

# Statistical Inference Course Notes

*Xing Su*

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## Overview

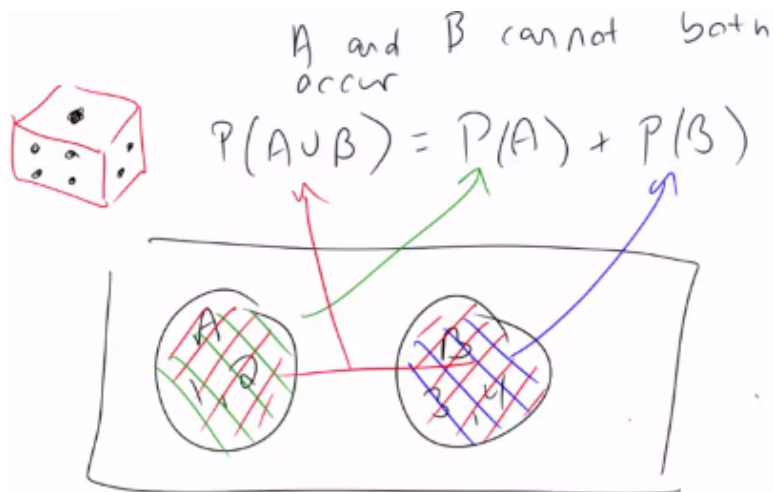
- **Statistical Inference** = generating conclusions about a population from a noisy sample
- Goal = extend beyond data to population
- Statistical Inference = only formal system of inference we have
- many different modes, but **two** broad flavors of inference (inferential paradigms): **Bayesian**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

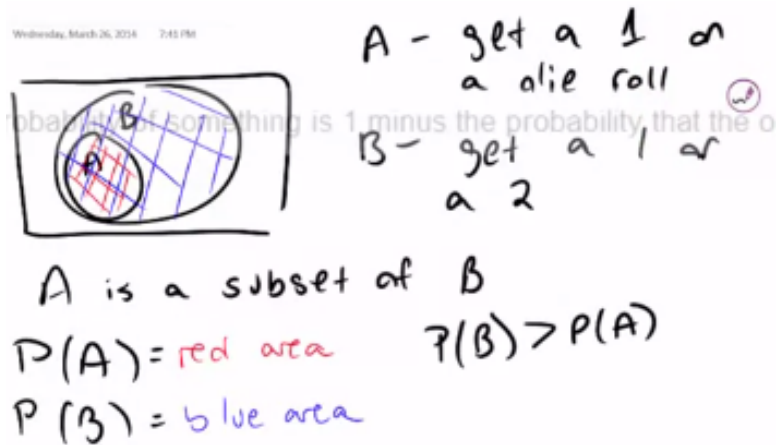
- **Probability** = the study of quantifying the likelihood of particular events occurring
  - given a random experiment, **probability** = population quantity that summarizes the randomness
    - \* not in the data at hand, but a conceptual quantity that exist in the population that we want to estimate

## General Probability Rules

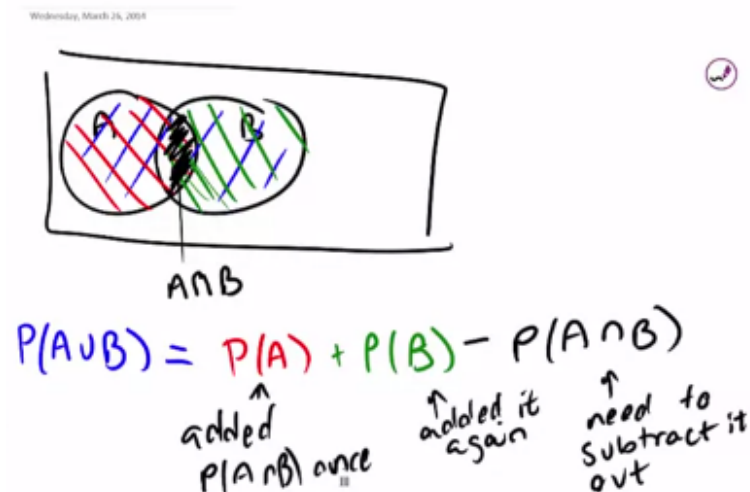
- discovered by Russian mathematician Kolmogorov, also known as “Probability Calculus”
- probability = function of any set of outcomes and assigns it a number between 0 and 1
  - $0 \leq P(E) \leq 1$ , where  $E$  = event
- probability that nothing occurs = 0 (impossible, have to roll dice to create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



- 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

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

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

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

- *example*

– for die roll,  $A = \{1\}$ ,  $B = \{1, 3, 5\}$ , then

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

### Baye's Rule

- definition

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

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  $\geq 0$  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  $\geq$  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)

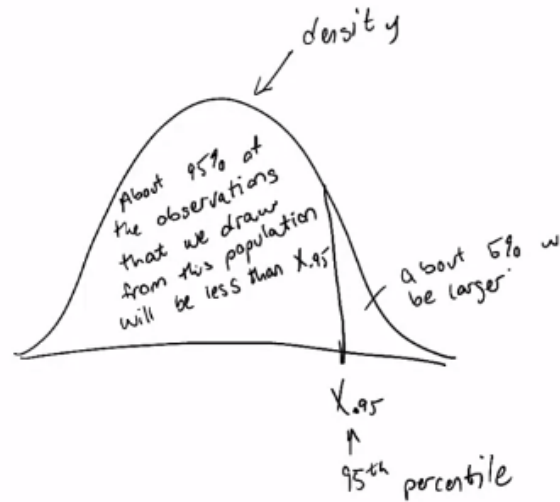
- CDF of a random variable  $X$  = probability that the random variable is  $\leq$  value  $x$ 
  - $F(x) = P(X \leq x)$  = applies when  $X$  is discrete/continuous
- PDF = derivative of CDF
  - integrate PDF  $\rightarrow$  CDF
    - \* `integrate(function, lower=0, upper=1)`  $\rightarrow$  can be 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  $\alpha^{th}$  quantile of a distribution with distribution function  $F$  = point  $x_\alpha$ 
  - $F(x_\alpha) = \alpha$
  - percentile = quantile with  $\alpha$  expressed as a percent
  - median = 50<sup>th</sup> 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
  - $P(A \cap B) = P(A)P(B)$
  - $P(A | B) = P(A)$
- two random variables  $X$  and  $Y$  are **independent**, if for any two sets,  $\mathbf{A}$  and  $\mathbf{B}$ , 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** =  $P(+ | D)$  = 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** =  $P(D | +)$  = probability that that subject has the disease given that the test is positive
- **negative predictive value** =  $P(D^c | -)$  = 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%

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

- low positive predictive value  $\rightarrow$  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

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

- **diagnostic likelihood ratio** of a **negative** test result is defined as

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

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

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

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

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

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

which can also be written as

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

- **odds** =  $p/(1 - p)$
  - $\frac{P(D)}{P(D^c)}$  = **pre-test odds**, or odds of disease in absence of test
  - $\frac{P(D|+)}{P(+|D^c)}$  = **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

$$DLR_+ = .997/(1 - .985) = 66 \quad DLR_- = (1 - .997)/.985 = 0.003$$

- 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

$$E[X] = \sum_x xp(x)$$

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 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
    - PDF =  $f(x)$
    - $\int xf(x) =$  area under the PDF curve = mean/expected value of  $X$

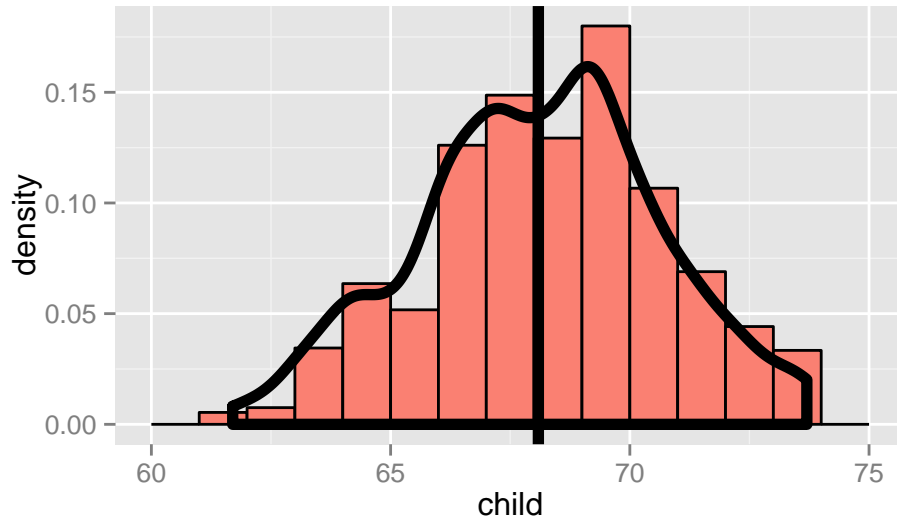
- **sample mean**

- 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
```



- **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 → estimates average of the population
  - if  $E[\text{sample mean}] = \text{population mean}$ , then estimator for the sample mean is **unbiased**
    - \* **[derivation]** let  $X_1, X_2, X_3, \dots, X_n$  be a collection of  $n$  samples from the population with mean  $\mu$
    - \* mean of this sample

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

- \* 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  $\mu$ , the expected value of each sample should be

$$E(X_i) = \mu$$

- \* therefore

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

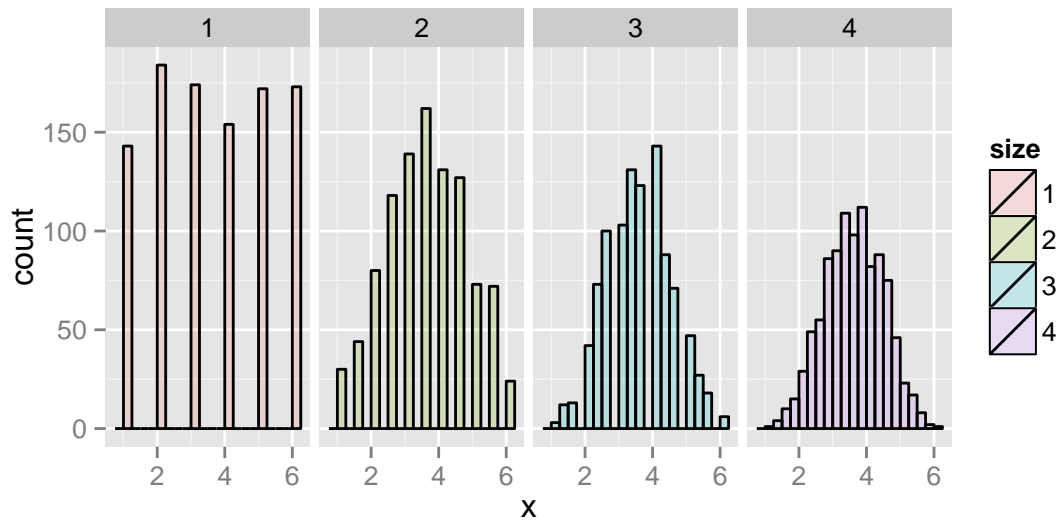
- **Note:** the more data that goes into the sample mean, the more concentrated its density/mass functions are around the population mean

```
nosim <- 1000
# simulate data for sample size 1 to 4
dat <- data.frame(
  x = c(sample(1 : 6, nosim, replace = TRUE),
    apply(matrix(sample(1 : 6, nosim * 2, replace = TRUE), nosim), 1, mean),
```

```

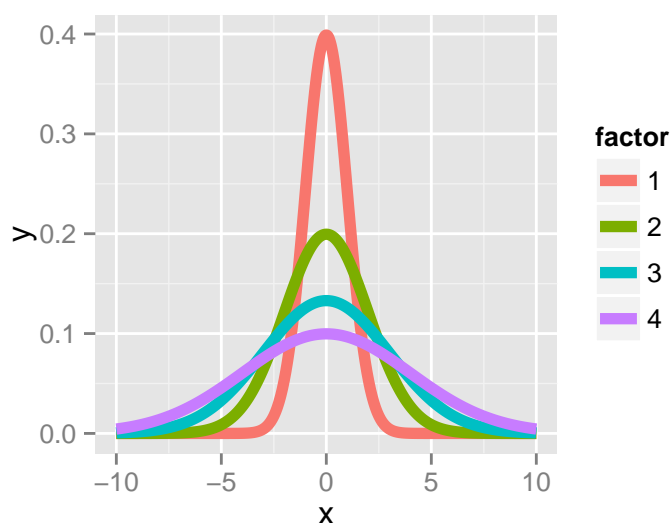
    apply(matrix(sample(1 : 6, nosim * 3, replace = TRUE), nosim), 1, mean),
    apply(matrix(sample(1 : 6, nosim * 4, replace = TRUE), nosim), 1, mean)),
    size = factor(rep(1 : 4, rep(nosim, 4))))
# plot histograms of means by sample size
g <- ggplot(dat, aes(x = x, fill = size)) + geom_histogram(alpha = .20, binwidth=.25, colour = "black")
g + facet_grid(. ~ size)

```



## 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)
```

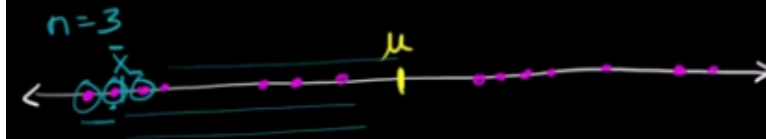


- **variance** = measure of spread, the square of expected distance from the mean (expressed in  $X$ 's units<sup>2</sup>)
  - as we can see from above, higher variances  $\rightarrow$  more spread, lower  $\rightarrow$  smaller spread
  - $Var(X) = E[(X - \mu)^2] = E[X^2] - E[X]^2$
  - **standard deviation**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

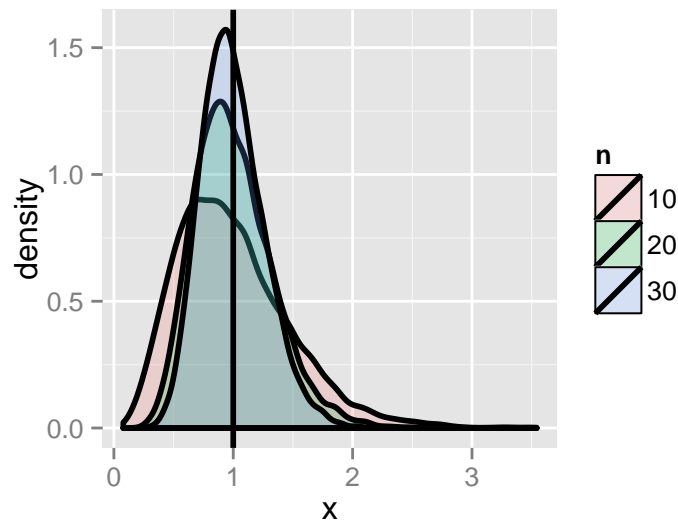
- the **sample variance** is defined as

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

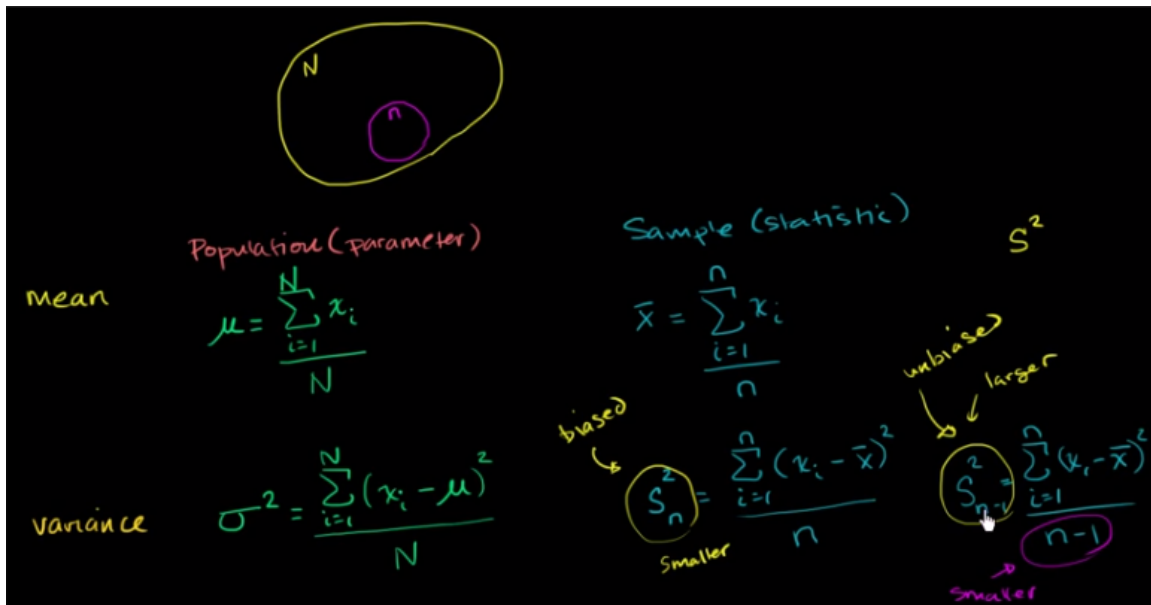


- on the above line representing the population (in magenta), any subset of data (3 of 14 selected, marked in blue) will most likely have a variance that is **lower than** the population variance
- dividing by  $n - 1$  will make the variance estimator **larger** to adjust for this fact → leads to more accurate estimation →  $S^2 =$  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
    - \* as we see from the simulation results below, with more data, the distribution for  $S^2$  gets more concentrated around population variance

```
# specify number of simulations
nosim <- 10000;
# simulate data for various sample sizes
dat <- data.frame(
  x = c(apply(matrix(rnorm(nosim * 10), nosim), 1, var),
    apply(matrix(rnorm(nosim * 20), nosim), 1, var),
    apply(matrix(rnorm(nosim * 30), nosim), 1, var))),
  n = factor(rep(c("10", "20", "30"), c(nosim, nosim, nosim))) )
# plot density function for different sample size data
ggplot(dat, aes(x = x, fill = n)) + geom_density(size = 1, alpha = .2) +
  geom_vline(xintercept = 1, size = 1)
```



- **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 = population mean
  - \*  $E[\bar{X}] = \mu$
- expected value of the variance of distribution of means
  - \*  $Var(\bar{X}) = \sigma^2/n$
  - \* as **n** becomes larger, the mean of random sample → more concentrated around the population mean → 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  $\sigma^2 \rightarrow$  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
- $S^2$  = sample variance
  - estimates how variable the population is
  - estimates population variance  $\sigma^2$
  - $S^2$  = a random variable and has its own distribution centered around  $\sigma^2$ 
    - \* more concentrated around  $\sigma^2$  as  $n$  increases
- $\bar{X}$  = sample mean
  - estimates population mean  $\mu$



- $\bar{X}$  = a random variable and has its own distribution centered around  $\mu$ 
  - \* more concentrated around  $\mu$  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))
```

```
## [1] 0.3080756
```

```
# 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 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] 0.08948087
```

```
# 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] 0.608916
```

```
# 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))
```

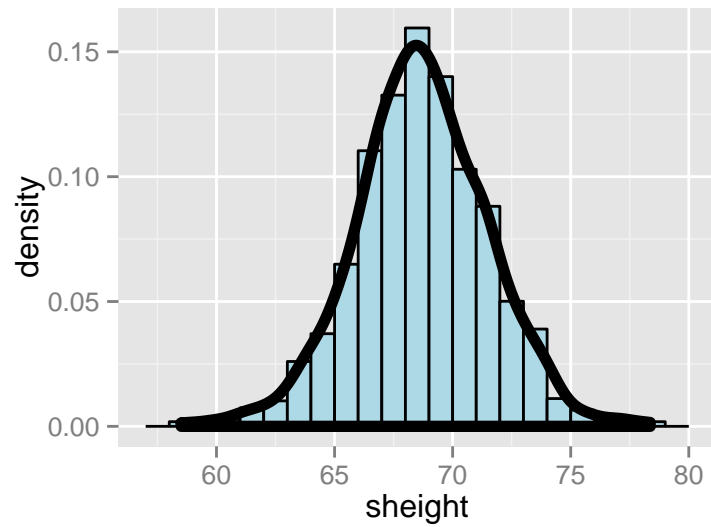
```
## [1] 0.1578129
```

```
# 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$height
# n is the length
n<-length(x)
# plot histogram for son's heights
g <- ggplot(data = father.son, aes(x = height))
g <- g + geom_histogram(aes(y = ..density..), fill = "lightblue", binwidth=1, colour = "black")
g <- g + geom_density(size = 2, colour = "black")
g
```



```
# 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  $X_1, \dots, X_n = \text{Bernoulli}(p)$

- 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  $x = 0, \dots, n$

- **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, what's 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 ^ 7 + 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  $X$

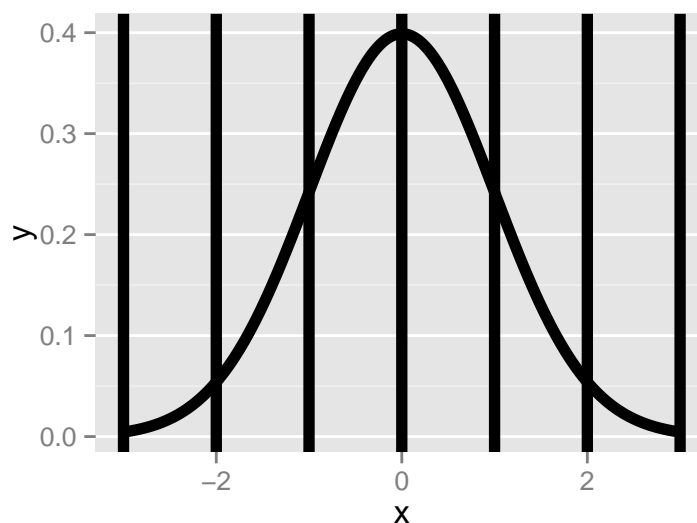
- notation =  $X \sim N(\mu, \sigma^2)$
- mean =  $E[X] = \mu$
- variance =  $Var(X) = \sigma^2$
- PMF is defined as

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

- $X \sim N(0, 1)$  = **standard normal distribution** (standard normal random variables often denoted using  $Z_1, Z_2, \dots$ )

- **Note:** see below graph for reference for the following observations
- ~68% of data/normal density → between  $\pm 1$  standard deviation from  $\mu$
- ~95% of data/normal density → between  $\pm 2$  standard deviation from  $\mu$
- ~99% of data/normal density → between  $\pm 3$  standard deviation from  $\mu$
- $\pm 1.28$  standard deviations from  $\mu \rightarrow 10^{th}$  (-) and  $90^{th}$  (+) percentiles
- $\pm 1.645$  standard deviations from  $\mu \rightarrow 5^{th}$  (-) and  $95^{th}$  (+) percentiles
- $\pm 1.96$  standard deviations from  $\mu \rightarrow 2.5^{th}$  (-) and  $97.5^{th}$  (+) percentiles
- $\pm 2.33$  standard deviations from  $\mu \rightarrow 1^{st}$  (-) and  $99^{th}$  (+) percentiles

```
# plot standard normal
x <- seq(-3, 3, length = 1000)
g <- ggplot(data.frame(x = x, y = dnorm(x)),
            aes(x = x, y = y)) + geom_line(size = 2)
g <- g + geom_vline(xintercept = -3 : 3, size = 2)
g
```



- 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 =  $\lambda$
  - PMF is defined as

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

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

- 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)
    - \*  $X \sim \text{Binomial}(n, p)$
    - \*  $\lambda = np$
  - rates →  $X \sim \text{Poisson}(\lambda t)$ 
    - \*  $\lambda = E[X/t] \rightarrow$  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  $\lambda$  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”)

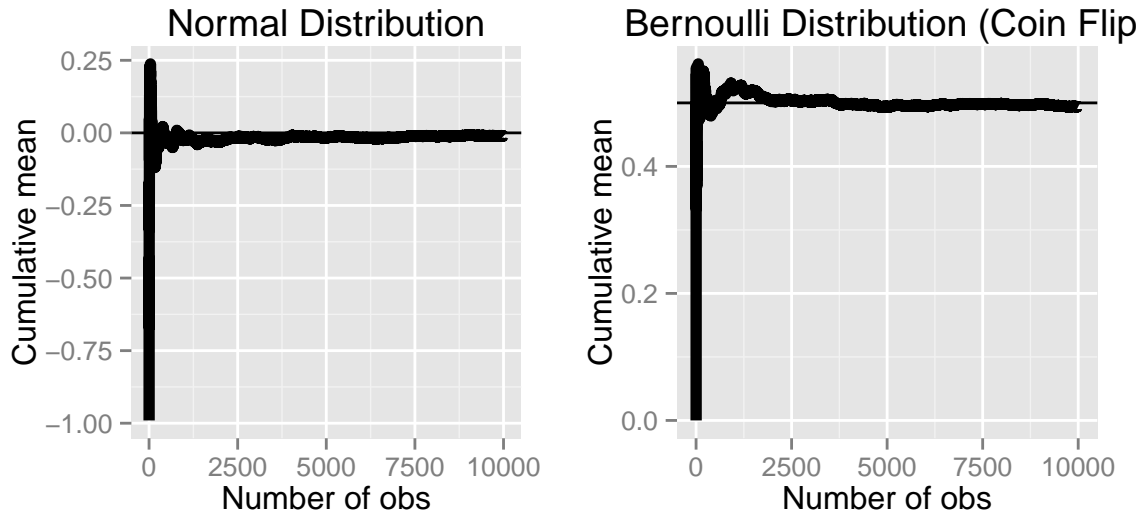
### Law of Large Numbers (LLN)

- 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
- 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)
# plot sample size vs sample mean
g <- 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")
# calculate sample (coin flips) means for different size of n
means <- cumsum(sample(0 : 1, n , replace = TRUE)) / (1 : n)
# plot sample size vs sample mean
p <- ggplot(data.frame(x = 1 : n, y = means), aes(x = x, y = y))
p <- p + geom_hline(yintercept = 0.5) + geom_line(size = 2)
p <- p + labs(x = "Number of obs", y = "Cumulative mean")
p <- p + ggtitle("Bernoulli Distribution (Coin Flip)")
# 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  $n$ ,

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

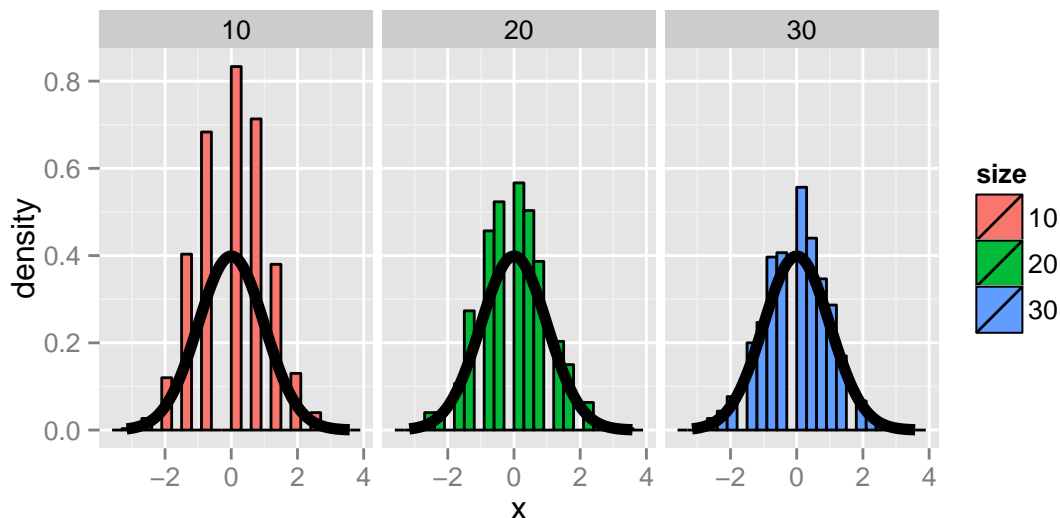
- this translates to the distribution of the sample mean  $\bar{X}_n$  is approximately  $N(\mu, \sigma^2/n)$ 
  - distribution is centered at the population mean
  - with standard deviation = standard error of the mean
- typically the Central Limit Theorem can be applied when  $n \geq 30$

### Example - CLT with Bernoulli Trials (Coin Flips)

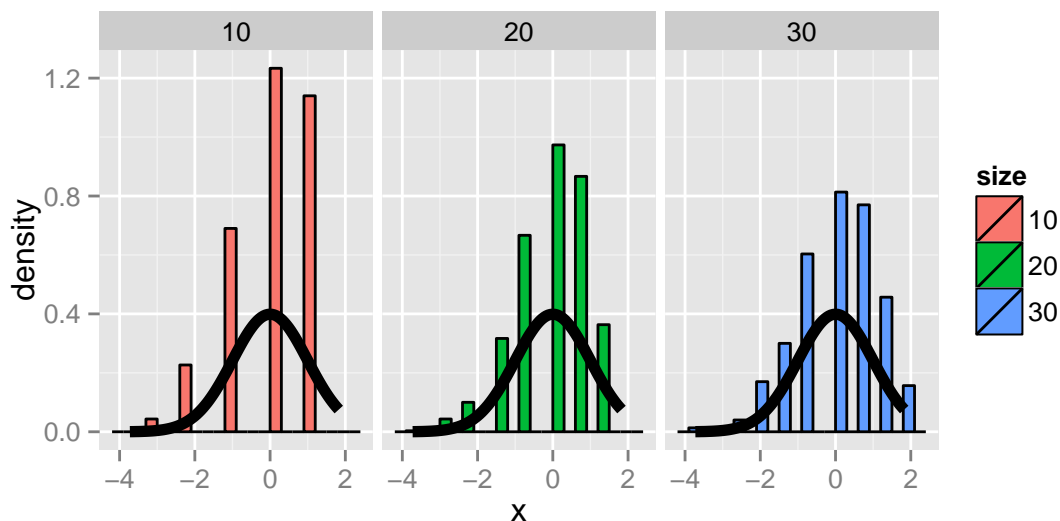
- for this example, we will simulate  $n$  flips of a possibly unfair coin
  - $X_i$  be the 0 or 1 result of the  $i^{th}$  flip of a possibly unfair coin
  - sample proportion,  $\hat{p}$ , is the average of the coin flips
  - $E[X_i] = p$  and  $Var(X_i) = p(1-p)$
  - standard error of the mean is  $SE = \sqrt{p(1-p)/n}$
- 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 divide 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  $n \rightarrow \infty$

### Confidence Intervals - Normal Distribution/Z Intervals

- **Z confidence interval** is defined as

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

where  $ZQ$  = quantile from the standard normal distribution

- according to CLT, the sample mean,  $\bar{X}$ , is approximately normal with mean  $\mu$  and sd  $\sigma/\sqrt{n}$

- **95% confidence interval for the population mean  $\mu$**  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 repeated samples of size  $n$  from the population and construct this confidence interval for each case, approximately 95% of the intervals will contain  $\mu$
- 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))
```

```
## [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  $\hat{p} = X/n$  as estimate
- $p(1 - p)$  is largest when  $p = 1/2$ , so 95% confidence interval can be calculated by

$$\begin{aligned} \hat{p} \pm Z_{0.95} \sqrt{\frac{0.5(1-0.5)}{n}} &= \hat{p} \pm 1.96 \sqrt{\frac{1}{4n}} \\ &= \hat{p} \pm \frac{1.96}{2} \sqrt{\frac{1}{n}} \\ &\approx \hat{p} \pm \frac{1}{\sqrt{n}} \end{aligned}$$

- 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

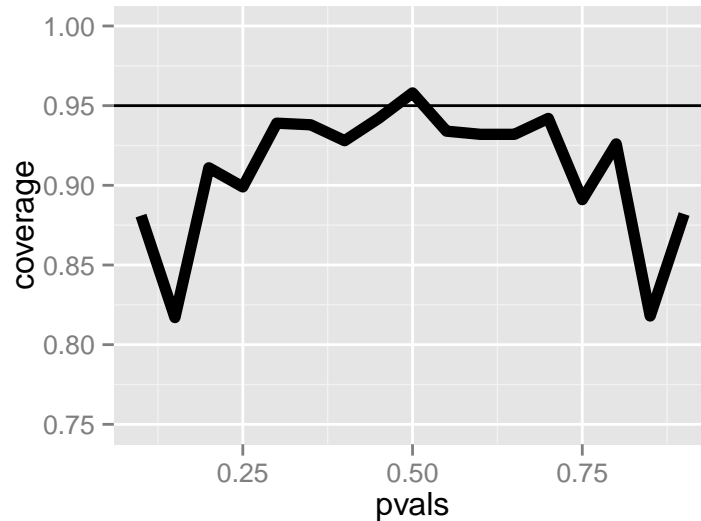
$$\hat{p} \pm z_{1-\alpha/2} \sqrt{\frac{p(1-p)}{n}}$$

**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 <- seq(.1, .9, by = .05)
# calculate the confidence intervals
coverage <- sapply(pvals, function(p){
  # simulate binomial data
  phats <- rbinom(nosim, prob = p, size = n) / n
  # calculate lower 95% CI bound
  ll <- phats - qnorm(.975) * sqrt(phats * (1 - phats) / n)
  # calculate upper 95% CI bound
  ul <- phats + qnorm(.975) * sqrt(phats * (1 - phats) / n)
  # calculate percent of intervals that contain p
  mean(ll < p & ul > 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

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

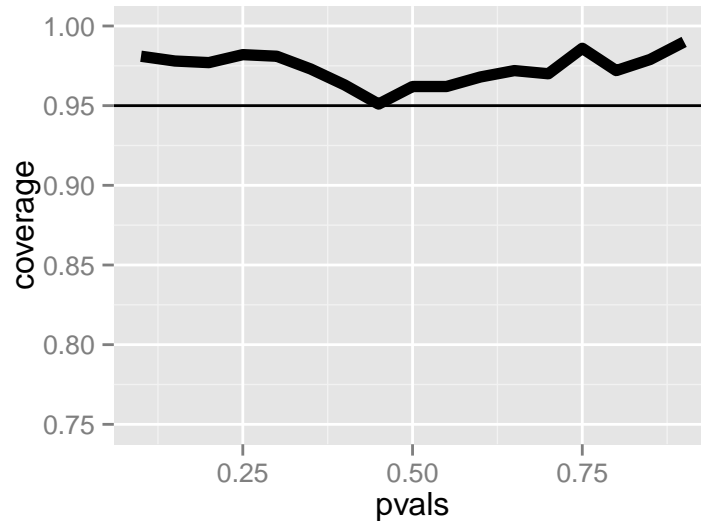
where we effectively **add 2** to number of successes,  $X$ , and **add 2** to number of failure

- 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 <- 20; nosim <- 1000
# simulate for p values from 0.1 to 0.9
pvals <- seq(.1, .9, by = .05)
# calculate the confidence intervals
coverage <- sapply(pvals, function(p){
  # simulate binomial data with Agresti/Coull Interval adjustment
  phats <- (rbinom(nosim, prob = p, size = n) + 2) / (n + 4)
  # calculate lower 95% CI bound
  ll <- phats - qnorm(.975) * sqrt(phats * (1 - phats) / n)
  # calculate upper 95% CI bound
  ul <- phats + qnorm(.975) * sqrt(phats * (1 - phats) / n)
  # calculate percent of intervals that contain p
  mean(ll < p & ul > 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 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  $X \sim \text{Poisson}(\lambda t)$ 
  - estimate rate  $\hat{\lambda} = X/t$
  - $\text{var}(\hat{\lambda}) = \lambda/t$
  - variance estimate =  $\hat{\lambda}/t$
- so the confidence interval is defined as

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

- however, for small values of  $\lambda$  (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  $\lambda$
  - \* 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

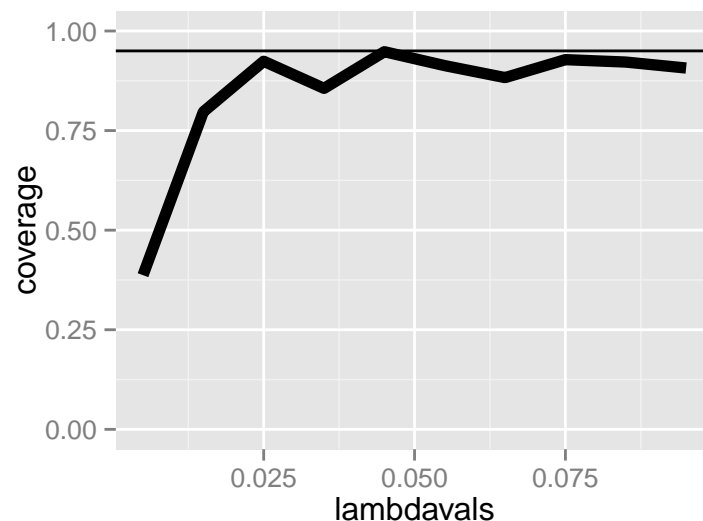
```
# define parameters
x <- 5; t <- 94.32; lambda <- x / t
# calculate confidence interval
round(lambda + c(-1, 1) * qnorm(.975) * sqrt(lambda / t), 3)
```

```
## [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
lambdavalss <- seq(0.005, 0.10, by = .01); nosim <- 1000; t <- 100
# calculate coverage using Poisson intervals
coverage <- sapply(lambdavalss, 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(lambdavalss, coverage), aes(x = lambdavalss, y = coverage)) + geom_line(size = 2) + geom_hline(y = 0.95)
```



- 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  $t \rightarrow \infty$ , the interval becomes the **true 95% interval**

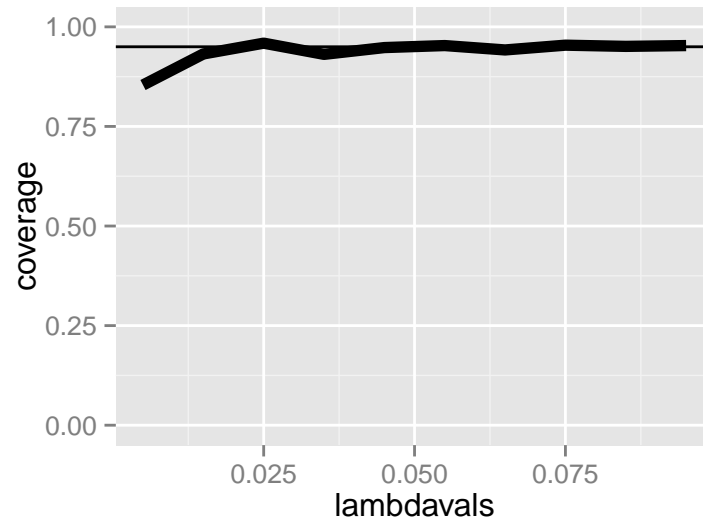
```
# small lambda simulations
lambdavalss <- seq(0.005, 0.10, by = .01); nosim <- 1000; t <- 1000
# calculate coverage using Poisson intervals
coverage <- sapply(lambdavalss, function(lambda){
  # calculate Poisson rates
  lhats <- rpois(nosim, lambda = lambda * t) / t
  # lower bound of 95% CI
  ll <- 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(lambdaval, coverage), aes(x = lambdaval, y = coverage)) + geom_line(size = 2) + geom

```



- 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

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

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

- works well with data distributions that are roughly symmetric/mound shaped, and **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

```

# Plot normal vs t distributions
k <- 1000; xvals <- seq(-5, 5, length = k); df <- 10
d <- data.frame(y = c(dnorm(xvals), dt(xvals, df)), x = xvals,
  dist = factor(rep(c("Normal", "T"), c(k,k))))

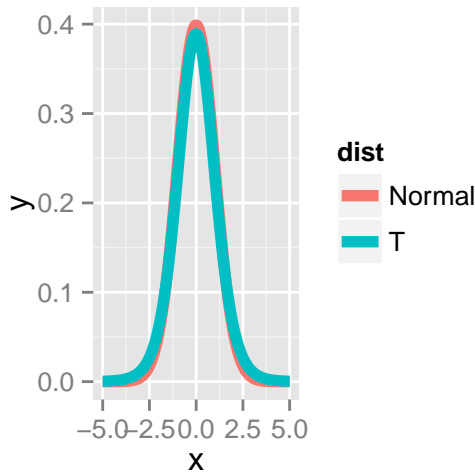
```

```

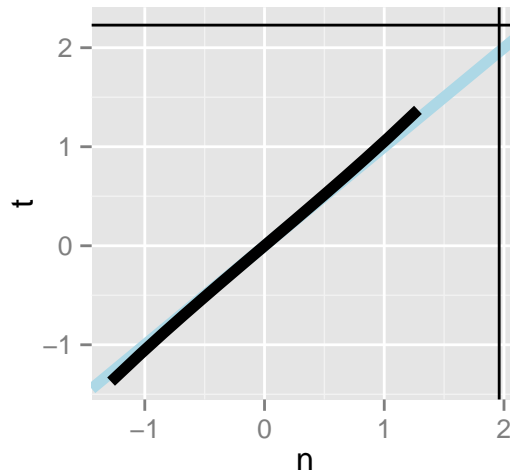
g <- ggplot(d, aes(x = x, y = y))
g <- g + geom_line(size = 2, aes(colour = dist)) + ggtitle("Normal vs T Distribution")
# plot normal vs t quantiles
d <- data.frame(n= qnorm(pvals),t=qt(pvals, df),p = pvals)
h <- ggplot(d, aes(x= n, y = t))
h <- h + geom_abline(size = 2, col = "lightblue")
h <- h + 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)

```

Normal vs T Distribution



Normal vs T Quantiles



- William Gosset's **t** Distribution ("Student's T distribution")
  - test = Gosset's pseudonym 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  $\frac{\bar{X} - \mu}{S/\sqrt{n}} \rightarrow t$  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

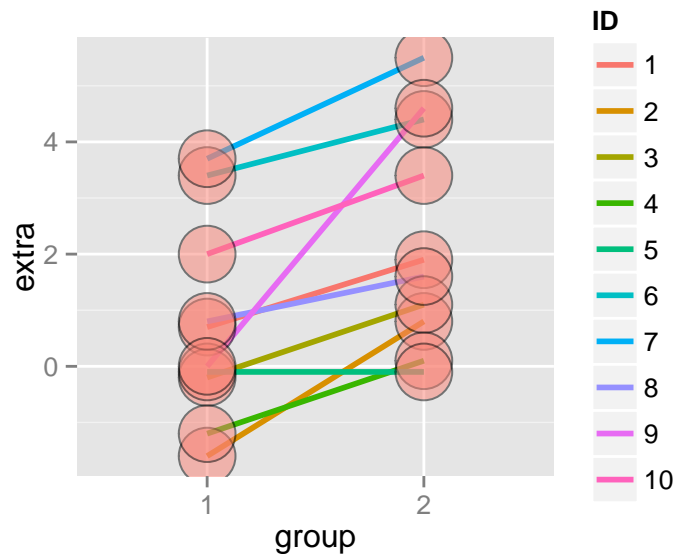
- `t.test(difference)` = performs group mean t test and returns metrics as results, which includes the confidence intervals

– `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 = 0.5)
g
```



```
# 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)
```

```
## [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:
```

```
## 0.7001142 2.4598858
## 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
##      1.58
```

## 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
- $t$  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
- $S_p \left( \frac{1}{n_x} + \frac{1}{n_y} \right)^{1/2}$  = 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  $\mu_y - \mu_x$  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

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

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

- Comparing other kinds of data
  - binomial → 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,  $\pm$
  - 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, nx + ny - 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 `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 ( $H_0$ ) = status quo
  - assumed to be **true** → statistical evidence required to reject it for **alternative** or “research” hypothesis ( $H_a$ )
    - \* alternative hypothesis typically take form of  $>$ ,  $<$  or  $\neq$
  - **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

- $\alpha$  = Type I error rate
  - probability of **rejecting** the null hypothesis when the hypothesis is **correct**
  - $\alpha = 0.5 \rightarrow$  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)
  - $\alpha$  = 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
    - \*  $H_1 : TS \leq T_\alpha$  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 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  $\alpha = 0.5$ , 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  $\mu$  = set of all possible values that fail to reject  $H_0$
  - if  $(1 - \alpha)\%$  confidence interval contains  $\mu_0$ , fail to reject  $H_0$
- **two-group intervals/test**
  - Rejection rules the same
  - Test  $H_0: \mu_1 = \mu_2 \rightarrow \mu_1 - \mu_2 = 0$
  - 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  $\alpha$  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 ( $X < \text{value}$ ,  $X > \text{value}$ ), 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*



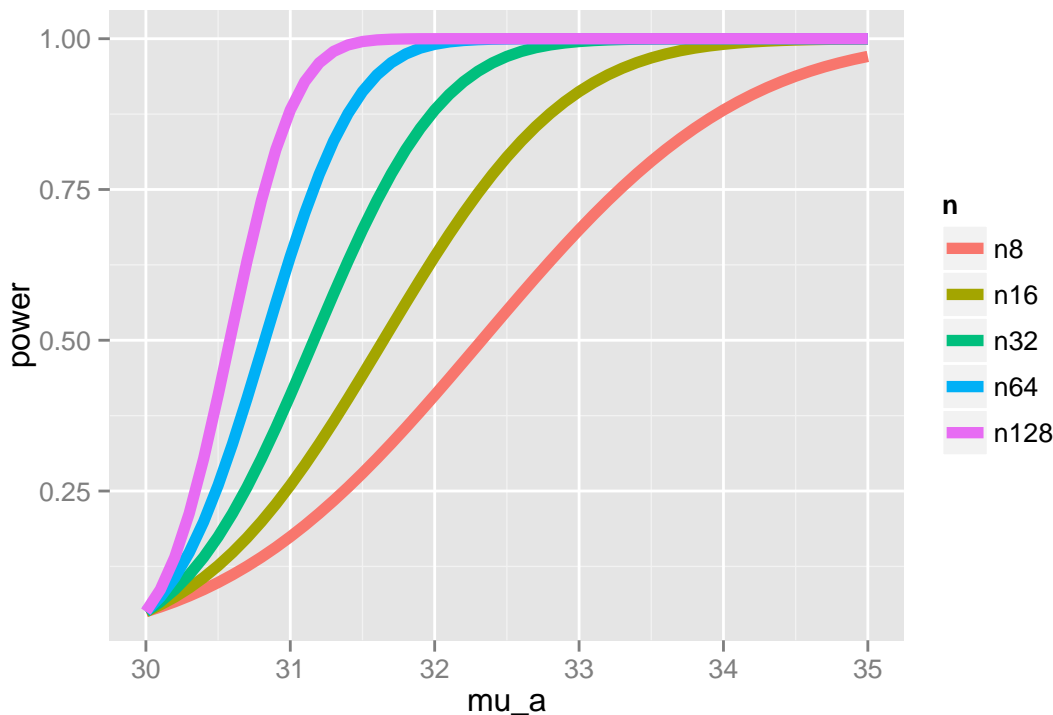
## Power

- **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
- $\beta$  = probability of type II error = failing to reject the null hypothesis when it's false
- power =  $1 - \beta$
- **example**
  - $H_0 : \mu = 30 \rightarrow \bar{X} \sim N(\mu_0, \sigma^2/n)$
  - $H_a : \mu > 30 \rightarrow \bar{X} \sim N(\mu_a, \sigma^2/n)$
  - Power:

$$\text{Power} = P\left(\frac{\bar{X} - 30}{s/\sqrt{n}} > t_{1-\alpha, n-1} ; \mu = \mu_a\right)$$

- \* **Note:** the above function depends on value of  $\mu_a$
- \* **Note:** as  $\mu_a$  approaches 30, power approaches  $\alpha$
- 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  $\mu_a$ 
    - \* **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  $\mu_a$

```
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 =  $\mu_a, \sigma, n, \beta$
- Knowns =  $\mu_0, \alpha$
- 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 excludes the probability of getting a large TS in the opposite direction of the truth, but this is only applicable when  $\mu_a$  and  $\mu_0$  are close together

- **Power Behavior**

- Power increases as  $\alpha$  becomes larger
- Power of one-sided test  $>$  power of associated two-sided test
- Power increases as  $\mu_a$  gets further away from  $\mu_0$
- Power increases as **n** increases (sample mean has less variability)
- Power increases as  $\sigma$  decreases (again less variability)
- Power usually depends only  $\frac{\sqrt{n}(\mu_a - \mu_0)}{\sigma}$ , and not  $\mu_a, \sigma$ , and  $n$ 
  - \* **effect size** =  $\frac{\mu_a - \mu_0}{\sigma} \rightarrow$  unit free, can be interpreted 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  $\mu_a$  and NOT  $\mu_0 \rightarrow$  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

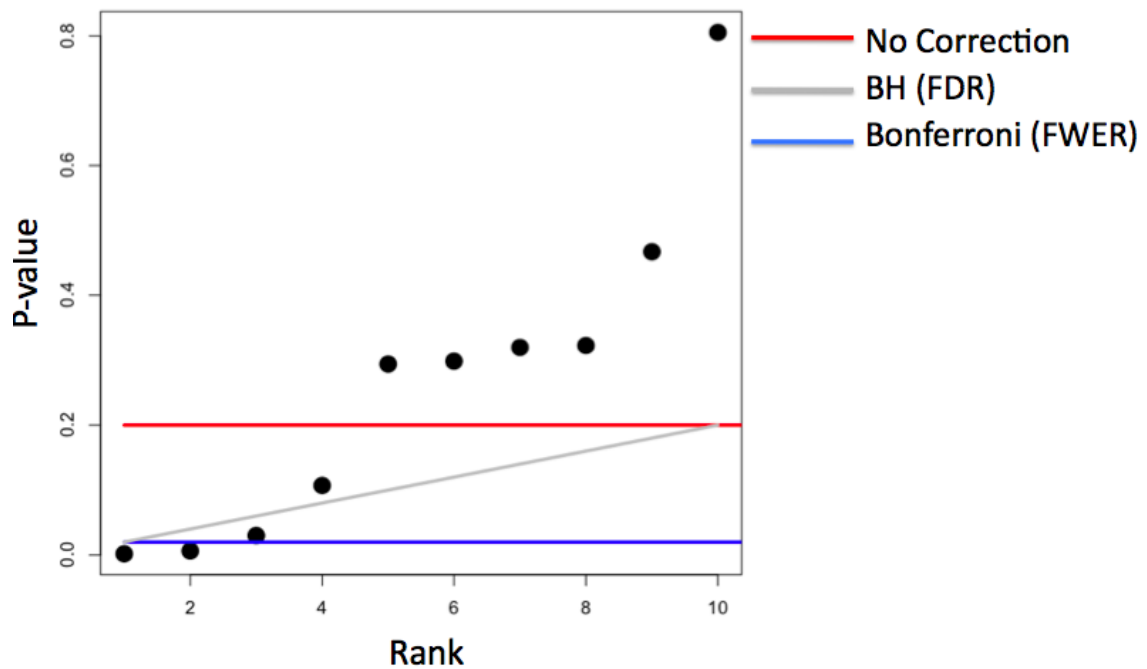
Actual $H_0 = \text{True}$	Actual $H_a = \text{True}$	Total	
Conclude $H_0 = \text{True}$ (non-significant)	$U$	$T$	$m - R$
Conclude $H_a = \text{True}$ (significant)	$V$	$S$	$R$
<b>Total</b>	$m_0$	$m - m_0$	$m$

- $m_0$  = 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  $H_a = \text{True}$  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  $E[\frac{V}{m_0}] \rightarrow$  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  $\rightarrow$  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  $\Pr(V \geq 1)$
- **false discovery rate (FDR)** = rate at which claims of significance are false  $E[\frac{V}{R}]$
- **controlling error rates (adjusting  $\alpha$ )**
  - 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  $\rightarrow P_{(1)}, P_{(1)}, \dots, P_{(m)}$
  - \* 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)
  - \*  $P_i^{fewer} = \max(mP_i, 1) \rightarrow$  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 calculating 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 (2.5<sup>th</sup> and 97.5<sup>th</sup>) 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

```
# 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 from
        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)
```

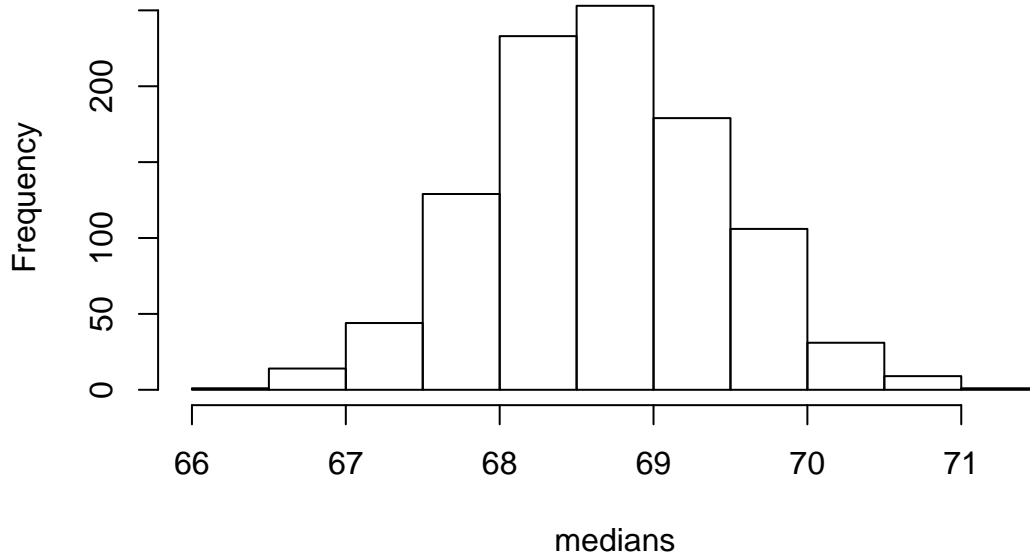
```
## [1] 0.76595
```

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

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

```
# histogram of bootstrapped 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
  - T statistic
- \* Calculate the percentage of simulations where the simulated statistic was more extreme (toward the alternative) than the observed

- *variations*

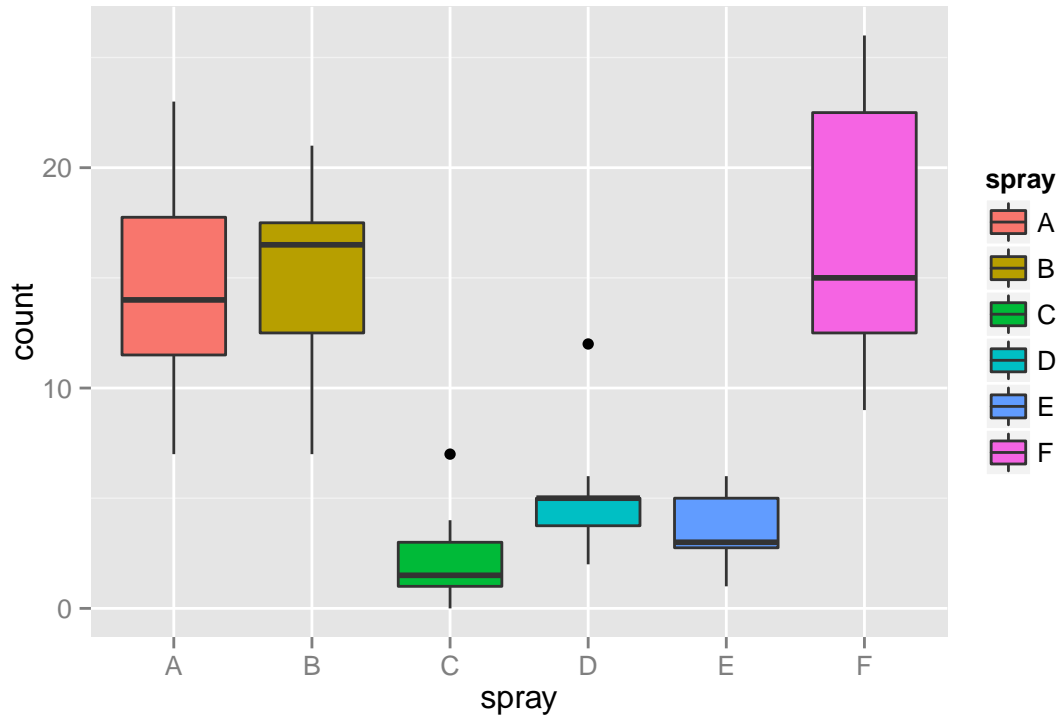
Data type	Statistic	Test name
Ranks	rank sum	rank sum test
Binary	hypergeometric prob	Fisher’s exact test
Raw data		ordinary permutation test

- \* **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
```

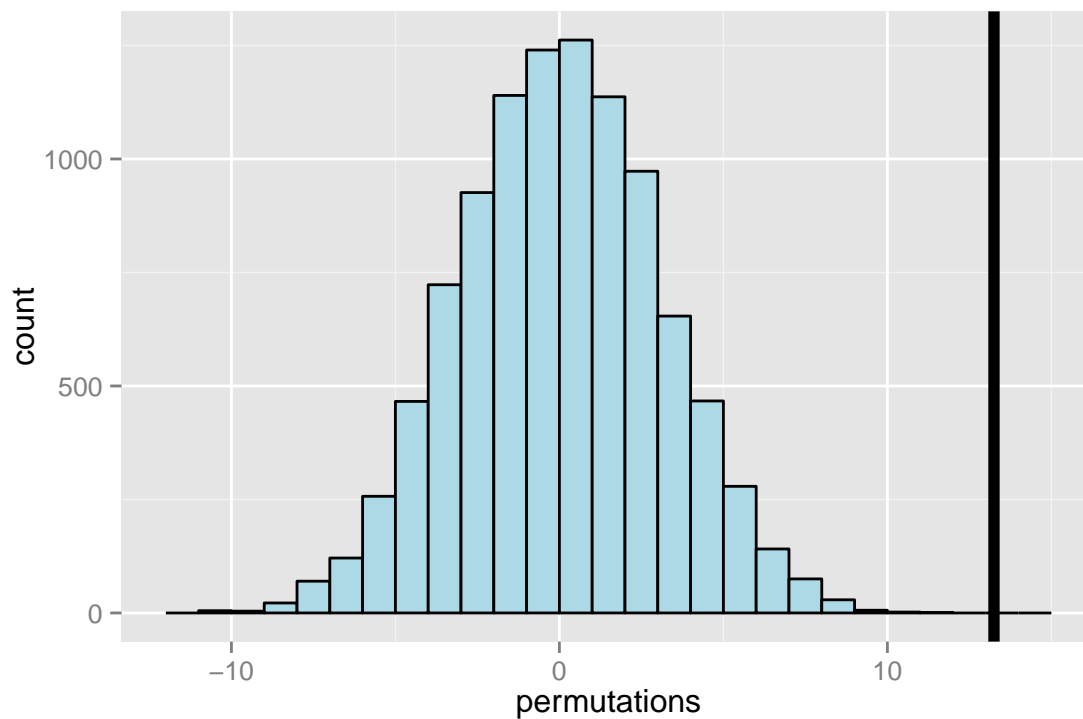
```
## [1] 13.25
```

- the observed difference between the groups is 13.25
- now we changed the resample the labels 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 reasonable  $\alpha$  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