Statistical Inference Course Notes

Xing Su

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Overview

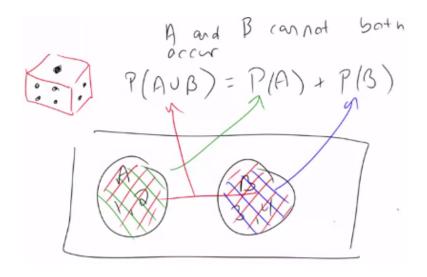
- Statistical Inference = generating conclusions about a population from a noisy sample
- Goal = extend beyond data to population
- Statistical Inference = only formal system of inference we have
- ullet many different modes, but ${f two}$ broad flavors of inference (inferential paradigms): ${m Bayesian}$ vs ${m Frequencist}$
 - 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

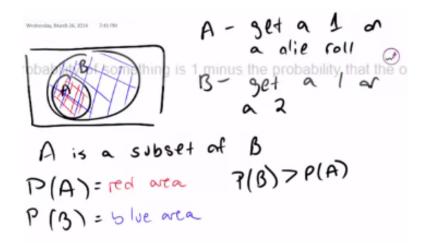
- Probability = the study of quantifying the likelihood of particular events occurring
 - given a random experiment, *probability* = population quantity that summarizes the randomness
 - * not in the data at hand, but a conceptual quantity that exist in the population that we want to estimate

General Probability Rules

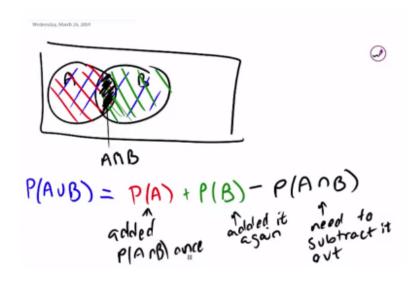
- discovered by Russian mathematician Kolmogorov, also known as "Probability Calculus"
- probability = function of any set of outcomes and assigns it a number between 0 and 1
 - $-0 \le P(E) \le 1$, where E = event
- probability that nothing occurs = 0 (impossible, have to roll dice to create outcome), 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 $\langle P(B) \rangle$



• 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

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

- \bullet 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

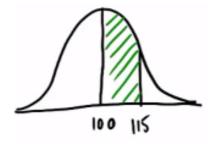
- random variable = numeric outcome of experiment
- discrete (what you can count/categories) = assign probabilities to every number/value the variable can take
 - coin flip, rolling a die, web traffic in a day
- continuous (any number within a continuum) = assign probabilities to the range the variable 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 \rightarrow linking sample to population

Probability Mass Function (PMF)

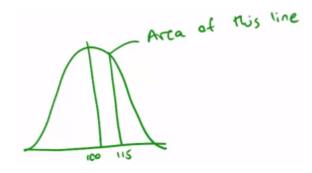
- evaluates the probability that the **discrete random variable** takes on a specific value
 - measures the chance of a particular outcome happening
 - always ≥ 0 for every possible outcome
 - $-\sum$ possible values that the variable can take = 1
- Bernoulli distribution example
 - $-X = 0 \rightarrow tails, X = 1 \rightarrow heads$
 - * 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 $\rightarrow p(x) = (\theta)^x (1-\theta)^{1-x}$
- 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 ≥ 0 everywhere
 - total area under curve 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)

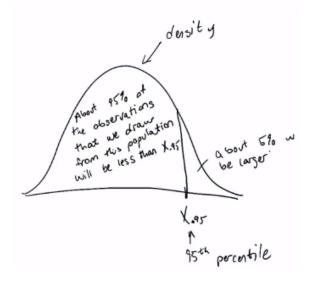
- CDF of a random variable $X = \text{probability that the random variable is } \leq \text{value } x$
 - $-F(x) = P(X \le x) = \text{applies when } X \text{ is discrete/continuous}$
- PDF = derivative of CDF
 - integrate PDF \rightarrow CDF
 - * integrate(function, lower=0, upper=1) \rightarrow can be 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 = 50^{th} percentile
 - $-\alpha\%$ of the possible outcomes lie below it



- 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, $D^c = \text{subject does not}$
- sensitivity = P(+ | D) = probability that the test is positive given that the subject has the disease (the higher the better)
- specificity = $P(-|D^c)$ = 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%

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

$$= \frac{P(+ \mid D)P(D)}{P(+ \mid D)P(D) + \{1 - P(- \mid D^c)\}\{1 - P(D)\}}$$

$$= \frac{.997 \times .001}{.997 \times .001 + .015 \times .999}$$

$$= .062$$

- ullet low positive predictive value o 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

• diagnostic likelihood ratio of a positive test result is defined as

$$DLR_{+} = \frac{sensitivity}{1 - specificity} = \frac{P(+ \mid D)}{P(+ \mid D^{c})}$$

• diagnostic likelihood ratio of a negative test result is defined as

$$DLR_{-} = \frac{1 - sensitivity}{specificity} = \frac{P(- \mid D)}{P(- \mid D^c)}$$

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

$$P(D \mid +) = \frac{P(+ \mid D)P(D)}{P(+ \mid D)P(D) + P(+ \mid D^c)P(D^c)}$$
(1)

$$P(D^c \mid +) = \frac{P(+ \mid D^c)P(D^c)}{P(+ \mid D)P(D) + P(+ \mid D^c)P(D^c)}$$
(2)

• if we divide equation (1) over (2), the quantities over have the same denominator so we get the following

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

which can also be written as

post-test odds of D =
$$DLR_+ \times$$
 pre-test odds of D

- $\mathbf{odds} = p/(1-p)$
- $-\frac{P(D)}{P(D^c)} = \frac{P(D)}{\text{pre-test odds}}$, or odds of disease in absence of test
- $-\frac{P(D \mid +)}{P(+ \mid D^c)} =$ **post-test odds**, or odds of disease given a positive test result
- $-DLR_{+}$ = factor by which the odds in the presence of a positive test can be multiplied to obtain the post-test odds
- $-DLR_{-}$ = relates the decrease in odds of disease after a negative result
- following the previous example, for sensitivity of 0.997 and specificity of 0.985, so the diagnostic likelihood ratios are as follows

$$DLR_{+} = .997/(1 - .985) = 66$$
 $DLR_{-} = (1 - .997)/.985 = 0.003$

- this indicates that the result of the positive test is the odds of disease is 66 times the pretest 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 = $linear \rightarrow E(aX + bY) = aE(X) + bE(Y)$
- 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 as

$$E[X] = \sum_{x} x p(x)$$

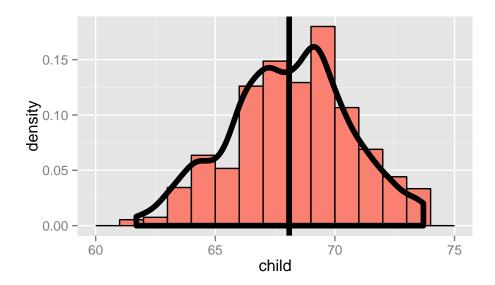
where the sum is taken over all possible values of x

- * E[X] = center of mass of a collection of location and weights x, p(x)
- * coin flip example: $E[X] = 0 \times (1-p) + 1 \times p = p$
- continuous variable
 - * for X with PDF 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
 - $\cdot PDF = f(x)$
 - f(x) = area under the PDF 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 $p(x_i) = 1/n$

```
# load relevant packages
library(UsingR); data(galton); library(ggplot2)
# plot galton data
g <- ggplot(galton, aes(x = child))
# add histogram for children data
g <- g + geom_histogram(fill = "salmon", binwidth=1, aes(y=..density..), colour="black")
# add density smooth
g <- g + geom_density(size = 2)
# add vertical line
g <- g + geom_vline(xintercept = mean(galton$child), size = 2)
# print graph
g</pre>
```



- average of random variables = a new random variable where 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 \rightarrow estimates average of the population
 - if E[sample mean] = population mean, then estimator for the sample mean is**unbiased**
 - * [derivation] let $X_1, X_2, X_3, \ldots X_n$ be a collection of n samples from the population with mean μ
 - * mean of this sample

$$\bar{X} = \frac{X_1 + X_2 + X_3 + . + X_n}{n}$$

* since E(aX) = aE(X), the expected value of the mean is can be written as

$$E\left[\frac{X_1 + X_2 + X_3 + \dots + X_n}{n}\right] = \frac{1}{n} \times [E(X_1) + E(X_2) + E(X_3) + \dots + E(X_n)]$$

* since each of the $E(X_i)$ is drawn from the population with mean μ , the expected value of each sample should be

$$E(X_i) = \mu$$

* therefore

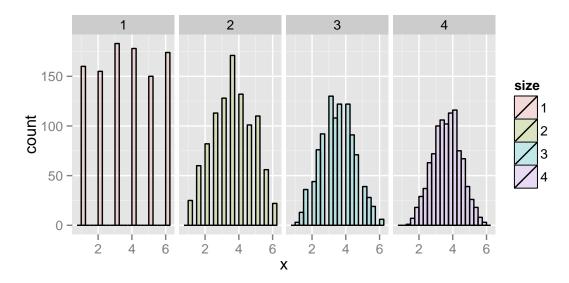
$$E\left[\frac{X_1 + X_2 + X_3 + \dots + X_n}{n}\right] = \frac{1}{n} \times [E(X_1) + E(X_2) + E(X_3) + \dots + E(X_n)]$$

$$= \frac{1}{n} \times [\mu + \mu + \mu + \dots + \mu]$$

$$= \frac{1}{n} \times n \times \mu$$

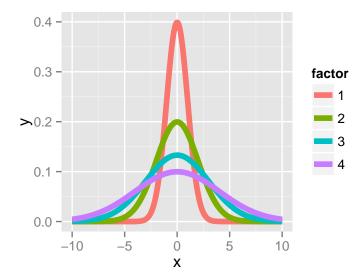
$$= \mu$$

• Note: the more data that goes into the sample mean, the more concentrated its density/mass functions are around the population mean



Variance

```
# generate x value ranges
xvals <- seq(-10, 10, by = .01)
# generate data from normal distribution for sd of 1 to 4
dat <- data.frame(
    y = c(dnorm(xvals, mean = 0, sd = 1),
        dnorm(xvals, mean = 0, sd = 2),
        dnorm(xvals, mean = 0, sd = 3),
        dnorm(xvals, mean = 0, sd = 4)),
    x = rep(xvals, 4),
    factor = factor(rep(1 : 4, rep(length(xvals), 4)))
)
# plot 4 lines for the different standard deviations
ggplot(dat, aes(x = x, y = y, color = factor)) + geom_line(size = 2)</pre>
```

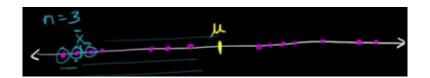


- **variance** = measure of spread or dispersion, the expected squared distance of the variable from its mean (expressed in X's units²)
 - as we can see from above, higher variances \rightarrow more spread, lower \rightarrow smaller spread
 - $Var(X) = E[(X \mu)^{2}] = E[X^{2}] E[X]^{2}$
 - standard deviation = $\sqrt{Var(X)}$ \rightarrow has same units as X
 - example
 - * for die roll, E[X] = 3.5
 - * $E[X^2] = 1^2 \times 1/6 + 2^2 \times 1/6 + 3^2 \times 1/6 + 4^2 \times 1/6 + 5^2 \times 1/6 + 6^2 \times 1/6 = 15.17$
 - * $Var(X) = E[X^2] E[X]^2 \approx 2.92$
 - example
 - * for coin flip, E[X] = p
 - $*E[X^2] = 0^2 \times (1-p) + 1^2 \times p = p$
 - * $Var(X) = E[X^2] E[X]^2 = p p^2 = p(1-p)$

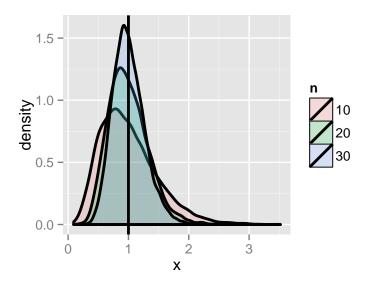
Sample Variance

• the sample variance is defined as

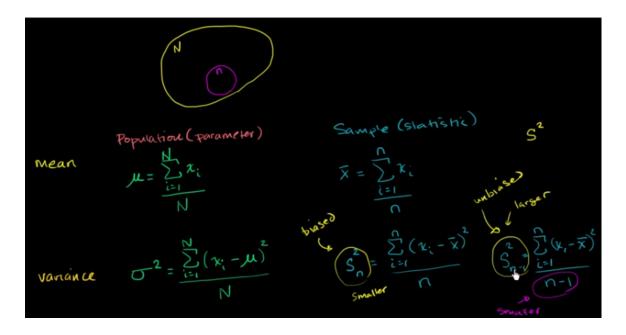
$$S^{2} = \frac{\sum_{i=1} (X_{i} - \bar{X})^{2}}{n-1}$$



- on the above line representing the population (in magenta), any subset of data (3 of 14 selected, marked in blue) 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 \rightarrow leads to more accurate estimation $\rightarrow S^2 =$ so called *unbiased estimate of population variance*
 - S^2 is a random variable, and therefore has an associated population distribution
 - * $E[S^2]$ = population variance, where S = sample standard deviation
 - st as we see from the simulation results below, with more data, the distribution for S^2 gets more concentrated around population variance



- Note: for any variable, properties of the population = parameter, estimates of properties for samples = statistic
 - below is a summary for the mean and variance for population and sample



· distribution for mean of random samples

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

• standard error (SE)

- the standard error of the mean is defined as

$$SE_{mean} = \sigma/\sqrt{n}$$

- this quantity is 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
- $S^2 = \text{sample variance}$
 - 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
- $\bar{X} = \text{sample mean}$
 - 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} \rightarrow "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 = $1/\sqrt{n}$

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

[1] 0.31781

```
# actual standard deviation of mean of standard normals
1 / sqrt(n)
```

[1] 0.3162278

- 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

Example - Standard Uniform

- standard uniform \rightarrow triangle straight line distribution \rightarrow mean = 1/2 and variance = 1/12
- means of random samples of n uniforms have have standard deviation of $1/\sqrt{12\times n}$

```
# estimated standard deviation of the sample means
sd(apply(matrix(runif(nosim * n), nosim), 1, mean))
```

[1] 0.08998201

```
# actual standard deviation of the means
1/sqrt(12*n)
```

[1] 0.09128709

Example - Poisson

- $Poisson(x^2)$ have variance of x^2
- means of random samples of $n\ Poisson(4)$ have standard deviation of $2/\sqrt{n}$

```
# estimated standard deviation of the sample means
sd(apply(matrix(rpois(nosim * n, lambda=4), nosim), 1, mean))

## [1] 0.615963

# actual standard deviation of the means
2/sqrt(n)

## [1] 0.6324555
Example - Bernoulli
```

- for p = 0.5, the Bernoulli distribution has variance of 0.25
- means of random samples of n coin flips have standard deviations of $1/(2\sqrt{n})$

```
# estimated standard deviation of the sample means
sd(apply(matrix(sample(0 : 1, nosim * n, replace = TRUE), nosim), 1, mean))

## [1] 0.156531

# actual standard deviation of the means
1/(2*sqrt(n))

## [1] 0.1581139
```

Example - Father/Son

```
# load data
library(UsingR); data(father.son);
# define son height as the x variable
x <- father.son$sheight
# n is the length
n<-length(x)
# plot histogram for son's heights
g <- ggplot(data = father.son, aes(x = sheight))
g <- g + geom_histogram(aes(y = ..density..), fill = "lightblue", binwidth=1, colour = "black")
g <- g + geom_density(size = 2, colour = "black")
g</pre>
```

```
0.15 - 20.10 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 - 20.00 -
```

```
# we calculate the parameters for variance of distribution and sample mean,
round(c(sampleVar = var(x),
    sampleMeanVar = var(x) / n,
    # as well as standard deviation of distribution and sample mean
    sampleSd = sd(x),
    sampleMeanSd = sd(x) / sqrt(n)),2)
```

sampleVar sampleMeanVar sampleSd sampleMeanSd ## 7.92 0.01 2.81 0.09

Binomial Distribution

• binomial random variable = sum of n Bernoulli variables

$$X = \sum_{i=1}^{n} X_i$$

where $X_1, \ldots, X_n = Bernoulli(p)$

- PMF is defined as

$$P(X = x) = \binom{n}{x} p^x (1 - p)^{n - x}$$

where $\binom{n}{x}$ = number of ways selecting x items out of n options without replacement or regard to order and for $x = 0, \ldots, n$

- combination or "n choose x" is defined as

$$\binom{n}{x} = \frac{n!}{x!(n-x)!}$$

- the base cases are

$$\binom{n}{n} = \binom{n}{0} = 1$$

- Bernoulli distribution = binary outcome
 - only possible outcomes
 - * 1 = "success" with probability of p
 - * 0 = "failure" with probability of 1 p
 - PMF is defined as

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

- mean = p
- variance = p(1-p)

Example

• of 8 children, whats the probability of 7 or more girls (50/50 chance)?

$$\binom{8}{7}.5^7(1-.5)^1 + \binom{8}{8}.5^8(1-.5)^0 \approx 0.04$$

calculate probability using PMF
choose(8, 7) * .5 ^ 8 + choose(8, 8) * .5 ^ 8

[1] 0.03515625

```
# calculate probability using CMF from distribution
pbinom(6, size = 8, prob = .5, lower.tail = FALSE)
```

[1] 0.03515625

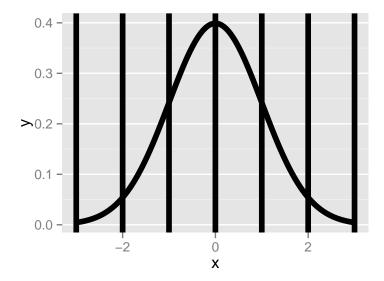
- choose(8, 7) = R function to calculate n choose x
- pbinom(6, size=8, prob =0.5, lower.tail=TRUE) = probability of 6 or less successes out of 8 samples with probability of 0.5 (CMF)
 - lower.tail=FALSE = returns the complement, in this case it's the probability of greater than 6 successes out of 8 samples with probability of 0.5

Normal Distribution

- normal/Gaussian distribution for random variable X
 - notation = $X \sim N(\mu, \sigma^2)$
 - mean $= E[X] = \mu$
 - variance = $Var(X) = \sigma^2$
 - PMF is defined as

$$f(x) = (2\pi\sigma^2)^{-1/2}e^{-(x-\mu)^2/2\sigma^2}$$

- $X \sim N(0,1) =$ standard normal distribution (standard normal random variables often denoted using $Z_1, Z_2, ...$)
 - Note: see below graph for reference for the following observations
 - $-\sim68\%$ of data/normal density \rightarrow between \pm 1 standard deviation from μ
 - ~95% of data/normal density \rightarrow between \pm 2 standard deviation from μ
 - $-\sim99\%$ of data/normal density \rightarrow between \pm 3 standard deviation from μ
 - $-\pm 1.28$ standard deviations from $\mu \to 10^{th}$ (-) and 90^{th} (+) percentiles
 - $-\pm 1.645$ standard deviations from $\mu \to 5^{th}$ (-) and 95^{th} (+) percentiles
 - $-\pm 1.96$ standard deviations from $\mu \to 2.5^{th}$ (-) and 97.5^{th} (+) percentiles
 - $-\pm 2.33$ standard deviations from $\mu \to 1^{st}$ (-) and 99^{th} (+) percentiles



• for any $X \sim N(\mu, \sigma^2)$, calculating the number of standard deviations each observation is from the mean **converts** the random variable to a **standard normal** (denoted as Z below)

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

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

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

- qnorm(n, mean=mu, sd=sd) = returns the n^{th} percentiles for the given normal distribution
- pnorm(x, mean=mu, sd=sd, lower.tail=F) = returns the probability of an observation drawn from the given distribution is larger in value than the specified threshold x

Example

- the number of daily ad clicks for a company is (approximately) normally distributed with a mean of 1020 and a standard deviation of 50
- What's the probability of getting more than 1,160 clicks in a day?

```
# calculate number of standard deviations from the mean
(1160 - 1020) / 50
```

[1] 2.8

```
# calculate probability using given distribution
pnorm(1160, mean = 1020, sd = 50, lower.tail = FALSE)
```

[1] 0.00255513

```
# calculate probability using standard normal
pnorm(2.8, lower.tail = FALSE)
```

[1] 0.00255513

- therefore, it is not very likely (0.255513% chance), since 1,160 is 2.8 standard deviations from the mean
- What number of daily ad clicks would represent the one where 75% of days have fewer clicks (assuming days are independent and identically distributed)?

```
qnorm(0.75, mean = 1020, sd = 50)
```

[1] 1053.724

• therefore, 1053.7244875 would represent the threshold that has more clicks than 75% of days

Poisson Distribution

- used to model counts
 - mean $= \lambda$
 - variance = λ
 - PMF is defined as

$$P(X = x; \lambda) = \frac{\lambda^x e^{-\lambda}}{x!}$$

where $X = 0, 1, 2, ... \infty$

- modeling uses for Poisson distribution
 - count data
 - event-time/survival \rightarrow cancer trials, some patients never develop and some do, dealing with the data for both ("censoring")
 - contingency tables \rightarrow record results for different characteristic measurements
 - approximating binomials \rightarrow instances where **n** is large and **p** is small (i.e. pollution on lung disease)
 - * $X \sim Binomial(n, p)$
 - $* \lambda = np$
 - $\text{ rates } \rightarrow X \sim Poisson(\lambda t)$
 - * $\lambda = E[X/t] \rightarrow$ expected count per unit of time
 - * t = total monitoring time
- ppois(n, lambda = lambda*t) = returns probability of n or fewer events happening given the rate λ
 and time t

Example

- number of people that show up at a bus stop can be modeled with Poisson distribution with a mean of 2.5 per hour
- after watching the bus stop for 4 hours, what is the probability that 3 or fewer people show up for the whole time?

```
# calculate using distribution
ppois(3, lambda = 2.5 * 4)
```

[1] 0.01033605

• as we can see from above, there is a 1.0336051% chance for 3 or fewer people show up total at the bus stop during 4 hours of monitoring

Example - Approximating Binomial Distribution

- flip a coin with success probability of 0.01 a total 500 times (low p, large n)
- what's the probability of 2 or fewer successes?

```
# calculate correct probability from Binomial distribution
pbinom(2, size = 500, prob = .01)
```

[1] 0.1233858

```
# estimate probability using Poisson distribution
ppois(2, lambda=500 * .01)
```

[1] 0.124652

• as we can see from above, the two probabilities (12.3385774% vs 12.3385774%) are extremely close

Asymptotics

- asymptotics = behavior of statistics as sample size $\rightarrow \infty$
- useful for simple statistical inference/approximations
- form basis for frequentist interpretation of probabilities ("Law of Large Numbers")

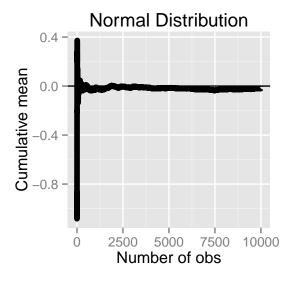
Law of Large Numbers (LLN)

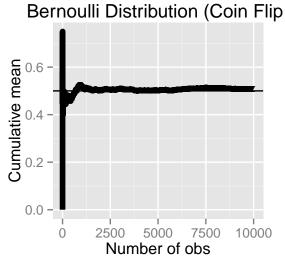
- IID sample statistic that estimates property of the sample (i.e. mean, variance) **becomes** the population statistic (i.e. population mean, population variance) as n increases
- Note: an estimator is consistent if it converges to what it is estimating
- \bullet sample mean/variance/standard deviation are all consistent estimators for their population counterparts
 - $-\bar{X}_n$ is average of the result of n coin flips (i.e. the sample proportion of heads)
 - as we flip a fair coin over and over, it **eventually converges** to the true probability of a head

Example - LLN for Normal and Bernoulli Distribution

- for this example, we will simulate 10000 samples from the normal and Bernoulli distributions respectively
- we will plot the distribution of sample means as n increases and compare it to the population means

```
# load library
library(gridExtra)
# specify number of trials
n <- 10000
# calculate sample (from normal distribution) means for different size of n
means <- cumsum(rnorm(n)) / (1 : n)</pre>
# plot sample size vs sample mean
g \leftarrow ggplot(data.frame(x = 1 : n, y = means), aes(x = x, y = y))
g <- g + geom_hline(yintercept = 0) + geom_line(size = 2)
g <- g + labs(x = "Number of obs", y = "Cumulative mean")
g <- g + ggtitle("Normal Distribution")</pre>
# calculate sample (coin flips) means for different size of n
means <- cumsum(sample(0 : 1, n , replace = TRUE)) / (1 : n)</pre>
# plot sample size vs sample mean
p \leftarrow ggplot(data.frame(x = 1 : n, y = means), aes(x = x, y = y))
p <- p + geom_hline(yintercept = 0.5) + geom_line(size = 2)</pre>
p <- p + labs(x = "Number of obs", y = "Cumulative mean")</pre>
p <- p + ggtitle("Bernoulli Distribution (Coin Flip)")</pre>
# combine plots
grid.arrange(g, p, ncol = 2)
```





• as we can see from above, for both distributions the sample means undeniably approach the respective population means as n increases

Central Limit Theorem

- one of the most important theorems in statistics
- distribution of means of IID variables approaches the standard normal as sample size n increases
- in other words, for large values of n,

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

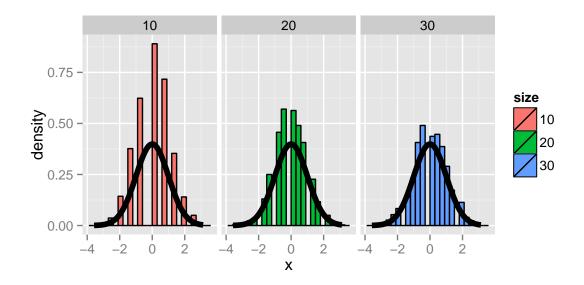
- this translates to the distribution of the sample mean \bar{X}_n is approximately $N(\mu, \sigma^2/n)$
 - distribution is centered at the population mean
 - with standard deviation = standard error of the mean
- typically the Central Limit Theorem can be applied when $n \geq 30$

Example - CLT with Bernoulli Trials (Coin Flips)

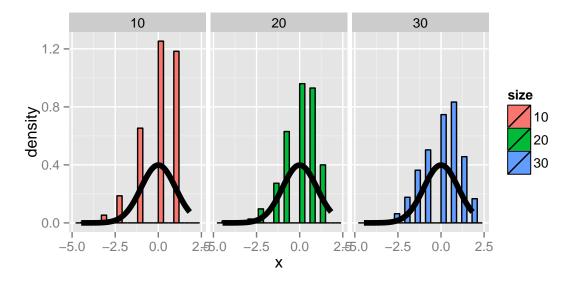
- for this example, we will simulate n flips of a possibly unfair coin
 - let X_i be the 0 or 1 result of the i^{th} flip of a possibly unfair coin
 - sample proportion, \hat{p} , is the average of the coin flips
 - $-E[X_i] = p$ and $Var(X_i) = p(1-p)$
 - standard error of the mean is $SE = \sqrt{p(1-p)/n}$
- in principle, normalizing the random variable X_i , we should get an approximately standard normal distribution

$$\frac{\hat{p}-p}{\sqrt{p(1-p)/n}} \sim N(0, 1)$$

• therefore, we will flip a coin n times, take the sample proportion of heads (successes with probability p), subtract off 0.5 (ideal sample proportion) and multiply the result by $\frac{1}{2\sqrt{n}}$ and compare it to the standard normal



• now, we can run the same simulation trials for an extremely unfair coin with p=0.9



- as we can see from both simulations, the converted/standardized distribution of the samples convert to the standard normal distribution
- 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 $n \to \infty$

Confidence Intervals - Normal Distribution/Z Intervals

ullet Z confidence interval is defined as

$$Estimate \pm ZQ \times SE_{Estimate}$$

where ZQ = quantile from the standard normal distribution

• according to CLT, the sample mean, \bar{X} , is approximately normal with mean μ and sd σ/\sqrt{n}

• 95% confidence interval for the population mean μ is defined as

$$\bar{X} \pm 2\sigma/\sqrt{n}$$

for the sample mean $\bar{X} \sim N(\mu, \sigma^2/n)$

- you can choose to use 1.96 to be more accurate for the confidence interval
- $-P(\bar{X} > \mu + 2\sigma/\sqrt{n} \text{ or } \bar{X} < \mu 2\sigma/\sqrt{n}) = 5\%$
- **interpretation**: if we were to repeatedly draw samples of size n from the population and construct this confidence interval for each case, approximately 95% of the intervals will contain μ
- confidence intervals get narrower with less variability or larger sample sizes
- Note: Poisson and binomial distributions have exact intervals that don't require CLT
- example
 - for this example, we will compute the 95% confidence interval for sons height data in inches

```
# load son height data
data(father.son); x <- father.son$sheight
# calculate confidence interval for sons height in inches
mean(x) + c(-1, 1) * qnorm(0.975) * sd(x)/sqrt(length(x))</pre>
```

[1] 68.51605 68.85209

Confidence Interval - Bernoulli Distribution/Wald Interval

- for Bernoulli distributions, X_i is 0 or 1 with success probability p and the variance is $\sigma^2 = p(1-p)$
- the confidence interval takes the form of

$$\hat{p} \pm z_{1-\alpha/2} \sqrt{\frac{p(1-p)}{n}}$$

- since the population proportion p is unknown, we can use the sampled proportion of success $\hat{p} = X/n$ as estimate
- p(1-p) is largest when p=1/2, so 95% confidence interval can be calculated by

$$\hat{p} \pm Z_{0.95} \sqrt{\frac{0.5(1-0.5)}{n}} = \hat{p} \pm qnorm(.975) \sqrt{\frac{1}{4n}}$$
$$= \hat{p} \pm 1.96 \sqrt{\frac{1}{4n}}$$
$$= \hat{p} \pm \frac{1.96}{2} \sqrt{\frac{1}{n}}$$
$$\approx \hat{p} \pm \frac{1}{\sqrt{n}}$$

- this is known as the Wald Confidence Interval and 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

• example

- suppose a random sample of 100 likely voters, 56 intent to vote for you, can you secure a victory?
- we can use the Wald interval to quickly estimate the 95% confidence interval
- as we can see below, because the interval [0.46, 0.66] contains values below 50%, victory is not guaranteed

- binom.test(k, n)\$conf = returns confidence interval binomial distribution (collection of Bernoulli trial) with k successes in n draws

```
# define sample probability and size
p = 0.56; n = 100
# Wald interval
c("WaldInterval" = p + c(-1, 1) * 1/sqrt(n))
## WaldInterval1 WaldInterval2
##
            0.46
                          0.66
# 95% confidence interval
c("95CI" = p + c(-1, 1) * qnorm(.975) * sqrt(p * (1-p)/n))
       95CI1
                 95CI2
## 0.4627099 0.6572901
# perform binomial test
binom.test(p*100, n*100)$conf.int
## [1] 0.004232871 0.007265981
## attr(,"conf.level")
## [1] 0.95
```

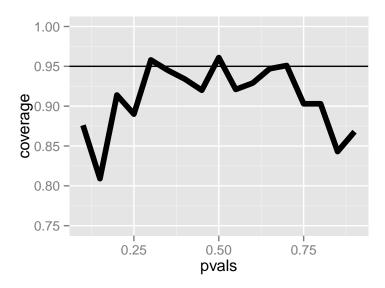
Confidence Interval - Binomial Distribution/Agresti-Coull Interval

• for a binomial distribution with smaller values of n (when n < 30, thus not large enough for CLT), often time the normal confidence intervals, as defined by

$$\hat{p} \pm z_{1-\alpha/2} \sqrt{\frac{p(1-p)}{n}}$$

do not provide accurate estimates

```
# simulate 1000 samples of size 20 each
n < -20; nosim < -1000
# simulate for p values from 0.1 to 0.9
pvals \leftarrow seq(.1, .9, by = .05)
# calculate the confidence intervals
coverage <- sapply(pvals, function(p){</pre>
    # simulate binomial data
    phats <- rbinom(nosim, prob = p, size = n) / n</pre>
    # calculate lower 95% CI bound
    11 <- phats - qnorm(.975) * sqrt(phats * (1 - phats) / n)</pre>
    # calculate upper 95% CI bound
    ul <- phats + qnorm(.975) * sqrt(phats * (1 - phats) / n)
    # calculate percent of intervals that contain p
    mean(11  p)
})
# plot CI results vs 95%
ggplot(data.frame(pvals, coverage), aes(x = pvals, y = coverage)) + geom_line(size = 2) + geom_hline(yi
```



- as we can see from above, the interval do not provide adequate coverage as 95% confidence intervals (frequently only provide 80 to 90% coverage)
- we can construct the **Agresti-Coull Interval**, which is defined uses the adjustment

$$\hat{p} = \frac{X+2}{n+4}$$

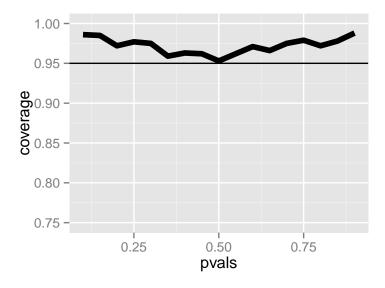
where we effectively add 2 to number of successes, X, and add 2 to number of failure

• therefore the interval becomes

$$\frac{X+2}{n+4} \pm z_{1-\alpha/2} \sqrt{\frac{p(1-p)}{n}}$$

- Note: interval tend to be conservative
- example

```
# simulate 1000 samples of size 20 each
n \leftarrow 20; nosim \leftarrow 1000
# simulate for p values from 0.1 to 0.9
pvals \leftarrow seq(.1, .9, by = .05)
# calculate the confidence intervals
coverage <- sapply(pvals, function(p){</pre>
    # simulate binomial data with Agresti/Coull Interval adjustment
    phats <- (rbinom(nosim, prob = p, size = n) + 2) / (n + 4)
        # calculate lower 95% CI bound
    11 <- phats - qnorm(.975) * sqrt(phats * (1 - phats) / n)</pre>
    # calculate upper 95% CI bound
    ul <- phats + qnorm(.975) * sqrt(phats * (1 - phats) / n)
    # calculate percent of intervals that contain p
    mean(ll  p)
# plot CI results vs 95%
ggplot(data.frame(pvals, coverage), aes(x = pvals, y = coverage)) + geom_line(size = 2) + geom_hline(yi
```



- $\bullet\,$ as we can see from above, the coverage is much better for the 95% interval
- in fact, all of the estimates are more conservative as we previously discussed, indicating the Agresti-Coull intervals are *wider* than the regular confidence intervals

Confidence Interval - Poisson Interval

- for $X \sim Poisson(\lambda t)$
 - estimate rate $\hat{\lambda} = X/t$
 - $-var(\hat{\lambda}) = \lambda/t$
 - variance estimate = $\hat{\lambda}/t$
- so the confidence interval is defined as

$$\hat{\lambda} \pm z_{1-\alpha/2} \sqrt{\frac{\lambda}{t}}$$

- however, for small values of λ (few events larger time interval), we **should not** use the asymptotic interval estimated
- example
 - * for this example, we will go through a specific scenario as well as a simulation exercise to demonstrate the ineffectiveness of asymptotic intervals for small values of λ
 - * nuclear pump failed 5 times out of 94.32 days, give a 95% confidence interval for the failure rate per day?
 - * poisson.test(x, T)\$conf = returns Poisson 95% confidence interval for given x occurrence over T time period

```
# define parameters
x <- 5; t <- 94.32; lambda <- x / t
# calculate confidence interval
round(lambda + c(-1, 1) * qnorm(.975) * sqrt(lambda / t), 3)</pre>
```

[1] 0.007 0.099

```
# return accurate confidence interval from poisson.test
poisson.test(x, T = 94.32)$conf
```

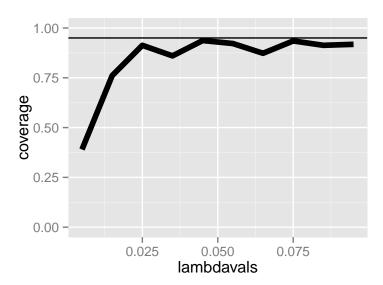
```
## [1] 0.01721254 0.12371005

## attr(,"conf.level")

## [1] 0.95

# small lambda simulations
```

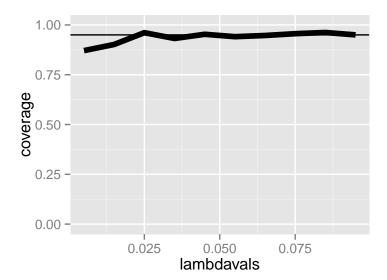
```
# small lambda simulations
lambdavals <- seq(0.005, 0.10, by = .01); nosim <- 1000; t <- 100
# calculate coverage using Poisson intervals
coverage <- sapply(lambdavals, function(lambda){
    # calculate Poisson rates
    lhats <- rpois(nosim, lambda = lambda * t) / t
    # lower bound of 95% CI
    11 <- lhats - qnorm(.975) * sqrt(lhats / t)
    # upper bound of 95% CI
    ul <- lhats + qnorm(.975) * sqrt(lhats / t)
    # calculate percent of intervals that contain lambda
    mean(ll < lambda & ul > lambda)
})
# plot CI results vs 95%
ggplot(data.frame(lambdavals, coverage), aes(x = lambdavals, y = coverage)) + geom_line(size = 2) + geom_line(size = 2) + geom_line(size = 2)
```



- as we can see above, for small values of $\lambda = X/t$, the confidence interval produced by the asymptotic interval is **not** an accurate estimate of the actual 95% interval (not enough coverage)
- however, as $t \to \infty$, the interval becomes the true 95% interval

```
# small lambda simulations
lambdavals <- seq(0.005, 0.10, by = .01); nosim <- 1000; t <- 1000
# calculate coverage using Poisson intervals
coverage <- sapply(lambdavals, function(lambda){
    # calculate Poisson rates
    lhats <- rpois(nosim, lambda = lambda * t) / t
    # lower bound of 95% CI
    ll <- lhats - qnorm(.975) * sqrt(lhats / t)
    # upper bound of 95% CI
    ul <- lhats + qnorm(.975) * sqrt(lhats / t)
    # calculate percent of intervals that contain lambda
    mean(ll < lambda & ul > lambda)
```

plot CI results vs 95%
ggplot(data.frame(lambdavals, coverage), aes(x = lambdavals, y = coverage)) + geom_line(size = 2) + ge



• as we can see from above, as t increases, the Poisson intervals become closer to the actual 95% confidence intervals

Confidence Intervals - T Distribution(Small Samples)

• t confidence interval is defined as

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

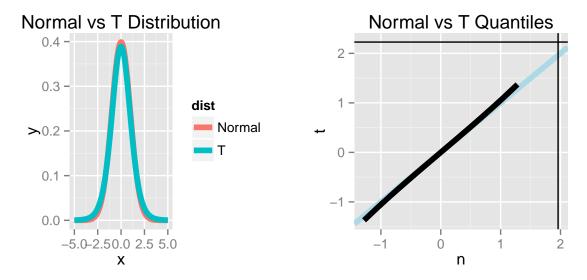
- -TQ =quantile from T distribution
- $-t_{n-1}$ = relevant quantile
- t interval assumes data is IID normal so that

$$\frac{X-\mu}{S/\sqrt{n}}$$

follows Gosset's t distribution with n-1 degrees of freedom

- works well with data distributions that are roughly symmetric/mound shaped, and $\operatorname{\textit{does not}}$ work with skewed distributions
 - * skewed distribution \rightarrow 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 \rightarrow z interval
- qt(0.975, df=n-1) = calculate the relevant quantile using t distribution

```
g <- ggplot(d, aes(x = x, y = y))
g <- g + geom_line(size = 2, aes(colour = dist)) + ggtitle("Normal vs T Distribution")
# plot normal vs t quantiles
d <- data.frame(n= qnorm(pvals),t=qt(pvals, df),p = pvals)
h <- ggplot(d, aes(x= n, y = t))
h <- h + geom_abline(size = 2, col = "lightblue")
h <- h + geom_line(size = 2, col = "black")
h <- h + geom_vline(xintercept = qnorm(0.975))
h <- h + geom_hline(yintercept = qt(0.975, df)) + ggtitle("Normal vs T Quantiles")
# plot 2 graphs together
grid.arrange(g, h, ncol = 2)</pre>
```



- 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 $\frac{\bar{X}-\mu}{S/\sqrt{n}} \to t$ 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

Confidence Interval - Paired T Tests

- compare observations for the same subjects over two different sets of data (i.e. different times, different treatments)
- the confidence interval is defined by

$$\bar{X}_1 - \bar{X}_2 \pm \frac{t_{n-1}S}{\sqrt{n}}$$

where \bar{X}_1 represents the first observations and \bar{X}_2 the second set of observations

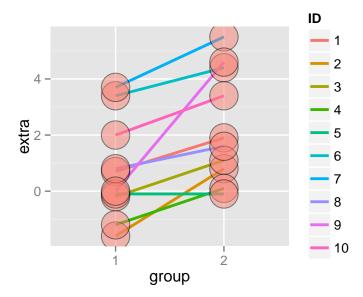
• t.test(difference) = performs group mean t test and returns metrics as results, which includes the confidence intervals

- t.test(g2, g1, paired = TRUE) = performs the same paired t test with data directly

• example

- the data used here is for a study of the effects of two soporific drugs (increase in hours of sleep compared to control) on 10 patients

```
# load data
data(sleep)
# plot the first and second observations
g <- ggplot(sleep, aes(x = group, y = extra, group = factor(ID)))
g <- g + geom_line(size = 1, aes(colour = ID)) + geom_point(size = 10, pch = 21, fill = "salmon", alpha
g</pre>
```



```
# define groups
g1 <- sleep$extra[1 : 10]; g2 <- sleep$extra[11 : 20]
# define difference
difference <- g2 - g1
# calculate mean and sd of differences
mn <- mean(difference); s <- sd(difference); n <- 10
# calculate intervals manually
mn + c(-1, 1) * qt(.975, n-1) * s / sqrt(n)</pre>
```

[1] 0.7001142 2.4598858

```
# perform the same test to get confidence intervals
t.test(difference)
```

```
##
## One Sample t-test
##
## data: difference
## t = 4.0621, df = 9, p-value = 0.002833
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
```

```
## sample estimates:
## mean of x
##
        1.58
t.test(g2, g1, paired = TRUE)
##
##
    Paired t-test
##
## data: g2 and g1
## t = 4.0621, df = 9, p-value = 0.002833
\#\# alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
  0.7001142 2.4598858
## sample estimates:
## mean of the differences
##
```

Independent Group t Intervals - Same Variance

0.7001142 2.4598858

- 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
- t confidence interval for $\mu_y \mu_x$ is defined as

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

- $-t_{n_x+n_y-2,1-\alpha/2}$ = relevant quantile
- $-n_x + n_y 2 =$ degrees of freedom
- $-\ S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2} = \text{standard error}$
- $-S_p^2 = \{(n_x 1)S_x^2 + (n_y 1)S_y^2\}/(n_x + n_y 2) = \text{pooled variance estimator}$
 - * this is effectively a weighted average between the two variances, such that different sample sizes are taken in to account
 - * For equal sample sizes, $n_x = n_y$, $S_p^2 = \frac{S_x^2 + S_y^2}{2}$ (average of variance of two groups)
- 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 $\mu_y - \mu_x$ is defined as

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

- $-t_{df}$ = 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

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

*
$$\left(\frac{s_x^2}{n_x} + \frac{s_y^2}{n_y}\right)^{1/2} = \text{standard error}$$

- Comparing other kinds of data
 - binomial \rightarrow relative risk, risk difference, odds ratio
 - binomial \rightarrow Chi-squared test, normal approximations, exact tests
 - count \rightarrow 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, \pm
- 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) \rightarrow TRUE for paired, FALSE for independent
 - · var.equal = whether or not the variance of the datasets should be treated as equal \rightarrow 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 \rightarrow doing this here is so that the second set of measurements come first $(1, 2 \rightarrow 2, 1)$ in order to perform mean₂ mean₁
 - 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 $true \rightarrow statistical$ evidence required to reject it for alternative or "research" hypothesis (\mathbf{H}_a)
 - * alternative hypothesis typically take form of >, < or \neq
 - Results

Truth	Decide	Result
$\overline{H_0}$	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

- $\alpha = \text{Type I error rate}$
 - probability of *rejecting* the null hypothesis when the hypothesis is *correct*
 - $-\alpha = 0.05 \rightarrow \text{standard for hypothesis testing}$
 - 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
 - * $H_1: TS \leq Z_{\alpha} \text{ OR } -Z_{1-\alpha}$
 - * $H_2: |TS| \ge Z_{1-\alpha/2}$
 - * $H_3: TS \geq Z_{1-\alpha}$
 - Note: In case of $\alpha = 0.05$ (most common), $Z_{1-\alpha} = 1.645$ (95 percentile)
 - $-\alpha = \text{low}$, so that when H_0 is rejected, original model \rightarrow 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
 - * $H_1: TS \leq T_\alpha \text{ OR } -T_{1-\alpha}$
 - * $H_2: |TS| \geq T_{1-\alpha/2}$
 - * $H_3: TS \geq T_{1-\alpha}$
 - Note: In case of $\alpha = 0.05$ (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 interpret 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 $\rightarrow H_a: \mu \neq \mu_0$
 - reject H_0 only if test statistic is too larger/small
 - for $\alpha = 0.05,$ 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 $\mu = \text{set of all possible values that fail to reject } H_0$
 - if $(1-\alpha)\%$ confidence interval contains μ_0 , fail to reject H_0
- two-group intervals/test
 - Rejection rules the same
 - Test H_0 : $\mu_1 = \mu_2 \to \mu_1 \mu_2 = 0$
 - Test statistic:

$$\frac{Estimate - H_0Value}{SE_{Estimate}} = \frac{\bar{X}_1 - \bar{X}_2 - 0}{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}}$$

- 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 \rightarrow 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 observed 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 \neq): 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

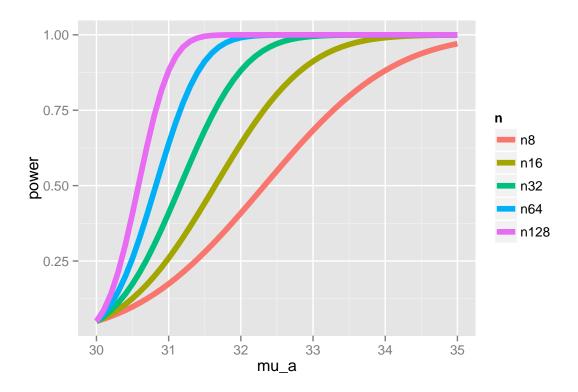
Power

- 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 = 1β
- example
 - $H_0: \mu = 30 \to \bar{X} \sim N(\mu_0, \sigma^2/n)$
 - $-H_a: \mu > 30 \rightarrow \bar{X} \sim N(\mu_a, \sigma^2/n)$
 - 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) \rightarrow calculates $Z_{1-\alpha}$
 - pnorm(mu0 + z * sigma/sqrt(n), mean = mua, sd = sigma/sqrt(n), lower.tail = FALSE) \rightarrow 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 = α
 - Power curve behavior
 - * Power increases as mu_a increases \rightarrow we are more likely to detect the difference in mu_a and mu_0
 - * Power increases as **n** increases \rightarrow with more data, more likely to detect any alternative mu_a

```
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 = "")</pre>
d <- data.frame(mu a, power)</pre>
library(reshape2)
d2 <- melt(d, id.vars = "mu_a")</pre>
names(d2) <- c("mu_a", "n", "power")</pre>
g <- ggplot(d2,
             aes(x = mu \ a, y = power, col = n)) + geom line(size = 2)
```



• 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 $\bf n$ to produce desired power (designing experiment/trial)
 - 2. Given the size \mathbf{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 ${\bf n}$ 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 = $\frac{\mu_a \mu_0}{\sigma}$ \rightarrow 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 $\mu_0 \to$ 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 $H_0 = \text{True}$	Actual H_a = True	Total	
Conclude $H_0 = \text{True (non-significant)}$	U	T	m-R
Conclude $H_a = \text{True (significant)}$	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 $H_a = \text{concluded to be true (measurable)}$
- m-R = number of null hypotheses that failed to be rejected, or cases where H_0 = concluded to be true (measurable)
- $V = \text{Type I Error} / \text{false positives, concludes } H_a = \text{True when } H_0 = \text{actually True}$
- T = Type II Error / false negatives, concludes $H_0 = \text{True when } H_a = \text{actually True}$
- S = true positives, concludes $H_a = \text{True when } H_a = \text{actually True}$
- U = true negatives, concludes $H_0 = \text{True when } H_0 = \text{actually True}$

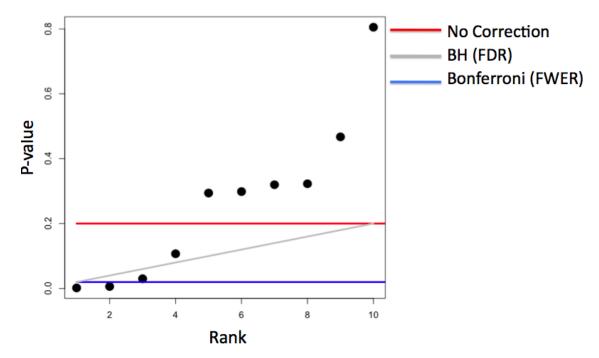
Error Rates

- false positive rate = rate at which false results are called significant $E\left[\frac{V}{m_0}\right] \to \text{average fraction of times that } H_a \text{ is claimed to be true when } H_0 \text{ is actually true}$
 - 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) = probability of at least one false positive $Pr(V \ge 1)$
- 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 $Pr(V \ge 1) < \alpha$
 - · 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 $E\left[\frac{V}{R}\right] \leq \alpha$
 - * calculate P-values normally and sort some from smallest to largest $\rightarrow P_{(1)}, P_{(1)}, ..., P_{(m)}$
 - * deem the P-values significant if $P_{(i)} \le \alpha \times \frac{i}{m}$
 - * 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)
 - * $P_i^{fewer} = max(mP_i, 1) \rightarrow \text{since p cannot exceed value of } 1$
 - * deem P-values significant if $P_i^{fewer} < \alpha$
 - * similar to controlling FWER

Example

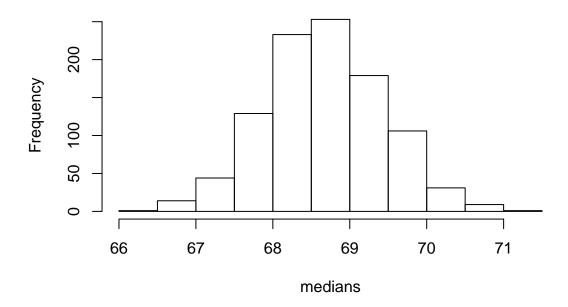
```
set.seed(1010093)
pValues <- rep(NA,1000)
for(i in 1:1000){
 x \leftarrow rnorm(20)
  # First 500 beta=0, last 500 beta=2
  if(i \le 500){y \le rnorm(20)}else{ y \le rnorm(20,mean=2*x)}
  # calculating p-values by using linear model; the [2, 4] coeff in result = pvalue
  pValues[i] <- summary(lm(y ~ x))$coeff[2,4]</pre>
# Controls false positive rate
trueStatus <- rep(c("zero", "not zero"), each=500)</pre>
table(pValues < 0.05, trueStatus)</pre>
##
         trueStatus
##
         not zero zero
## FALSE 0 476
              500 24
##
    TRUE
# Controls FWER
table(p.adjust(pValues,method="bonferroni") < 0.05,trueStatus)</pre>
##
         trueStatus
##
         not zero zero
## FALSE 23 500
    TRUE
              477 0
##
# Controls FDR (Benjamin Hochberg)
table(p.adjust(pValues,method="BH") < 0.05,trueStatus)</pre>
##
         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 \rightarrow 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 \rightarrow approximate sampling distribution

```
# load data
library(UsingR); data(father.son)
# observed dataset
x <- father.son$sheight
# number of simulated statistic
B <- 1000
# generate samples
resamples <- matrix(</pre>
                            # sample to draw frome
    sample(x,
           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)</pre>
# estimated standard error of median
sd(medians)
## [1] 0.76595
# confidence interval of median
quantile(medians, c(.025, .975))
##
       2.5%
               97.5%
## 67.18292 70.16488
# histogram of bootstraped samples
hist(medians)
```

Histogram of 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
 - \cdot T statistic
- * Calculate the percentage of simulations where the simulated statistic was more extreme (toward the alternative) than the observed

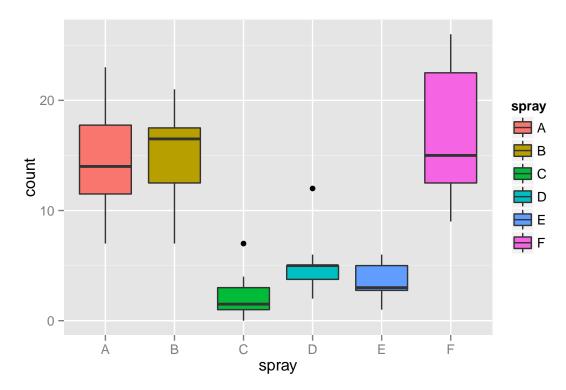
- variations

Data type	Statistic	Test name
Ranks Binary Raw data	rank sum hypergeometric prob	rank sum test Fisher's exact test 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</pre>
```

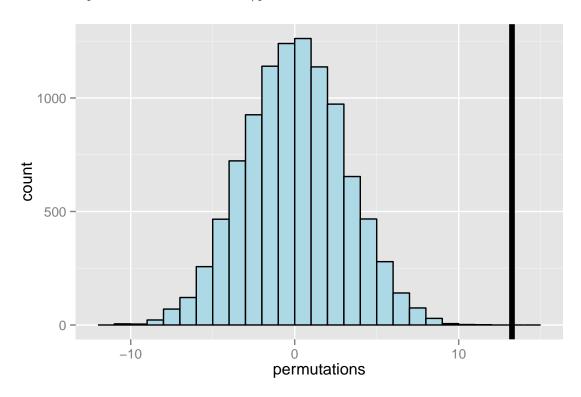
[1] 13.25

- the observed difference between the groups is 13.25
- now we changed the resample the lables for groups ${\bf B}$ and ${\bf C}$

```
# 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 ${\bf B}$ and ${\bf C}$ larger than the original data
- therefore, p-value is very small and we can reject the null hypothesis with any reasonable 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 \rightarrow likely 0 is not the true difference
 - with this information, formal confidence intervals can be constructed and p-values can be calculated