

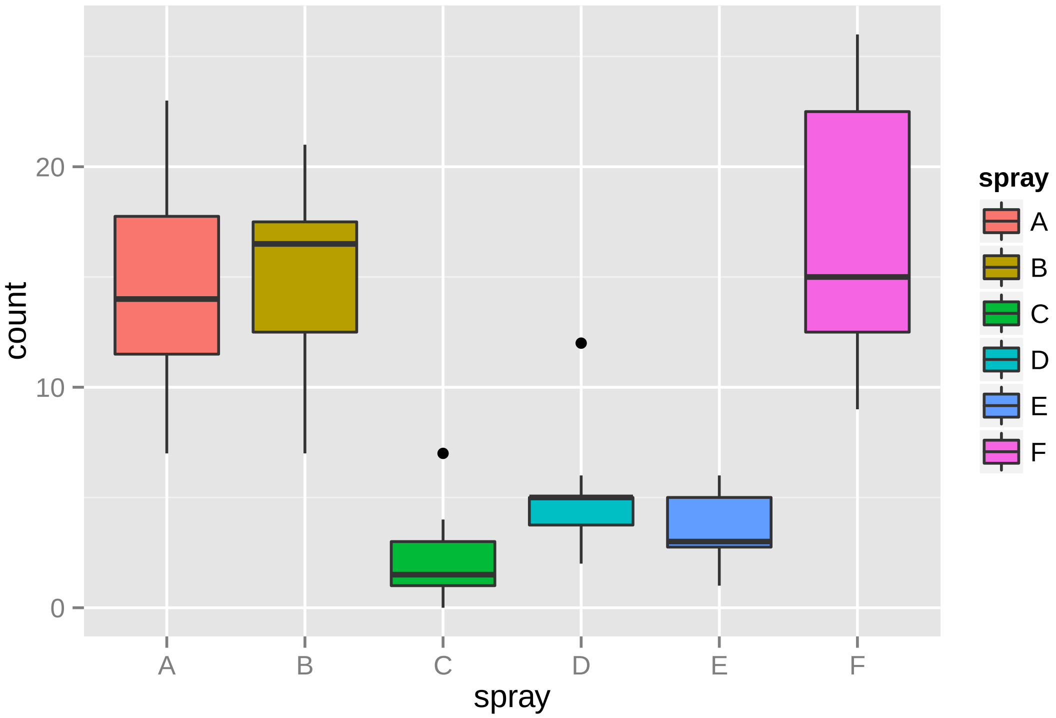


- ***Note:*** *better percentile bootstrap confidence interval = "bias corrected and accelerated interval" in* `bootstrap` *package*
- **Permutation Tests**
  - ***procedures***
    - compare groups of data and test the null hypothesis that the distribution of the observations from each group = same
      - ***Note****: if this is true, then group labels/divisions are irrelevant*
    - permute the labels for the groups
    - recalculate the statistic
      - Mean difference in counts
      - Geometric means
      - T statistic
    - Calculate the percentage of simulations wherethe simulated statistic was more extreme (toward the alternative) than the observed
  - ***variations***

Data type	Statistic	Test name
Ranks	rank sum	rank sum test
Binary	hypergeometric prob	Fisher's exact test
Raw data		ordinary permutation test

- ***Note****: randomization tests are exactly permutation tests, with a different motivation*
- For matched data, one can randomize the signs
- For ranks, this results in the **signed rank test**
- Permutation strategies work for regression by permuting a regressor of interest
- Permutation tests work very well in multivariate settings

- ***example***
    - we will compare groups **B** and **C** in this dataset for null hypothesis H_0 : there are no difference between the groups



- we will compare groups **B** and **C** in this dataset for null hypothesis H_0 : there are no difference between the groups

```
# subset to only "B" and "C" groups
subdata <- InsectSprays[InsectSprays$spray %in% c("B", "C"),]
# values
y <- subdata$count
# labels
group <- as.character(subdata$spray)
# find mean difference between the groups
testStat <- function(w, g) mean(w[g == "B"]) - mean(w[g == "C"])
observedStat <- testStat(y, group)
observedStat
```

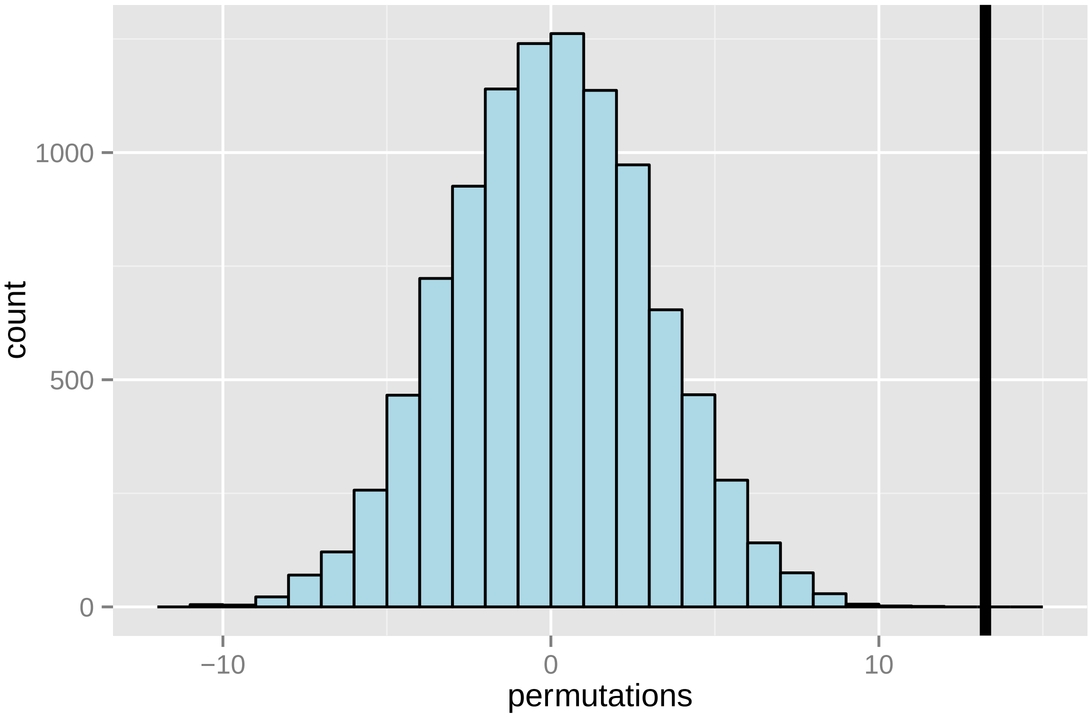
```
## [1] 13.25
```

- the observed difference between the groups is 13.25
- now we changed the resample the lables for groups **B** and **C**

```
# create 10000 permutations of the data with the labels' changed
permutations <- sapply(1 : 10000, function(i) testStat(y, sample(group)))
# find the number of permutations whose difference that is bigger than the observed
mean(permutations > observedStat)
```

```
## [1] 0
```

- we created 1000 permutations from the observed dataset, and found ***no datasets*** with mean differences between groups **B** and **C** larger than the original data
- therefore, p-value is very small and we can ***reject the null*** hypothesis with any resonable α levels
- below is the plot for the null distribution/permutations



- as we can see from the black line, the observed difference/statistic is very far from the mean –> likely 0 is ***not*** the true difference
  - with this information, formal confidence intervals can be constructed and p-values can be calculated