STA305/1004-Class 17

Nov. 26, 2019

Today's Class

- Sample size for ANOVA
- Randomized block designs
  - Linear model and ANOVA
  - Assumptions
- Other Blocking Designs
  - Latin Square
  - Graeco Latin Square
  - hypo-Graeco Latin Square
  - Randomized incomplete block design

Sample size for ANOVA - Designing a study to compare more than two treatments

- Consider the hypothesis that k means are equal vs. the alternative that at least two differ.
- What is the probability that the test rejects if at least two means differ?
- Power $= 1 - P(\text{Type II error})$ is this probability.

Sample size for ANOVA - Designing a study to compare more than two treatments

The null and alternative hypotheses are:

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_k \text{ vs. } H_1 : \mu_i \neq \mu_j.$$

The test rejects at level α if

$$MS_{Treat}/MS_E \geq F_{k-1,N-K,\alpha}.$$

The power of the test is

$$1 - \beta = P\left(MS_{Treat}/MS_E \geq F_{k-1,N-K,\alpha}\right),$$

when H_0 is false.

Sample size for ANOVA - Designing a study to compare more than two treatments

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- MS_{Treat}/σ^2 has a non-central Chi-square distribution with $k-1$ degrees of freedom and non-centrality parameter δ.

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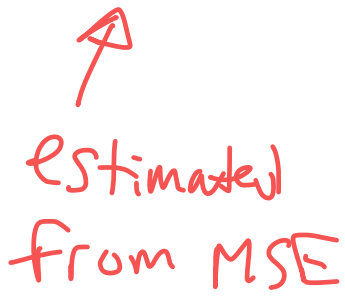
- $$\delta = \frac{\sum_{i=1}^{k} n_i \left(\mu_i - \bar{\mu}\right)^2}{\sigma^2},$$

  where n_i is the number of observations in group i, $\bar{\mu} = \sum_{i=1}^{k} \mu_i/k$, and σ^2 is the within group error variance .



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- This is dentoted by $F_{k-1,N-k}(\delta)$.

Direct calculation of Power

- The power of the test is

$$P\left(F_{k-1,N-k}(\delta) > F_{k-1,N-K,\alpha}\right).$$

- The power is an increasing function δ
- The power depends on the true values of the treatment means μ_i, the error variance σ^2, and sample size n_i.
- If the experimentor has some prior idea about the treament means and error variance, and the sample size (number of replications) the formula above will calculate the power of the test.

The treatment means can be obtained from the table below.

Blood coagulation example - sample size

Suppose that an investigator would like to replicate the blood coagulation study with only 3 animals per diet. In this case $k = 4, n_i = 3$. The treatment means from the initial study are:

Diet	A	B	C	D
Average	61	66	68	61

← Mean Coagulation time.

```
lm.diets <- lm(y~diets,data = tab0401)
anova(lm.diets)
```

```
## Analysis of Variance Table
##
## Response: y
##           Df Sum Sq Mean Sq F value    Pr(>F)
## diets      3    228    76.0  13.571 4.658e-05 ***
## Residuals 20    112     5.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

← MSE

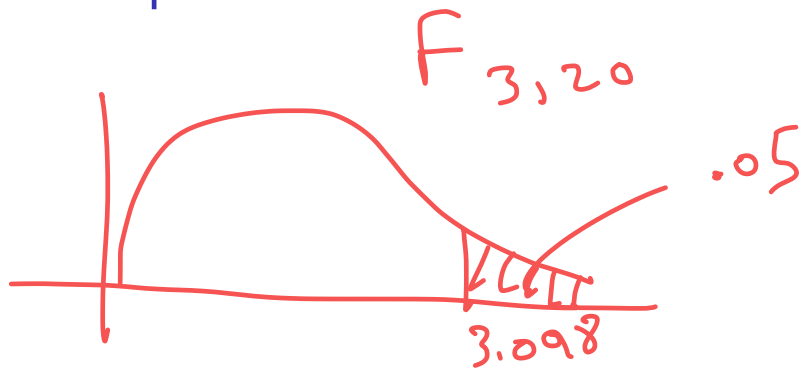
Blood coagulation example - sample size

- $\mu_1 = 61$, $\mu_2 = 66$, $\mu_3 = 68$, $\mu_4 = 61$.
- The error variance σ^2 was estimated as $MS_E = 5.6$.
- Assuming that the estimated values are the true values of the parameters, the non-centrality parameter of the F distribution is:
-

$$\delta = 3 \times \left((61-64)^2 + (66-64)^2 + (68-64)^2 + (61-64)^2\right)/5.6 = 20.35714$$

$$= \sum_{i=1}^{4} n_i (\mu_i - \bar{\mu})^2 / \sigma^2$$

Blood coagulation example - sample size



If we choose $\alpha = 0.05$ as the significance level then $F_{3,20,0.05} = 3.0983912$. The power of the test is then

$$P\left(F_{3,20}(20.36) > 3.10\right) = 0.94.$$

This was calculated using the CDF for the F distribution in R `pf()`.

```
1-pf(q = 3.10,df1 = 3,df2 = 20,ncp = 20.36)
```

```
## [1] 0.9435208
```

cdf F

Calculating power and sample size using the `pwr` library

There are several libraries in R which can calculate power and sample size for statistical tests.

The library `pwr()` has a function

```
pwr.anova.test(k = NULL, n = NULL, f = NULL, sig.level = 0.05, power = NULL)
```

For computing power and sample size.

`k`: Number of groups

`n`: Number of observations (per group)

`f`: Effect size

The effect size is the square root of the non-centrality parameter of the non-central F distribution.

$$f = \sqrt{\frac{\sum_{i=1}^{k} n_i \left(\mu_i - \bar{\mu}\right)^2}{\sigma^2}},$$

where n_i is the number of observations in group i, $\bar{\mu} = \sum_{i=1}^{k} \mu_i / k$, and σ^2 is the within group error variance.

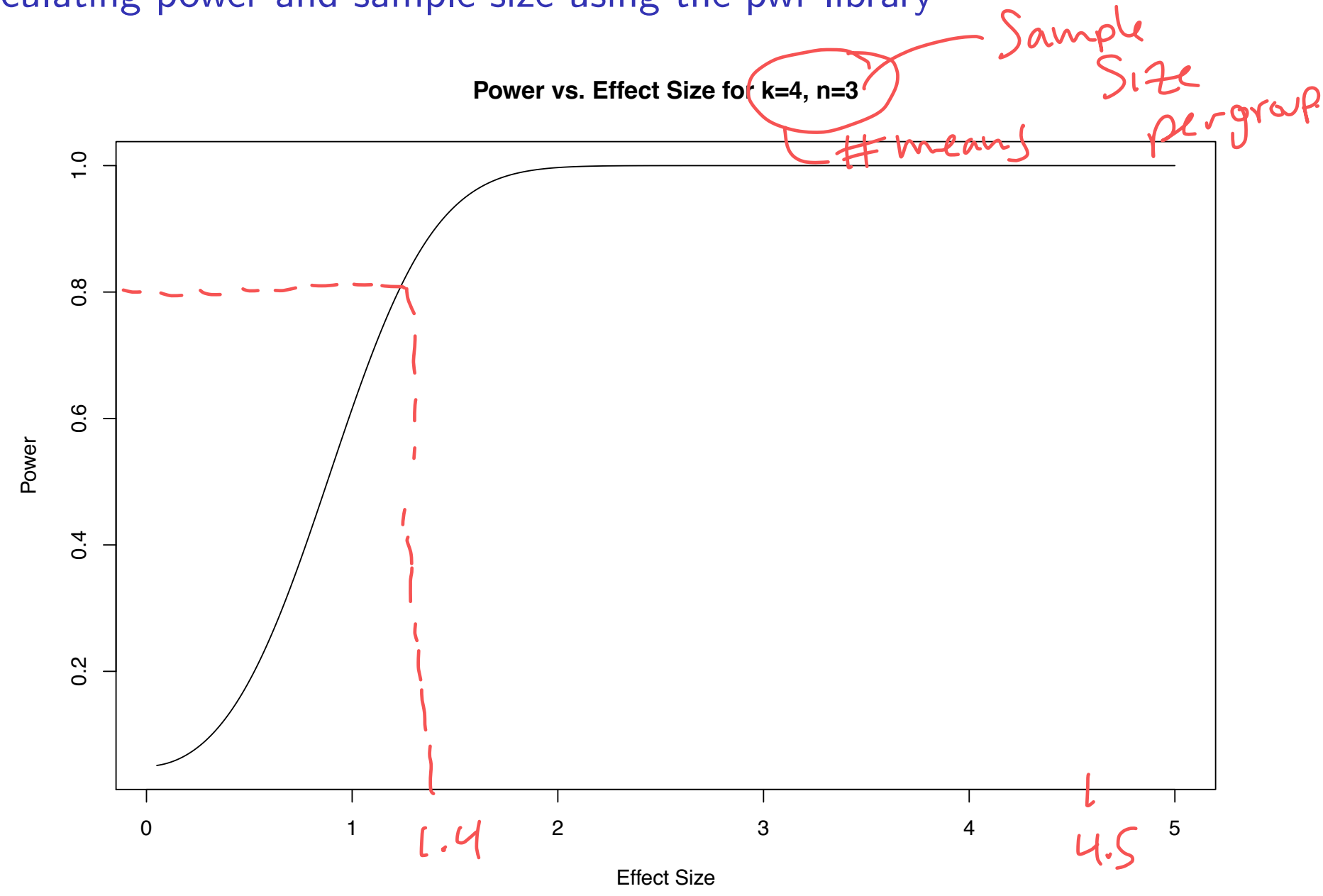
Calculating power and sample size using the pwr library

In the previous example $\delta = 20.35714$ so $f = \sqrt{20.35714} = 4.5118887$.

```
library(pwr)
pwr.anova.test(k = 4,n = 3,f = 4.5)
```

```
##
##      Balanced one-way analysis of variance power calculation
##
##               k = 4
##               n = 3
##               f = 4.5
##       sig.level = 0.05
##           power = 1
##
## NOTE: n is number in each group
```

Calculating power and sample size using the pwr library



Calculating power using simulation

The general procedure for simulating power is:

- Use the underlying model to generate random data with (a) specified sample sizes, (b) parameter values that one is trying to detect with the hypothesis test, and (c) nuisance parameters such as variances.
- Run the estimation program (e.g., `t.test()`,`lm()`) on these randomly generated data.
- Calculate the test statistic and p-value.
- Do the previous steps many times, say, N, and save the p-values. The estimated power for a level alpha test is the proportion of observations (out of N) for which the p-value is less than alpha.

Calculating power using simulation - R program

```r
#Simulate power of ANOVA for three groups

NSIM <- 1000 # number of simulations
res <- numeric(NSIM) # store p-values in res

mu1 <- 2; mu2 <- 2.5;mu3 <- 2  # true mean values of treatment groups
sigma1 <- 1; sigma2 <- 1; sigma3 <- 1 #variances in each group
n1 <- 40; n2 <- 40; n3 <- 40 #sample size in each group

for (i in 1:NSIM) # do the calculations below N times
  {
# generate sample of size n1 from N(mu1,sigma1^2)
y1 <- rnorm(n = n1,mean = mu1,sd = sigma1)
# generate sample of size n2 from N(mu2,sigma2^2)
y2 <- rnorm(n = n2,mean = mu2,sd = sigma2)
# generate sample of size n3 from N(mu3,sigma3^2)
y3 <- rnorm(n = n3,mean = mu3,sd = sigma3)
y <- c(y1,y2,y3) # store all the values from the groups
# generate the treatment assignment for each group
trt <- as.factor(c(rep(1,n1),rep(2,n2),rep(3,n3)))
m <- lm(y~trt) # calculate the ANOVA
res[i] <- anova(m)[1,5] # p-value of F test
}
sum(res<= 0.05)/NSIM # calculate p-value
```

```
## [1] 0.642
```

Change 1st.

Change σ_i^2 in each group.

40 obs. from $N(2,1)$

$N(2.5, 1)$

$N(2, 1)$.

This means that with 40 per group the test will detect a diff. in μ_1, μ_3 $\approx$ 64% of the time.

Blocking - Example: penicillin yield

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Blocking - Example: penicillin yield

Balanced Randomized Block Design.

Key idea: You must know what to block for to implement

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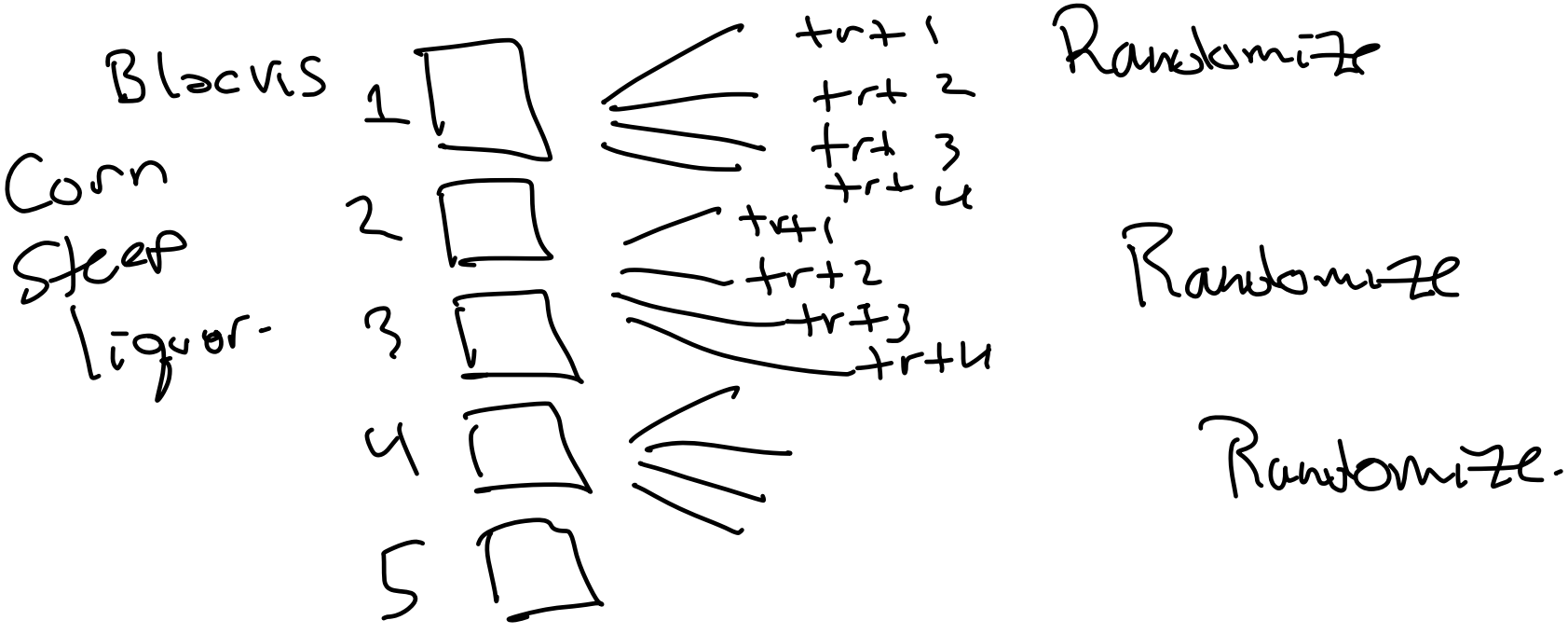
- Within each blend the order in which the four treatments were run was random.



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- Experimenters decided to study 5 blends of corn steep liquor.
- Within each blend the order in which the four treatments were run was random.
- Randomization done separately within each block. Within each blend the order in which the treatments were run were randomized.

Blocking - Example: penicillin yield

	SS	df	MS
Treat	SST	df_T	
Error	SSE	df_E	

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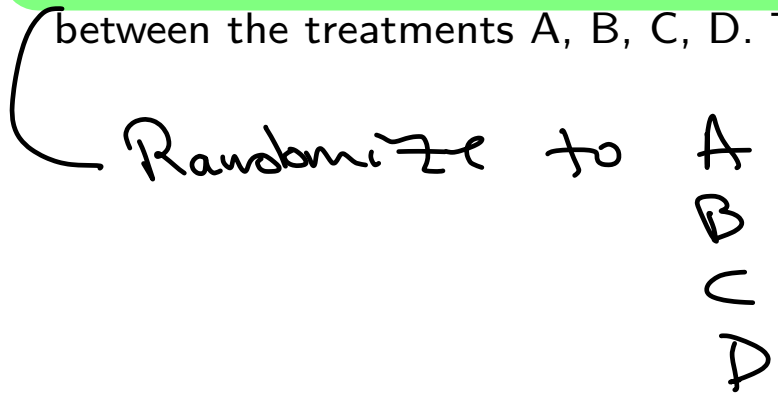
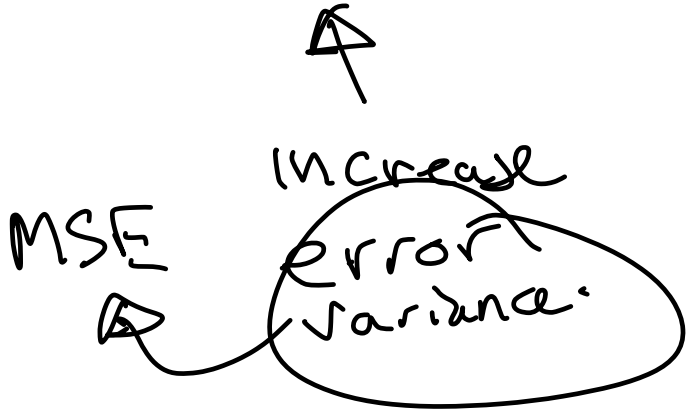
- It was thought that corn steep liquor might causes significant differences in yield.
- Experimenters decided to study 5 blends of corn steep liquor.
- Within each blend the order in which the four treatments were run was random.
- Randomization done separately within each block. Within each blend the order in which the treatments were run were randomized.
- In a fully randomized one-way design blend differences might not be balanced between the treatments A, B, C, D. This might increase the experimental noise.





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- Randomization done separately within each block. Within each blend the order in which the treatments were run were randomized.
- In a fully randomized one-way design blend differences might not be balanced between the treatments A, B, C, D. This might increase the experimental noise.
- But, by randomly assigning the order in which the four treatments were run within each blend (block), blend differences between the groups were largely eliminated.

Example: penicillin yield

The results of the experiment for blend 1

run	blend	treatment	y
1	1	A	89
3	1	B	88
2	1	C	97
4	1	D	94

Seperate Randomizations.

The results of the experiment for blend 2

run	blend	treatment	y
4	2	A	84
2	2	B	77
3	2	C	92
1	2	D	79

Randomization of treatments was done separately within each block.

The ANOVA identity for randomized block designs

The total sum of squares can be re-expressed by adding and subtracting the treatment and block averages as:

$$\sum_{i=1}^{a}\sum_{j=1}^{b}(y_{ij}-\bar{y}_{\cdot\cdot})^2=\sum_{i=1}^{a}\sum_{j=1}^{b}[(\bar{y}_{i\cdot}-\bar{y}_{\cdot\cdot})+(\bar{y}_{\cdot j}-\bar{y}_{\cdot\cdot})+(y_{ij}-\bar{y}_{i\cdot}-\bar{y}_{\cdot j}+\bar{y}_{\cdot\cdot}))]^2 .$$

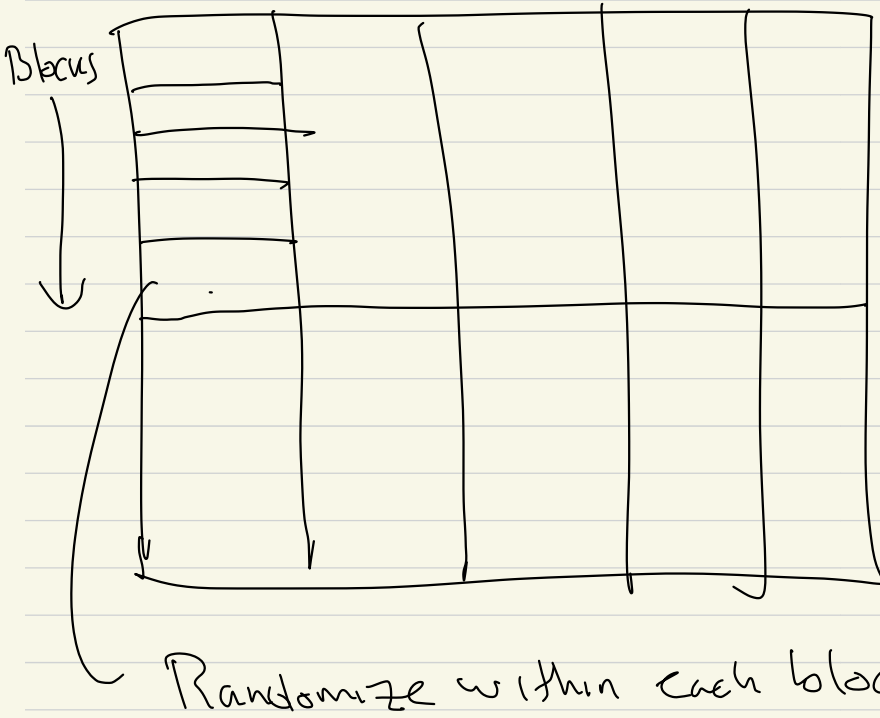
After some algebra ... $SS_T=\sum_{i=1}^{a}\sum_{j=1}^{b}(y_{ij}-\bar{y}_{\cdot\cdot})^2$ is equal to

$$b\sum_{i=1}^{a}(\bar{y}_{i\cdot}-\bar{y}_{\cdot\cdot})^2+a\sum_{j=1}^{b}(\bar{y}_{\cdot j}-\bar{y}_{\cdot\cdot})^2+\sum_{i=1}^{a}\sum_{j=1}^{b}(y_{ij}-\bar{y}_{i\cdot}-\bar{y}_{\cdot j}+\bar{y}_{\cdot\cdot})^2$$

So,

$$SS_T=SS_{Treat}+SS_{Blocks}+SS_E$$

Poll answer is B



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- There are N observations so SS_T has $N-1$ degrees of freedom.
- There are a treatments and b blocks so SS_{Treat} and SS_{Blocks} have $a-1$ and $b-1$ degrees of freedom, respectively.
- The sum of squares on the left hand side the equation should add to the sum of squares on the right hand side of the equation. Therefore, the error sum of squares has

$$(N-1)-(a-1)-(b-1) = (ab-1)-(a-1)-(b-1) = (a-1)(b-1)$$

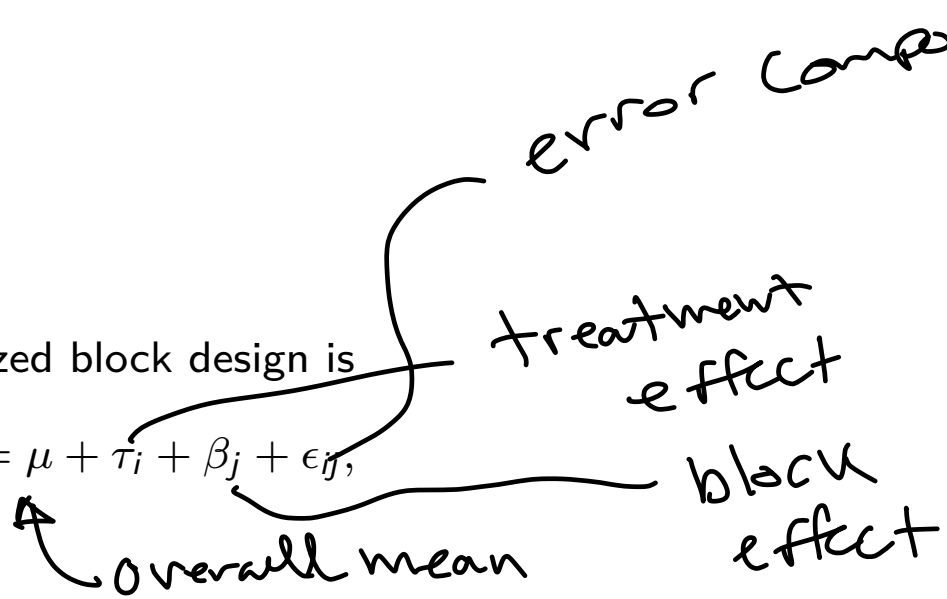
degrees of freedom.

Linear Model for Randomized Block Design

- The linear model for the randomized block design is

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij},$$

where $E(\epsilon_{ij}) = 0$.



- The model is completely additive.
- It assumes that there is no interaction between blocks and treatments.
- An interaction could occur if an impurity in blend 3 poisoned treatment B and made it ineffective, even though it did not affect the other treatments.

Linear Model for Randomized Block Design

treatment　　block.

```
pen.model <- lm(y~as.factor(treatment)+as.factor(blend),data=tab0404)
anova(pen.model)
```

```
Analysis of Variance Table

Response: y
                     Df Sum Sq Mean Sq F value  Pr(>F)
as.factor(treatment)  3     70  23.333  1.2389 0.33866
as.factor(blend)      4    264  66.000  3.5044 0.04075 *
Residuals            12    226  18.833
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

treatment

block.

Calculation of the p-value assumes that

$$\epsilon_{ij} \sim N(0, \sigma^2).$$

So that $MS_{Treat}/MS_E \sim F_{a-1,(a-1)(b-1)}$, $MS_{Blocks} \sim F_{b-1,(a-1)(b-1)}$.

Penicillin example - interpretation

- There is no evidence that the four treatments produce different yields.

∴ large p-value.

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- The differences between the blocks might be informative.
- In particular the investigators might speculate about why blend 1 has such a different influence on yield.
- Perhaps now the experimenters should study the characteristics of the different blends of corn steep liquor. (Box, Hunter, Hunter, 2005)

Other blocking designs

- Latin square
- Graeco-Latin squares,
- Hyper-Graeco-Latin Squares,
- Balanced incomplete block designs.

The Latin Square Design

- There are several other types of designs that utilize the blocking principle such as The Latin Square design.
- If there is more than one nuisance source that can be eliminated then a Latin Square design might be appropriate.

Latin Square Design - Automobile Emissions

- An experiment to test the feasibility of reducing air pollution.

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Latin Square Design - Automobile Emissions

- An experiment to test the feasibility of reducing air pollution.
- A gasoline mixture was modified by changing the amounts of certain chemicals.
- This produced four different types of gasoline: A, B, C, D ← treatments
- These four treatments were tested with four different drivers and four different cars.

4 4 4

Latin Square Design - Automobile Emissions

- Two blocking factors: cars and drivers.
- The Latin square design was used to help eliminate possible differences between drivers I, II, III, IV and cars 1, 2, 3, 4.
- Randomly allocate treatments, drivers , and cars.

Driver	Car 1	Car 2	Car 3	Car 4
Driver I	A	B	D	C
Driver II	D	C	A	B
Driver III	B	D	C	A
Driver IV	C	A	B	D

Latin Square Design - Automobile Emissions

- The data from the experiment.

Driver	Car 1	Car 2	Car 3	Car 4
Driver I	A	B	D	C
	19	24	23	26
Driver II	D	C	A	B
	23	24	19	30
Driver III	B	D	C	A
	15	14	15	16
Driver IV	C	A	B	D
	19	18	19	16

Latin Square Design - Automobile Emissions

- Why not standardize the conditions and make the 16 experimental runs with a single car and single driver for the four treatments?
- Could also be valid but Latin square provides a wider inductive basis.

Latin Square Design - Automobile Emissions

```
latinsq.auto <- lm(y~additive+as.factor(cars)+as.factor(driver),data=tab0408)
anova(latinsq.auto)
```

```
Analysis of Variance Table

Response: y
                   Df Sum Sq Mean Sq F value   Pr(>F)
additive            3     40  13.333     2.5 0.156490
as.factor(cars)     3     24   8.000     1.5 0.307174
as.factor(driver)   3    216  72.000    13.5 0.004466 **
Residuals           6     32   5.333
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

treat.
Block
Block

No evidence of treatment effect, but there is an effect due to driver.

$$SS_T = SS_{cars} + SS_{drivers} + SS_{Additives} + SS_E$$

Latin Square Design - Automobile Emissions

- Assumming that the residuals are independent and normally distributed and the null hypothesis that there are no treatment differences is true then the ratio of mean squares for treatments and residuals has an $F_{3,6}$ distribution.
- This analysis assumes that treatments, cars, and drivers are additive.
- If the design was replicated then this would increase the degrees of freedom for the residuals and reduce the mean square error.

General Latin Square

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General Latin Square

- A Latin square for p factors of a $p \times p$ Latin square, is a square containing p rows and p columns
- Each of the p^2 cells contains one of the p letters that correspond to a treatment.
- Each letter occurs once and only once in each row and column.
- There are many possible $p \times p$ Latin squares.

- Magic Squares.
- Sudoku.

General Latin Square

Which of the following is a Latin square?

	Col1	Col2	Col3
Row 1	B	A	C
Row 2	A	C	B
Row 3	C	B	A

	Col1	Col2	Col3
Row 1	A	B	C
Row 2	C	A	B
Row 3	B	B	A

Not a Latin Square.

Misuse of the Latin Square

- Inappropriate to use Latin square to study factors that can interact.
- Effects of one factor can then be mixed up with interactions of other factors.
- Outliers can occur as a result of these interactions.
- When interactions between factors are likely possible need to use a factorial design.

Graeco-Latin Square

treatment = # levels of each blocking variable.

A Graeco-Latin square is a $k \times k$ pattern that permits study of k treatments simultaneously with three different blocking variables each at k levels.

	Car 1	Car 2	Car 3	Car 4
Driver I	A α	B β	C γ	D δ
Driver II	B δ	A γ	D β	C α
Driver III	C β	D α	A δ	B γ
Driver IV	D γ	C δ	B α	A β

Graeco-Latin Square

- This is a Latin square in which each Greek letter appears once and only once with each Latin letter.
- Can be used to control three sources of extraneous variability (i.e. block in three different directions).

Driver	Car 1	Car 2	Car 3	Car 4
Driver I	A α	B β	C γ	D δ
Driver II	B δ	A γ	D β	C α
Driver III	C β	D α	A δ	B γ
Driver IV	D γ	C δ	B α	A β

Latin letters

Greek letters.

Controlling for three blocking variables: Driver, Car, another blocking factor.

Graeco-Latin Square

To generate a 3×3 Graeco-Latin square design, superimpose two designs using the Greek letters for the second 3×3 Latin square.

	Col1	Col2	Col3
Row 1	B	A	C
Row 2	A	C	B
Row 3	C	B	A

Blocking var 1

	Col1	Col2	Col3
Row 1	A α	B β	C γ
Row 2	C γ	A α	B β
Row 3	B β	C γ	A α

Blocking var 2

	Col 1	Col 2	Col 3
Row 1	B α	A β	C γ
Row 2	A γ	C α	B β
Row 3	C β	B γ	A α

Superimpose

Blocking var 3 has levels α, β, γ

Treatments are A, B, C.

To implement:

Randomly assign levels of blocks to Col 1, Col 2, Col 3 Row 1, Row 2, Row 3

α, β, γ, Randomly assign treatments to letters A, B, C.

hyper-Graeco-Latin Square

These three Latin squares can be superimposed to form a hyper-Graeco-Latin square. Can be used to control 4 nuisance factors (i.e. block 4 factors).

Row	Col1	Col2	Col3	Col4
Row 1	B	A	D	C
Row 2	C	D	A	B
Row 3	D	B	C	A
Row 4	A	C	B	D

Row	Col1	Col2	Col3	Col4
Row 1	D	A	C	B
Row 2	A	D	B	C
Row 3	B	C	A	D
Row 4	C	B	D	A

Row	Col1	Col2	Col3	Col4
Row 1	A	D	B	C
Row 2	C	A	D	B
Row 3	B	C	A	D
Row 4	D	B	C	A

hyper-Graeco-Latin Square

- A machine used for testing the wear on types of cloth.
- Four pieces of cloth can be compared simultaneously on one machine.
- Response is weight loss in tenths of mg when rubbed against a standard grade of emery paper for 1000 revolutions of the machine.

hyper-Graeco-Latin Square

- Specimens of 4 different cloths (A, B,C,D) are compared.
- The wearing qualities can be in any one of 4 positions P_1, P_2, P_3, P_4 on the machine.
- Each emery $(\alpha, \beta, \gamma, \delta)$ paper used to cut into for quarters and each quarter used to complete a cycle C_1, C_2, C_3, C_4 of 1000 revolutions.
- Object was to compare treatments.

treatments to compare.

block variable #1

Block variable #2

block variable #3.

Block variable #4 — type of specimen holders

See next slide.

hyper-Graeco-Latin Square

i) type of specimen holders 1, 2, 3, 4
ii) position on the machine P_1, P_2, P_3, P_4.
iii) emory paper sheet $\alpha, \beta, \gamma, \delta$.
iv) machine cycle C_1, C_2, C_3, C_4.

4 blocking variables

The design was replicated. The first replicate is shown in the table below.

	P_1	P_2	P_3	P_4
C_1	A α 1	B β 2	C γ 3	D δ 4
	320	297	299	313
C_2	C β 4	D α 3	A δ 2	B γ 1
	266	227	260	240
C_3	D γ 2	C δ 1	B α 4	A β 3
	221	240	267	252
C_4	B δ 3	A γ 4	D β 1	C α 2
	301	238	243	290

← weights

hyper-Graeco-Latin Square

A linear model can be fit so that the ANOVA table and parameter treatment effects can be calculated.

```
wear.hypsq <- lm(y~treatment+as.factor(rep)+as.factor(position)+
                   as.factor(cycle)+as.factor(holder)+
                   as.factor(paper),data=tab0412)
anova(wear.hypsq)
```

```
Analysis of Variance Table

Response: y
                    Df  Sum Sq Mean Sq F value    Pr(>F)
treatment            3  1705.3  568.45  5.3908  0.021245 *
as.factor(rep)       1   603.8  603.78  5.7259  0.040366 *
as.factor(position)  3  2217.3  739.11  7.0093  0.009925 **
as.factor(cycle)     6 14770.4 2461.74 23.3455 5.273e-05 ***
as.factor(holder)    3   109.1   36.36  0.3449  0.793790
as.factor(paper)     6  6108.9 1018.16  9.6555  0.001698 **
Residuals            9   949.0  105.45
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

treatment

Blocking variables

replication #

there is evidence that a diff. between treatments exist!

$$SS_{Treat} = SS_{Rep} + SS_{position} + SS_{cycle} + SS_{holder} + SS_{paper} + SS_{Error}$$

Block what you can and randomize the rest...

Balanced incomplete block design

- Suppose that instead of four samples to be included on each 1000 revolution cycle only three could be included, but the experimenter still wanted to compare four treatments.
- The size of the block is now 3 - too small to accommodate all treatments simultaneously.
- A balanced incomplete block design has the property that every pair of treatments occurs together in a block the same number of times.

Cycle block			
1	A	B	C
2	A	B	D
3	A	C	D
4	B	C	D

Cycle block	A	B	C	D
1	x	x	x	
2	x	x		x
3	x		x	x
4		x	x	x