STA2453 - Randomization

January 22, 2019

Today's Class

- The concepts of: Randomization, Blocking, Replication
- Summaries of sample populations
- Hypothesis testing via randomization

Randomized Experiments and Observational Studies

- A technical definition of an observational study is given by Imbens and Rubin (2015)
- The process that determines which experimental units receive which treatments is called the assignment mechanisim.
- When the assignment mechanism is unknown then the design is called an observational study.

Randomized Experiments and Observational Studies

In randomized experiments (pg. 20, Imbens and Rubin, 2015): "... the assignment mechanism is under the control of the experimenter, and the probability of any assignment of treatments across the units in the experiment is entirely knowable before the experiment begins."

Treatment Assignment

Suppose, for example, that we have two breast cancer patients and we want to randomly assign these two patients to two treatments (A and B). Then how many ways can this be done?

1. patient 1 receives A and patient 2 receives A
2. patient 1 receives A and patient 2 receives B
3. patient 1 receives B and patient 2 receives A
4. patient 1 receives B and patient 2 receives B

- There are 4 possible treatment assignments.
- The probability of a treatment assignment is $1/4$,
- The probability that an individual patient receives treatment A (or B) is $1/2$.
- In general, if there are N experimental units then there are 2^N possible treatment assignments (provided there are two treatments).

Treatment Assignment

A treatment assignment vector records the treatmemnt that each experimental unit is assigned to receive. If $N = 2$ then the possible treatment assignment vectors are:

$$\begin{pmatrix}1\\0\end{pmatrix}, \begin{pmatrix}0\\1\end{pmatrix}, \begin{pmatrix}1\\1\end{pmatrix}, \begin{pmatrix}0\\0\end{pmatrix},$$

where 1= treatment A, and 0=treatment B.

Treatment Assignment

- It wouldn't be a very imformative expriment if both patients received A or both received B.
- Therefore, it makes sense to rule out this scenario.
- We want to assign treatments to patients such that one patient receives A and the other receives B.
- The possibile treatment assignments are:

1. patient 1 receives A and patient 2 receives B or (in vector notation) $\begin{pmatrix} 1 \\ 0 \end{pmatrix}$.
2. patient 1 receives B and patient 2 receives A or (in vector notation) $\begin{pmatrix} 0 \\ 1 \end{pmatrix}$.

- In this case the probability of a treatment assignment is $1/2$, and the probability that an individual patient receives treatment A (or B) is still $1/2$.

Randomized Experiments and Observational Studies

Randomized experiments are currently viewed as the most credible basis for determining cause and effect relationships. Health Canada, the U.S. Food and Drug Administration, European Medicines Agency, and other regulatory agencies all rely on randomized experiments in their approval processes for pharmaceutical treatments.

Randomization

- The primary objective in the design of experiments is the avoidance of bias or systematic error (Cox and Reid, 2005).
- One way to avoid bias is to use randomization.

Randomization

- Applied to the allocation of experimental units to treatments.
- Provides protection to experimenter against variables unknown to experimenter but may impact the response.
- Reduces influence of subjective judgement in treatment allocation.

Randomization

- National supported work demonstration program (NSW) included a randomized experiment to evaluate the effect of on the job training on unemployment. (Ref: Rosenbaum, pg. 22- 28)
- Treatment: work experience in form of subsidized employment then individuals transitioned to unsubsidized employment.
- Control: standard social programs

Randomization

- The response was earnings ($) in 1978.
- Later in course we will compare this with observational studies.
- So participants were matched on pre-treatment covariates.
- Results in 185 treated men matched to 185 treated controls.

Randomization

Covariate	Group	Earnings ($)
Age (Mean)	Treated	25.82
	Control	25.70
Years of education (Mean)	Treated	10.35
	Control	10.19
Black (%)	Treated	84%
	Control	85%
Married (%)	Treated	19%
	Control	20%
Earnings in 1974 $ (Mean)	Treated	2096
	Control	2009

Blocking

- To block an experiment is to divide the observations into groups called blocks so that observations in a block are collected under relatively similar conditions.
- Suppose that the yield of a manufacturing process for penicillin varies a lot depending on how much of a certain raw material is used in the process. To compare four variants of the manufacturing process we might randomize within blocks of the raw material.

Blocking

- NSW experiment: assume we paired similar men.
- One member of each pair was randomized to subsidized employment.
- The pair of men would form a block.
- Paired experiments are a form of blocking.

Replication

- One of the main principles of experimental design.
- Replication should be carried out several times.
- Which diet, A or B, results in a greater weight loss? Replication means that more than one subject should be assigned to the diets.
- This should be done in such a way that the variation among replicates can provide an accurate measure of errors that affect comparisons between A runs and B runs.

Example: Wheat Yield

Is one fertilizer better than another in terms of yield?

- What is the outcome variable?
- What are factor of interest?

Example: Wheat Yield

Experimental material?

Plot 1	Plot 2	Plot 3	Plot 4	Plot 5	Plot 6
Plot 7	Plot 8	Plot 9	Plot 10	Plot 11	Plot 12

Example: Wheat Yield

How should we assign treatments/factor levels to plots?

- We want to make sure that we can identify the treatment effect in the presence of other sources of variation.
- What other (besides fertilizer) potential sources could cause variation in wheat yield?

Example: Wheat Yield

- Assigning treatments randomly avoids any pre-experimental bias.
- 12 playing cards, 6 red, 6 black were shuffled (7 times??) and dealt
- 1st card black → 1^{st} plot gets B
- 2nd card red → 2^{nd} plot gets A
- 3rd card black → 3^{rd} plot gets B
- Completely randomized design

Wheat Yield Example

B 26.9	A 11.4	B 26.6	A 23.7	B 25.3	B 28.5
B 14.2	A 17.9	A 16.5	A 21.1	B 24.3	A 19.6

- Evidence that fertilizer type is a source of yield variation?
- Evidence about differences between two populations is generally measured by comparing summary statistics across two sample populations.
- A statistic is any computable function of the observed data.

Summarizing a Distribution

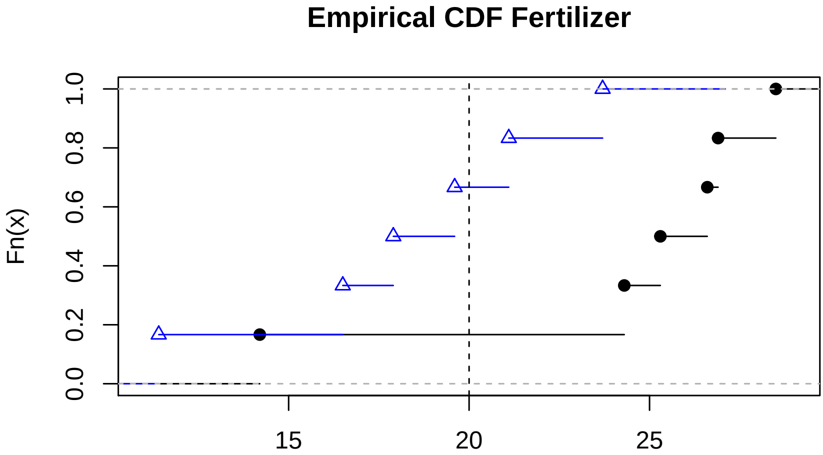
- The empirical cumulative distribution function is:

$$\hat{F}(y) = \frac{\#(y_i \leq y)}{n}$$

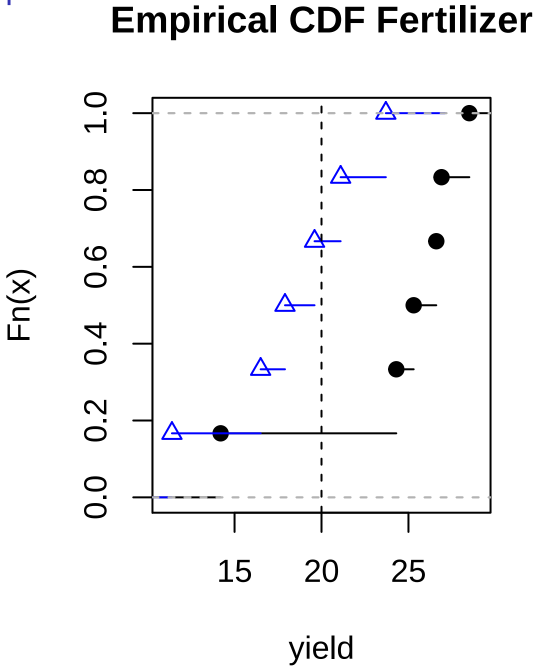
- Histograms, Boxplots, other graphical displays.

Empirical CDF

```r
yA <- c(11.4,23.7,17.9,16.5,21.1,19.6)
yB <- c(26.9,26.6,25.3,28.5,14.2,24.3)
plot.ecdf(yB,xlab="yield",xlim=c(11,29),
          main="Empirical CDF Fertilizer")
plot.ecdf(yA,col="blue",pch=2,add=T);abline(v=20,lty=2)
```



Empirical CDF



Summarizing a Distribution - Location

Let $x_1, x_2, \ldots, x_n$ be a sample from a distribution.

Sample mean:

$$\bar{x} = \sum_{i=1}^{n} x_i / n$$

The p^{th} quantile of a distribution with CDF F is the value x_p such that $F(x_p) = p$ or $x_p = F^{-1}(p) = \min\{x | F(x) \geq p\}$.

Sample percentile: A value $\hat{x_p}$ such that:

$$\hat{x_p} = \hat{F}(p)^{-1}$$

For example, $x_{0.25}, x_{0.5}, x_{0.75}$ are the $25^{th}, 50^{th}$, and 75^{th} percentiles.

Summarizing a Distribution - Scale

Sample variance of $x_1, x2, \ldots, x_n$ is

$$s^2 = \frac{1}{n-1} \sum_{i=1}^{n} (x_i - \bar{x})^2$$

The interquartile range is $x_{0.75} - x_{0.25}$.

Summarizing Wheat Yield

```r
summary(yA); sd(yA);quantile(yA,prob=c(0.25,0.75))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   11.40   16.85   18.75   18.37   20.73   23.70 

## [1] 4.234934

##    25%    75% 
## 16.850 20.725 
```

```r
summary(yB); sd(yA); quantile(yA,prob=c(0.25,0.75))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   14.20   24.55   25.95   24.30   26.82   28.50 

## [1] 4.234934

##    25%    75% 
## 16.850 20.725 
```

Results

```r
mean(yA)-mean(yB)
```

```
## [1] -5.933333
```

- So there is a moderate/large difference in mean yield for these fertilizers.
- Would you recommend B over A for future plantings?
- Do you think these results generalize to a larger population?
- Could the result be due to chance?

Hypothesis Testing Via Randomization

- Are the observed differences in yield due to fertilizer type?
- Are the observed differences in yield due to plot-to-plot variation?

Hypothesis Testing Via Randomization

Hypothesis tests:

- H_0 (null hypothesis): Fertilizer type does not affect yield.
- H_1 (alternative hypothesis): Fertilizer type does affect yield.
- A statistical hypothesis evaluates the compatibility of H_0 with the data

Test Statistics and Null Distributions

We can evaluate H_0 by answering:

- Is a mean difference of -5.93 plausible/probable if H0 true?
- Is a mean difference of -5.93 large compared to experimental noise?

Test Statistics and Null Distributions

- Compare $\bar{y}_a - \bar{y}_b$=-5.93 (observed difference in the experiment) to values of $\bar{y}_a - \bar{y}_b$ that could have been observed if H_0 were true.
- Hypothetical values of $\bar{y}_a - \bar{y}_b$ that could have been observed under H_0 are referred to as samples from the null distribution.

Test Statistics and Null Distributions

- $\bar{y}_a - \bar{y}_b$ is a function of the outcome of the experiment.
- If a different experiment were performed then we would obtain a diffrent value of $\bar{y}_a - \bar{y}_b$.

Test Statistics and Null Distributions

- In this experiment we observed $\bar{y}_a - \bar{y}_b$=-5.93.
- If there was no difference between fertilizers then what other possible values of $\bar{y}_a - \bar{y}_b$ could have been observed?

Experimental Procedure and Potential Outcomes

The cards were shuffled and we were dealt B, R, B, R, . . .

B	A	B	A	B	B
B	A	A	A	B	A

Under this treatment assignment then the yields of the different plots would be:

B 26.9	A 11.4	B 26.6	A 23.7	B 25.3	B 28.5
B 14.2	A 17.9	A 16.5	A 21.1	B 24.3	A 19.6

Experimental Procedure and Potential Outcomes

Another potential treatment assignment under H_0 is:

B	A	B	B	A	A
A	B	B	A	A	B

The yields obtained under this assignment are:

B 26.9	A 11.4	B 26.6	B 23.7	A 25.3	A 28.5
A 14.2	B 17.9	B 16.5	A 21.1	A 24.3	B 19.6

This data could occur of the experiment were run again.

Experimental Procedure and Potential Outcomes

- Under this hypothetical assignment the mean difference is:

```
yA <- c(11.4,25.3,28.5,14.2,21.1,24.3)
yB <- c(26.9,26.6,23.7,17.9,16.5,19.6)
mean(yA-yB)
```

```
## [1] -1.066667
```

This represents an outcome of the experiment in a universe where:

1. The treatment assignment is B, A, B, B, A, A, A, B, B, A, A, B
2. H_0 is true (i.e., $\mu_A = \mu_B$, where μ_A, μ_B are the mean yields of fertilizers A and B).

The Null distribution

- What potential outcomes would we see if H_0 is true?
- Compute $\bar{y}_a - \bar{y}_b$ for each possible treatment assignment.

The Null Distribution

- For each treatment assignment compute

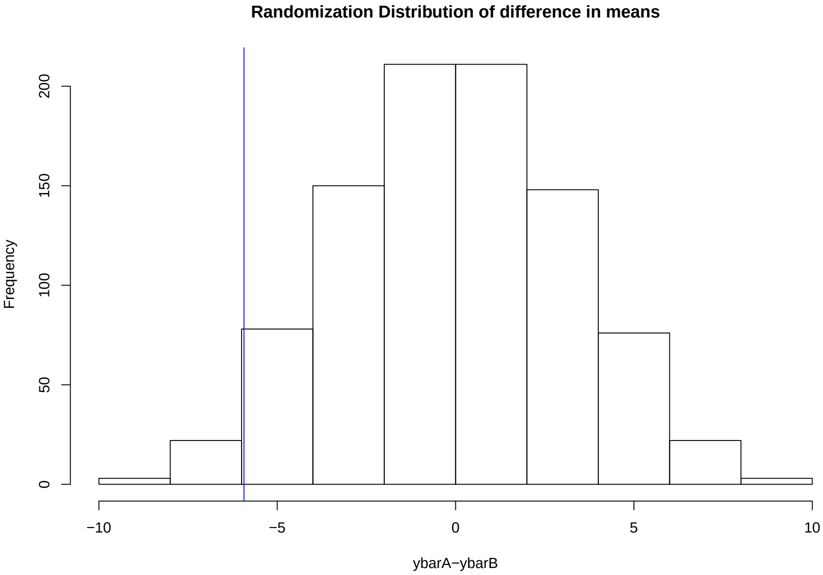
$$\delta_i = \bar{y}_a - \bar{y}_b, i = 1, 2, \ldots, 924.$$

- $\{\delta_1, \delta_2, \ldots, \delta_{924}\}$ enumerates all pre-randomisation outcomes assuming no treatment effect.
- Since each treatment assignment is equally likely under the null distribution, a probability distribution of experimental results if H_0 is true can be described as

$$\hat{F}(y) = \frac{\#(\delta_i \leq y)}{924}.$$

This is called the randomisation distribution.

Randomization Distribution



Hypothesis Testing

- Is there any contradiction between H_0 and the observed data?
- Calculate

$$\hat{F}(-5.93) = \frac{\#(\delta_i \leq -5.93)}{924}.$$

Hypothesis Testing

- A P-value is the probability, under the null hypothesis of obtaining a more extreme than the observed result.

$$\text{P-value} = P\left(\delta \leq -5.93\right)$$

- A small P-value implies evidence **against** null hypothesis.
- If the P-value is large does this imply that the null is true?

Randomization Test

- Assume H_0 is true.
- Calculate the difference in means for every possible way to split the data into two samples of size 6.
- This would result in $\binom{12}{6} = 924$ differences.
- Calculate the probability of observing a value as extreme of more extreme than the observed value of the test statistic (*P-value*).
- If the P-value is small then there are two possible explanations:

1. An unlikely value of the statistic has occurred, or
2. The assumption that H_0 is true is incorrect.

- If the P-value is large then the hypothesis test is inconclusive.

Hypothesis Testing Via Randomization

- Are the observed differences in yield due to fertilizer type?
- Are the observed differences in yield due to plot-to-plot variation?

Hypothesis Testing Via Randomization

Hypothesis tests:

- H_0 (null hypothesis): Fertilizer type does not affect yield.
- H_1 (alternative hypothesis): Fertilizer type does affect yield.
- A statistical hypothesis evaluates the compatibility of H_0 with the data

Test Statistics and Null Distributions

We can evaluate H_0 by answering:

- Is a mean difference of -5.93 plausible/probable if H0 true?
- Is a mean difference of -5.93 large compared to experimental noise?

Test Statistics and Null Distributions

- Compare $\bar{y}_a - \bar{y}_b$=-5.93 (observed difference in the experiment) to values of $\bar{y}_a - \bar{y}_b$ that could have been observed if H_0 were true.
- Hypothetical values of $\bar{y}_a - \bar{y}_b$ that could have been observed under H_0 are referred to as samples from the null distribution.

Test Statistics and Null Distributions

- $\bar{y}_a - \bar{y}_b$ is a function of the outcome of the experiment.
- If a different experiment were performed then we would obtain a diffrent value of $\bar{y}_a - \bar{y}_b$.

Test Statistics and Null Distributions

- In this experiment we observed $\bar{y}_a - \bar{y}_b$=-5.93.
- If there was no difference between fertilizers then what other possible values of $\bar{y}_a - \bar{y}_b$ could have been observed?

Experimental Procedure and Potential Outcomes

The cards were shuffled and we were dealt B, R, B, R, . . .

B	A	B	A	B	B
B	A	A	A	B	A

Under this treatment assignment we oberved the yields:

B 26.9	A 11.4	B 26.6	A 23.7	B 25.3	B 28.5
B 14.2	A 17.9	A 16.5	A 21.1	B 24.3	A 19.6

Experimental Procedure and Potential Outcomes

Another potential treatment assignment under H_0 is:

B	A	B	B	A	A
A	B	B	A	A	B

The yields obtained under this assignment are:

B 26.9	A 11.4	B 26.6	B 23.7	A 25.3	A 28.5
A 14.2	B 17.9	B 16.5	A 21.1	A 24.3	B 19.6

This data could occur if the experiment were run again.

Experimental Procedure and Potential Outcomes

- Under this hypothetical assignment the mean difference is:

```
yA <- c(11.4,25.3,28.5,14.2,21.1,24.3)
yB <- c(26.9,26.6,23.7,17.9,16.5,19.6)
mean(yA-yB)
```

```
## [1] -1.066667
```

This represents an outcome of the experiment in a universe where:

1. The treatment assignment is B, A, B, B, A, A, A, B, B, A, A, B
2. H_0 is true (i.e., $\mu_A = \mu_B$, where μ_A, μ_B are the mean yields of fertilizers A and B).

The Null distribution

- What potential outcomes **could** we see if H_0 is true?
- Compute $\bar{y}_a - \bar{y}_b$ for each possible treatment assignment.

The Null Distribution

- For each treatment assignment compute

$$\delta_i = \bar{y}_a - \bar{y}_b, i = 1, 2, \ldots, 924.$$

- $\{\delta_1, \delta_2, \ldots, \delta_{924}\}$ enumerates all pre-randomisation outcomes assuming no treatment effect.
- Since each treatment assignment is equally likely under the null distribution, a probability distribution of experimental results if H_0 is true can be described as

$$\begin{aligned}\hat{F}(y) &= \frac{\#(\delta_i \leq y)}{924} \\ &= \frac{\sum_{k=1}^{\binom{12}{6}} I(\delta_k \leq y)}{\binom{12}{6}}\end{aligned}$$

This is called the randomisation distribution.

Randomization Distribution

- The yield is not random since the plots were not chosen randomly.
- Their assignment to treatments is random.
- The basis for building a probability distribution for $\bar{y}_a - \bar{y}_b$ comes from the randomization of fertilizers to plots.

Randomization Distribution

- This randomization results in 6 plots getting fertilizer A and the remaining 6 plots receiving fertilizer B.
- This is one of $\binom{12}{6} = 924$ equally likely randomizations that could have occured.

Experimental Procedure and Potential Outcomes

This represents an outcome of the experiment in a universe where:

1. H_0 is true.
2. The yield will be the same regardless of which fertilizer a plot received.

For example a plot that had a yield of 26.9 given fertilizer B would have the same yield if the plot received fertilizer A if H_0 is true.

R Code for Randomization Distribution

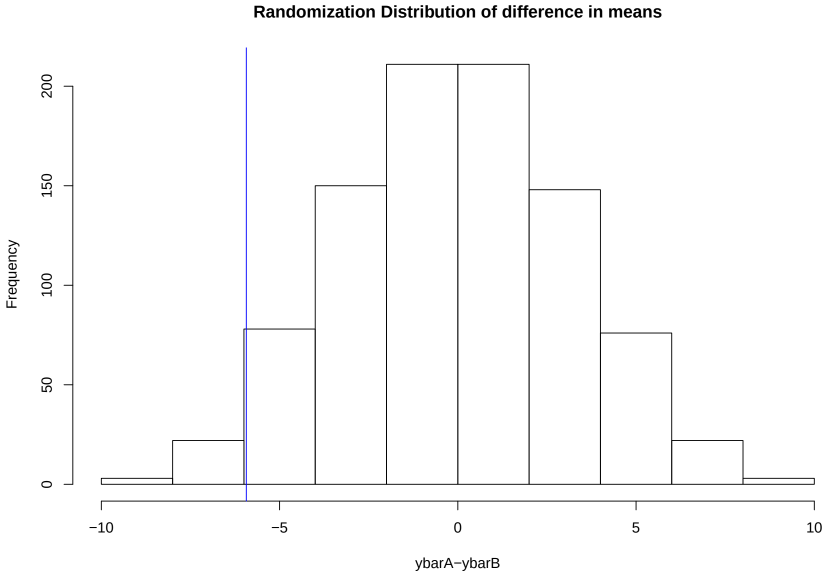
```r
yA <- c(11.4,23.7,17.9,16.5,21.1,19.6);yB <- c(26.9,26.6,25.3,28
fert <- c(yA,yB); N <- choose(12,6)
res <- numeric(N) # store the results
index <-combn(1:12,6) #Generate N treatment assignments
for (i in 1:N)
{res[i] <- mean(fert[index[,i]])-mean(fert[-index[,i]])}
index[,1:2] #output first two randomizations
```

```
##      [,1] [,2]
## [1,]    1    1
## [2,]    2    2
## [3,]    3    3
## [4,]    4    4
## [5,]    5    5
## [6,]    6    7
```

```r
res[1:2] #output first two mean diffs
```

```
## [1] -5.933333 -3.500000
```

Randomization Distribution



Hypothesis Testing

- Is there any contradiction between H_0 and the observed data?
- A **P-value** is the probability, under the null hypothesis of obtaining a more extreme than the observed result.

$$\text{P-value} = P\left(\delta \leq -5.93\right) = \hat{F}(-5.93)$$

- A small P-value implies evidence **against** null hypothesis.
- If the P-value is large does this imply that the null is true?

Randomization Test

- Assume H_0 is true.
- Calculate the difference in means for every possible way to split the data into two samples of size 6.
- This would result in $\binom{12}{6} = 924$ differences.
- Calculate the probability of observing a value as extreme of more extreme than the observed value of the test statistic (*P-value*).
- If the P-value is small then there are two possible explanations:

1. An unlikely value of the statistic has occurred, or
2. The assumption that H_0 is true is incorrect.

- If the P-value is large then the hypothesis test is inconclusive.

Computing the P-value

The observed value of the test statistic is -5.93. So, the p-value is

```r
# of times values from the mean randomization distribution
# less than observed value
sum(res<=observed)
```

```
## [1] 26
```

```r
N # Number of randomizations
```

```
## [1] 924
```

```r
pval <- sum(res<=observed)/N # Randomization p value
round(pval,2)
```

```
## [1] 0.03
```

Interpretation of P-value

- A p-value of 0.03 can be interpreted as: assume there is no difference in yield between fertilizers A and B then the proportion of randomizations that would produce an observed mean difference between A and B of at most -5.93 is 0.03.
- In other words, under the assumption that there is no difference between A and B only 3% of randomizations would produce an extreme or more extreme difference than the observed mean difference.
- Therefore it's unlikely (if we consider 3% unlikely) that an observed mean difference as extreme or more extreme than -5.93 would be observed if $\mu_A = \mu_B$.

Two-Sided Randomization P value

- If we are using a two-sided alternative then how do we calculate a p-value?
- The randomization distribution may not be symmetric so there is no justifcation for simply doubling the probability in one tail.

Let

$$\bar{t} = \left(1/\binom{N}{N_A}\right) \sum_{i=1}^{\binom{N}{N_A}} t_i$$

be the mean of the randomization distribution then we can define the two-sided p-value as

$$P(|T - \bar{t}| \geq |t^* - \bar{t}|\,|H_0) = \sum_{i=1}^{\binom{N}{N_A}} \frac{I(|t_i - \bar{t}| \geq |t^* - \bar{t}|)}{\binom{N}{N_A}},$$

The probability of obtaining an observed value of the test statistic as far, or farther, from the mean of the randomization distribution.

Two-Sided Randomization P value

```r
yA <- c(11.4,23.7,17.9,16.5,21.1,19.6)
yB <- c(26.9,26.6,25.3,28.5,14.2,24.3)
fert <- c(yA,yB) #pool data
N <- choose(12,6)
res <- numeric(N) # store the results
index <-combn(1:12,6)
for (i in 1:N)
{
  res[i] <- mean(fert[index[,i]])-mean(fert[-index[,i]])
}
tbar <- mean(res)
pval <- sum(abs(res-tbar)>=abs(observed-tbar))/N
round(pval,2)
```

```
## [1] 0.06
```

Randomization Test

- We could calculate the difference in means for every possible way to split the data into two samples of size 6.
- This would result in $\binom{12}{6} = 924$ differences.
- If there were 30 observations split evenly into two groups then there are $\binom{30}{15} = 155,117,520$ differences.
- So unless the sample sizes are small these exhaustive calculations are not practical.

Randomization Test

Instead we can create a permutation resample (Monte Carlo Sampling).

1. Draw 6 observations from the pooled data without replacement. (fert A)
2. The remaining 6 observations will be the second sample (fert B)
3. Calculate the difference in means of the two samples
4. Repeat 1-3 at least 250000 times.
5. P-value is the fraction of times the random statistics exceeds the original statistic.

Estimate P-value via Monte Carlo Sampling

If M test statistics, t_i, $i = 1, ..., M$ are randomly sampled from the permutation distribution, a one-sided Monte Carlo p value for a test of $H_0 : \mu_T = 0$ versus $H_1 : \mu_T > 0$ is

$$\hat{p} = \frac{1 + \sum_{i=1}^{M} I(t_i \geq t^*)}{M + 1}.$$

Including the observed value t^* there are $M + 1$ test statistics.

Estimate P-value via Monte Carlo Sampling

```
N <- 250000 # number of times to repeat this process
result <- numeric(N) # space to save random diffs.
for (i in 1:N)
{ #sample of size 6, from 1 to 12, without replacement
  index <- sample(12,size=6,replace=F)
  result[i] <- mean(fert[index])-mean(fert[-index])
}

#store observed mean difference
observed <- mean(yA)-mean(yB)

#P-value - mean - results will vary
pval <- (sum(result <= observed)+1)/(N+1)
round(pval,4)
```

```
## [1] 0.0287
```

Basic Decision Theory

	H_0 True	H_0 False
Accept H_0	correct	type II error
Reject H_0	type I error	correct

$$\text{P-value} = P\left(\text{test statistic} \geq \text{observed value of test statistic}\right)$$

$$\begin{aligned} \alpha &= P\left(\text{type I error}\right) \\ \beta &= P\left(\text{type II error}\right) \\ 1 - \beta &= \text{power} \end{aligned}$$

The Randomization P-value

- An achievable P-value of the randomization test must be a multiple of $\frac{k}{\binom{12}{6}} = \frac{k}{924}$, where $k = 1, 2, \ldots, 924$.
- If we choose a significance level of $\alpha = \frac{k}{924}$ that is one of the achievable P-values then $P\left(\text{type I error}\right) = \alpha$.
- The randomization test is an exact test.
- If α is not chosen to be one of the achievable P-values but $\alpha = \frac{k}{924}$ is the largest acheivable P-value less than α then $P\left(\text{type I error}\right) < \alpha$.

Choosing a Test Statistic

A test statistic should be able to differentiate between H_0 and H_a in ways that are scientifically relevant.

Other Test Statistics

- Other test statistics could be used instead of $T = \bar{Y}_A - \bar{Y}_B$ to measure the effectiveness of fertilizer A.
- The difference in group medians

$$median(Y_A) - median(Y_B)$$

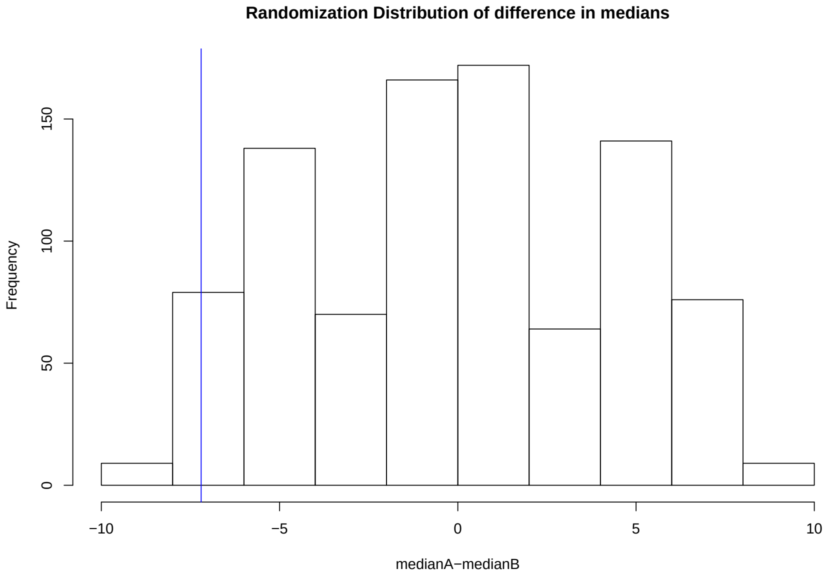
or trimmed means are examples of other test statistics.

Other Test Statistics

The randomiztion distribution of the difference in group medians can be obtained by modifying the R code used for the difference in group means.

```r
fert <- c(yA,yB) #pool data
N <- choose(12,6)
res <- numeric(N) # store the results
index <-combn(1:12,6) # Generate N treatment assignments
for (i in 1:N)
{
  res[i] <- median(fert[index[,i]])-median(fert[-index[,i]])
}
```

Other Test Statistics



Other Test Statistics

The p-value of the randomization test can be calculated

```
# of times values from the median randomization
# distribution less than observed value
sum(res<=observed)
```

```
## [1] 36
```

```
N # Number of randomizations
```

```
## [1] 924
```

```
pval <- sum(res<=observed)/N # Randomization p value
round(pval,2)
```

```
## [1] 0.04
```

The two-sample t-test

If the two wheat yield samples are independent random samples from a normal distribution with means μ_A and μ_B but the same variance then the statistic

$$\bar{y}_A - \bar{y}_b \sim N\left(\mu_A - \mu_B, \sigma^2(1/n_A + 1/n_B)\right).$$

So,

$$\frac{\bar{y}_A - \bar{y}_b - \delta}{\sigma\sqrt{(1/n_A + 1/n_B)}} \sim N(0, 1),$$

where $\delta = \mu_A - \mu_B$.

If we substitute

$$S^2 = \frac{\sum_{i=1}^{n_A}(y_{iA} - \bar{y}_A) + \sum_{i=1}^{n_B}(y_{iB} - \bar{y}_B)}{n_A + n_B - 2}$$

for σ^2 then

$$\frac{\bar{y}_A - \bar{y}_b - \delta}{\quad} \sim t_{n_A+n_B-2},$$

The two-sample t-test

In the wheat yield example $H_0 : \mu_A = \mu_B$ and suppose that $H_1 : \mu_A < \mu_B$. The p-value of the test is obtained by calculating the observed value of the two sample t-statistic under H_0.

$$t^* = \frac{\bar{y}_A - \bar{y}_b}{s\sqrt{(1/n_A + 1/n_B)}} = \frac{18.37 - 24.3}{4.72\sqrt{(1/6 + 1/6)}} = -2.18$$

The p-value is $P(t_{18} < -2.18) = 0.03$.

The calculation was done in R.

```r
s <- sqrt((5*var(yA)+5*var(yB))/10)
tstar <- (mean(yA)-mean(yB))/(s*sqrt(1/6+1/6)); round(tstar,2)
```

```
## [1] -2.18
```

```r
pval <- pt(tstar,10); round(pval,5)
```

```
## [1] 0.02715
```

The two-sample t-test

In R the command to run a two-sample t-test is `t.test()`.

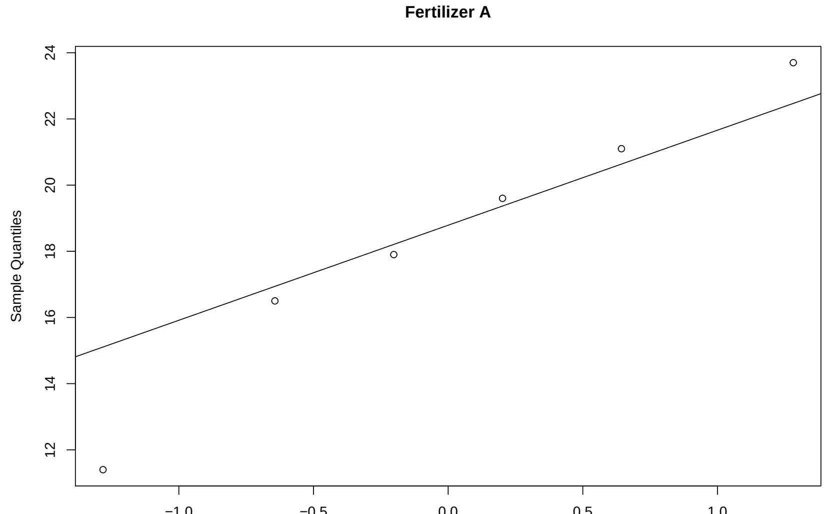
```
t.test(yA,yB,var.equal = TRUE,alternative = "less")
```

```
##
##  Two Sample t-test
##
## data:  yA and yB
## t = -2.1793, df = 10, p-value = 0.02715
## alternative hypothesis: true difference in means is less than
## 95 percent confidence interval:
##        -Inf -0.9987621
## sample estimates:
## mean of x mean of y
##  18.36667  24.30000
```

The two-sample t-test

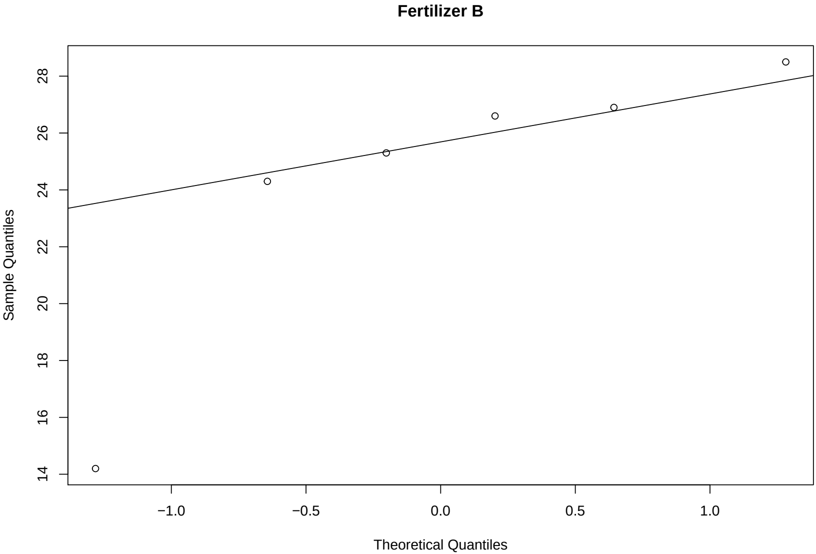
The assumption of normality can be checked using normal quantile plots, although the t-test is robust against non-normality.

```r
qqnorm(yA,main = "Fertilizer A");qqline(yA)
```



The two-sample t-test

```
qqnorm(yB,main = "Fertilizer B");qqline(yB)
```



Two-Sample t-test versus Randomization Test

- The p-value from the randomization test and the p-value from two-sample t-test are almost identical.
- The randomization test does not depend on normality or independence.

Two-Sample t-test versus Randomization Test

- The randomization test does depend on Fisher's concept that after randomization, if the null hypothesis is true, the two results obtained from each particular plot will be exchangeable.
- The randomization test tells you what you could say if exchangeability were true.

Paired Comparisons

- Increase precision by making comparisons within matched pairs of experimental material.
- Randomize within a pair.

Boy's Shoe Experiment

- Two materials to make boy's shoes, A and B, are tested to evaluate if B is more sturdy compared to A.
- During the experimental test some boys scuffed their shoes more than others.
- Each boy's two shoes were subjected to the same treatment by having each boy wear both materials.
- Working with 10 differences B-A most of the boy-to-boy variation could be eliminated.
- Called a randomized paired comparison design.

Boy's Shoe Experiment

- Toss a coin to randomize material to L/R foot of a boy.
- Head: Material A used on right foot.
- Null hypothesis: amount of wear associated with material A and B are the same.
- So labelling given to a pair of results only affects the sign of the difference.

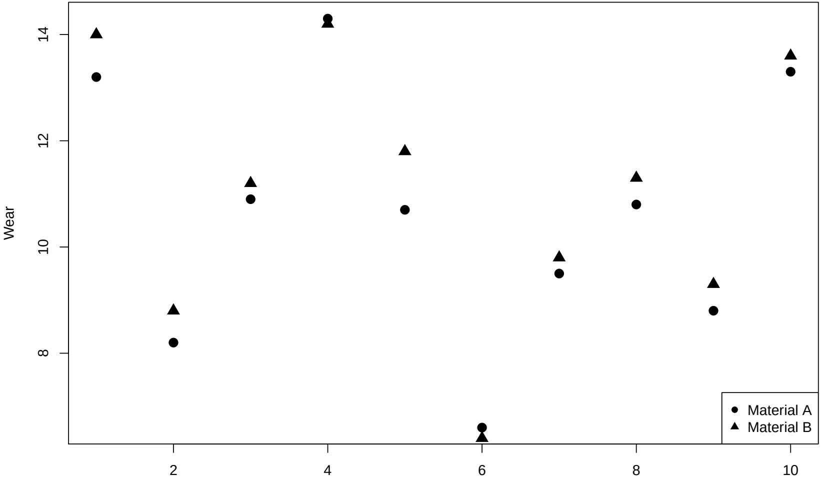
Randomized paired comparison

```r
library(BHH2)
data(shoes.data)
shoes.data
```

```
##    boy matA sideA matB sideB
## 1    1 13.2     L 14.0     R
## 2    2  8.2     L  8.8     R
## 3    3 10.9     R 11.2     L
## 4    4 14.3     L 14.2     R
## 5    5 10.7     R 11.8     L
## 6    6  6.6     L  6.4     R
## 7    7  9.5     L  9.8     R
## 8    8 10.8     L 11.3     R
## 9    9  8.8     R  9.3     L
## 10  10 13.3     L 13.6     R
```

Randomized paired comparison

```
plot(shoes.data$boy,shoes.data$matA,pch=16,cex=1.5,
     xlab="Boy",ylab="Wear")
points(shoes.data$boy,shoes.data$matB,pch=17,cex=1.5)
legend("bottomright",legend=c("Material A","Material B"),pch=c(1
```



Randomized paired comparison

```
diff <- shoes.data$matA-shoes.data$matB
meandiff <- mean(diff); meandiff
```

```
## [1] -0.41
```

```
shoe.dat2 <- data.frame(shoes.data,diff)
shoe.dat2
```

```
##    boy matA sideA matB sideB diff
## 1    1 13.2     L 14.0     R -0.8
## 2    2  8.2     L  8.8     R -0.6
## 3    3 10.9     R 11.2     L -0.3
## 4    4 14.3     L 14.2     R  0.1
## 5    5 10.7     R 11.8     L -1.1
## 6    6  6.6     L  6.4     R  0.2
## 7    7  9.5     L  9.8     R -0.3
## 8    8 10.8     L 11.3     R -0.5
## 9    9  8.8     R  9.3     L -0.5
## 10  10 13.3     L 13.6     R -0.3
```

Boy's Shoe Experiment

- The sequence of coin tosses is one of $2^{10} = 1024$ equiprobable outcomes.
- To test H_0 the average difference of -0.41 observed observed can be compared with the other 1023 averages by calculating the average difference for each of 1024 arrangements of signs in:

$$\bar{d} = \frac{\pm 0.8 \pm 0.6 \cdots \pm 0.3}{10}$$

Randomized paired comparison

```
N <- 2^(10) # number of treatment assignments
res <- numeric(N) #vector to store results
LR <- list(c(-1,1)) # difference is multiplied by -1 or 1
# generate all possible treatment assign
trtassign <- expand.grid(rep(LR, 10))

for(i in 1:N){
res[i] <- mean(as.numeric(trtassign[i,])*diff)
}
trtassign[1:2,]
```

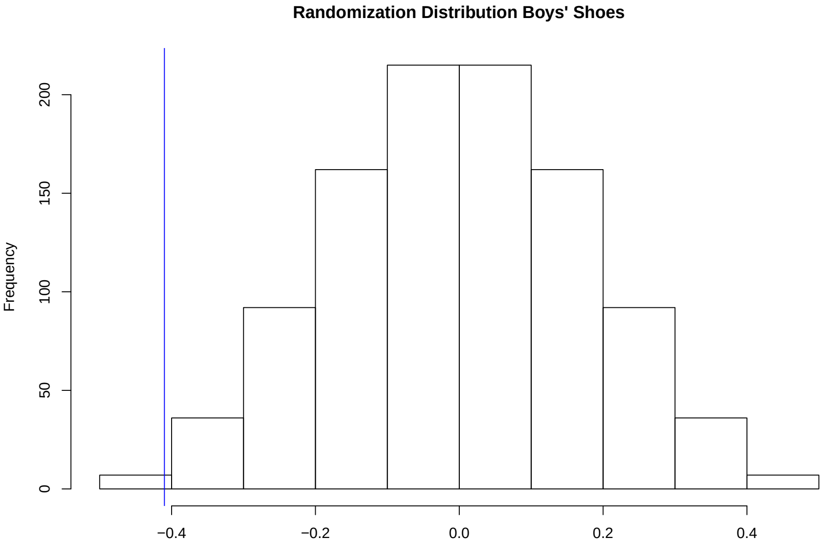
```
##   Var1 Var2 Var3 Var4 Var5 Var6 Var7 Var8 Var9 Var10
## 1   -1   -1   -1   -1   -1   -1   -1   -1   -1    -1
## 2    1   -1   -1   -1   -1   -1   -1   -1   -1    -1
```

```
res[1:2]
```

```
## [1] 0.41 0.25
```

Randomized paired comparison

```
hist(res, xlab="Mean Difference",main="Randomization Distributio
abline(v = meandiff,col="blue")
```



Randomized paired comparison

```
sum(res<=meandiff) # number of differences le observed diff
```

```
## [1] 7
```

```
sum(res<=meandiff)/N # p-value
```

```
## [1] 0.006835938
```

Paired t-test

If we assume that the differences -0.8, -0.6, -0.3, 0.1, -1.1, 0.2, -0.3, -0.5, -0.5, -0.3 are a random sample from a normal distribution then the statistic

$$t = \frac{\bar{d}}{s_{\bar{d}}/\sqrt{10}} \sim t_{10-1},$$

where, $s_{\bar{d}}$ is the sample standard deviation of the paired differences. The p-value for testing if $\bar{D} < 0$ is

$$P(t_9 < t).$$

Paired t-test

In general if there are n differences then

$$t = \frac{\bar{d}}{s_{\bar{d}}/\sqrt{n}} \sim t_{n-1},$$

where, $s_{\bar{d}}$ is the sample standard deviation of the paired differences. The p-value for testing if $\bar{D} < 0$ is

$$P(t_{n-1} < t).$$

NB: This is the same as a one-sample t-test of the differences.

Paired t-test

In R a paired t-test can be obtained by using the command `t.test()` with `paired=T`.

```r
t.test(shoes.data$matA,shoes.data$matB,paired = TRUE,
       alternative = "less")
```

```
##
##  Paired t-test
##
## data:  shoes.data$matA and shoes.data$matB
## t = -3.3489, df = 9, p-value = 0.004269
## alternative hypothesis: true difference in means is less than
## 95 percent confidence interval:
##        -Inf -0.1855736
## sample estimates:
## mean of the differences
##                   -0.41
```

Paired t-test

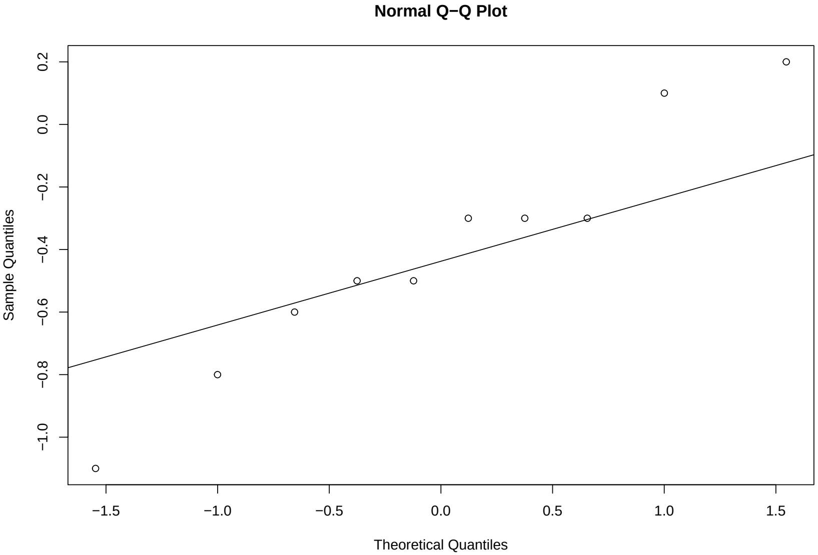
This is the same as a one-sample t-test on the difference.

```r
# same as a one-sample t-test on the diff
t.test(diff,alternative = "less")
```

```
##
##  One Sample t-test
##
## data:  diff
## t = -3.3489, df = 9, p-value = 0.004269
## alternative hypothesis: true mean is less than 0
## 95 percent confidence interval:
##        -Inf -0.1855736
## sample estimates:
## mean of x
##     -0.41
```

Paired t-test

```r
qqnorm(diff); qqline(diff)
```


Normal Q−Q Plot
Sample Quantiles
Theoretical Quantiles