R09 - Analysis of Experiments with Two Factors

Two-way ANOVA and Contrasts

STAT 5870 (Engineering)
Iowa State University

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Two factors

Consider the question of the affect of variety and density on yield under various experimental designs:

- Balanced, complete design
- Unbalanced, complete
- Incomplete

We will also consider the problem of finding the density that maximizes yield.

Data

An experiment was run on tomato plants to determine the effect of

- 3 different varieties (A,B,C) and
- 4 different planting densities (10,20,30,40)

on yield.

A balanced completely randomized design (CRD) with replication was used.

- complete: each treatment (variety × density) is represented
- balanced: each treatment has the same number of replicates
- randomized: treatment was randomly assigned to the plot
- replication: each treatment is represented more than once

This is also referred to as a full factorial or fully crossed design.

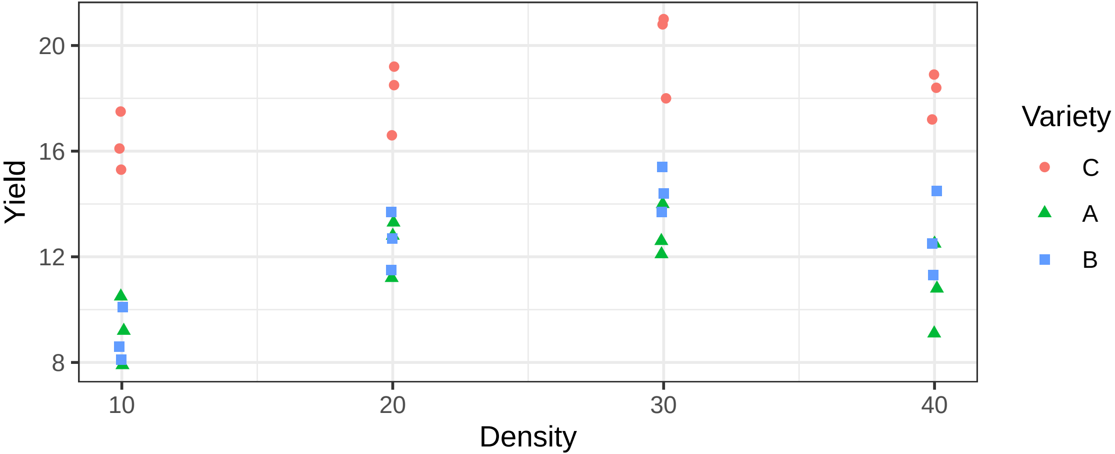
Hypotheses

- How does variety affect mean yield?
    - How is the mean yield for variety A different from B on average?
    - How is the mean yield for variety A different from B at a particular value for density?
- How does density affect mean yield?
    - How is the mean yield for density 10 different from density 20 on average?
    - How is the mean yield for density 10 different from density 20 at a particular value for variety?
- How does density affect yield differently for each variety?

For all of these questions, we want to know

- is there any effect and
- if yes, what is the magnitude and direction of the effect.

Confidence/credible intervals can answer these questions.


Yield
20
16
12
8
10
20
30
40
Density
Variety
C
A
B

Summary statistics

```
# A tibble: 12 x 5
# Groups:   Variety [3]
   Variety Density     n  mean    sd
   <fct>     <int> <int> <dbl> <dbl>
 1 C            10     3 16.3  1.11 
 2 C            20     3 18.1  1.35 
 3 C            30     3 19.9  1.68 
 4 C            40     3 18.2  0.874
 5 A            10     3  9.2  1.3  
 6 A            20     3 12.4  1.10 
 7 A            30     3 12.9  0.985
 8 A            40     3 10.8  1.7  
 9 B            10     3  8.93 1.04 
10 B            20     3 12.6  1.10 
11 B            30     3 14.5  0.854
12 B            40     3 12.8  1.62 
```

Two-way ANOVA

- Setup: Two categorical explanatory variables with I and J levels respectively
- Model:

$$Y_{ijk} \overset{ind}{\sim} N(\mu_{ij}, \sigma^2)$$

where Y_{ijk} is the

  - kth observation at the
  - ith level of variable 1 (variety) with $i = 1, \ldots, \mathrm{I}$ and the
  - jth level of variable 2 (density) with $j = 1, \ldots, \mathrm{J}$.

Consider the models:

  - Additive/Main effects: $\mu_{ij} = \mu + \nu_i + \delta_j$
  - Cell-means: $\mu_{ij} = \mu + \nu_i + \delta_j + \gamma_{ij}$

	10	20	30	40
A	$\mu_{A,10}$	$\mu_{A,20}$	$\mu_{A,30}$	$\mu_{A,40}$
B	$\mu_{B,10}$	$\mu_{B,20}$	$\mu_{B,30}$	$\mu_{B,40}$
C	$\mu_{B,10}$	$\mu_{C,20}$	$\mu_{C,30}$	$\mu_{C,40}$

As a regression model

1. Assign a reference level for both variety (C) and density (40).
2. Let V_i and D_i be the variety and density for observation i.
3. Build indicator variables, e.g. $\mathrm{I}(V_i = A)$ and $\mathrm{I}(D_i = 10)$.
4. The additive/main effects model:

$$\begin{aligned}\mu_i = \quad & \beta_0 \\ & +\beta_1 \mathrm{I}(V_i = A) + \beta_2 \mathrm{I}(V_i = B) \\ & +\beta_3 \mathrm{I}(D_i = 10) + \beta_4 \mathrm{I}(D_i = 20) + \beta_5 \mathrm{I}(D_i = 30)\end{aligned}$$

5. The cell-means model:

$$\begin{aligned}\mu_i = \quad & \beta_0 \\ & +\beta_1 \mathrm{I}(V_i = A) + \beta_2 \mathrm{I}(V_i = B) \\ & +\beta_3 \mathrm{I}(D_i = 10) + \beta_4 \mathrm{I}(D_i = 20) + \beta_5 \mathrm{I}(D_i = 30) \\ \\ & +\beta_6 \mathrm{I}(V_i = A)\mathrm{I}(D_i = 10) + \beta_7 \mathrm{I}(V_i = A)\mathrm{I}(D_i = 20) + \beta_8 \mathrm{I}(V_i = A)\mathrm{I}(D_i = 30) \\ & +\beta_9 \mathrm{I}(V_i = B)\mathrm{I}(D_i = 10) + \beta_{10} \mathrm{I}(V_i = B)\mathrm{I}(D_i = 20) + \beta_{11} \mathrm{I}(V_i = B)\mathrm{I}(D_i = 30)\end{aligned}$$

ANOVA Table

ANOVA Table - Additive/Main Effects model

Source	SS	df	MS	F
Factor A	SSA	(I-1)	SSA/(I-1)	MSA/MSE
Factor B	SSB	(J-1)	SSB/(J-1)	MSB/MSE
Error	SSE	n-I-J+1	SSE/(n-I-J+1)	
Total	SST	n-1		

ANOVA Table - Cell-means model

Source	SS	df	MS	F
Factor A	SSA	I-1	SSA/(I-1)	MSA/MSE
Factor B	SSB	J-1	SSB/(J-1)	MSB/MSE
Interaction AB	SSAB	(I-1)(J-1)	SSAB /(I-1)(J-1)	MSAB/MSE
Error	SSE	n-IJ	SSE/(n-IJ)	
Total	SST	n-1		

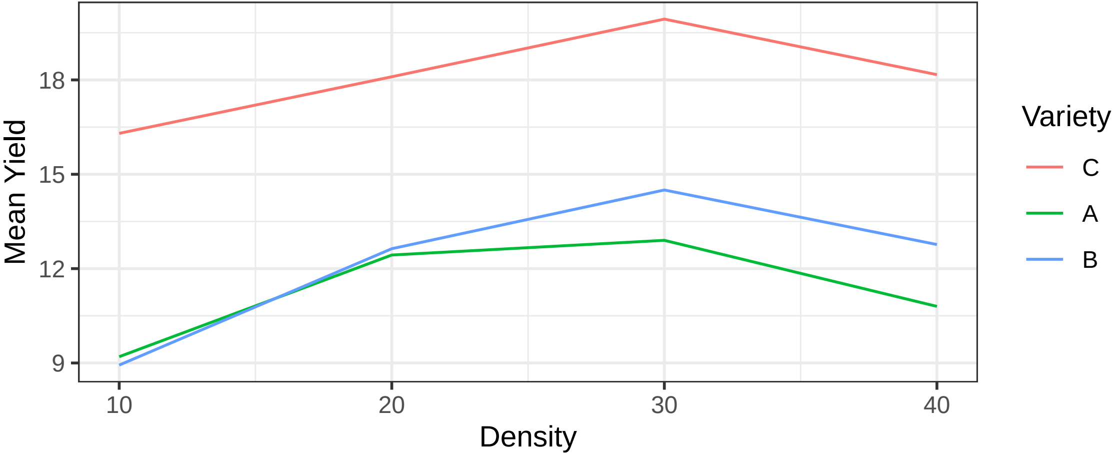
```
tomato$Density <- factor(tomato$Density)
m <- lm(Yield ~ Variety + Density, tomato)
drop1(m, test = "F")

Single term deletions

Model:
Yield ~ Variety + Density
        Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                46.07 20.880
Variety  2    327.60 373.67 92.235 106.659 2.313e-14 ***
Density  3     86.69 132.76 52.980  18.816 4.690e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

m <- lm(Yield ~ Variety * Density, tomato)
drop1(m, scope = ~ Variety + Density + Variety:Density, test = "F")

Single term deletions

Model:
Yield ~ Variety * Density
                Df Sum of Sq     RSS    AIC F value    Pr(>F)
<none>                        38.040 25.984
Variety          2   104.749 142.789 69.603 33.0438 1.278e-07 ***
Density          3    19.809  57.849 35.076  4.1660   0.01648 *
Variety:Density  6     8.032  46.072 20.880  0.8445   0.54836
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Additive vs cell-means

Opinions differ on whether to use an additive vs a cell-means model when the interaction is not significant. Remember that an insignificant test does not prove that there is no interaction.

	Additive	Cell-means
Interpretation	Direct	More complicated
Estimate of σ^2	Biased	Unbiased

We will continue using the cell-means model to answer the scientific questions of interest.


Mean Yield
18
15
12
9
10
20
30
40
Density
Variety
C
A
B

Two-way ANOVA in R

```
tomato$Density <- factor(tomato$Density)
m <- lm(Yield ~ Variety * Density, tomato)
anova(m)


Analysis of Variance Table

Response: Yield
                Df Sum Sq Mean Sq  F value    Pr(>F)
Variety          2 327.60 163.799 103.3430 1.608e-12 ***
Density          3  86.69  28.896  18.2306 2.212e-06 ***
Variety:Density  6   8.03   1.339   0.8445    0.5484
Residuals       24  38.04   1.585
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Variety comparison

```
library(emmeans)
em <- emmeans(m, pairwise ~ Variety)
confint(em)
```

```
$emmeans
 Variety emmean    SE df lower.CL upper.CL
 C         18.1 0.363 24     17.4     18.9
 A         11.3 0.363 24     10.6     12.1
 B         12.2 0.363 24     11.5     13.0

Results are averaged over the levels of: Density
Confidence level used: 0.95

$contrasts
 contrast estimate    SE df lower.CL upper.CL
 C - A       6.792 0.514 24     5.51    8.075
 C - B       5.917 0.514 24     4.63    7.200
 A - B      -0.875 0.514 24    -2.16    0.409

Results are averaged over the levels of: Density
Confidence level used: 0.95
Conf-level adjustment: tukey method for comparing a family of 3 estimates
```

Density comparison

```
em <- emmeans(m, pairwise ~ Density)
confint(em)


$emmeans
 Density emmean   SE df lower.CL upper.CL
 10        11.5 0.42 24     10.6     12.3
 20        14.4 0.42 24     13.5     15.3
 30        15.8 0.42 24     14.9     16.6
 40        13.9 0.42 24     13.0     14.8

Results are averaged over the levels of: Variety
Confidence level used: 0.95

$contrasts
 contrast              estimate    SE df lower.CL upper.CL
 Density10 - Density20   -2.911 0.593 24   -4.548   -1.274
 Density10 - Density30   -4.300 0.593 24   -5.937   -2.663
 Density10 - Density40   -2.433 0.593 24   -4.071   -0.796
 Density20 - Density30   -1.389 0.593 24   -3.026    0.248
 Density20 - Density40    0.478 0.593 24   -1.159    2.115
 Density30 - Density40    1.867 0.593 24    0.229    3.504

Results are averaged over the levels of: Variety
Confidence level used: 0.95
Conf-level adjustment: tukey method for comparing a family of 4 estimates
```

```
em <- emmeans(m, pairwise ~ Variety * Density)
confint(em)
```

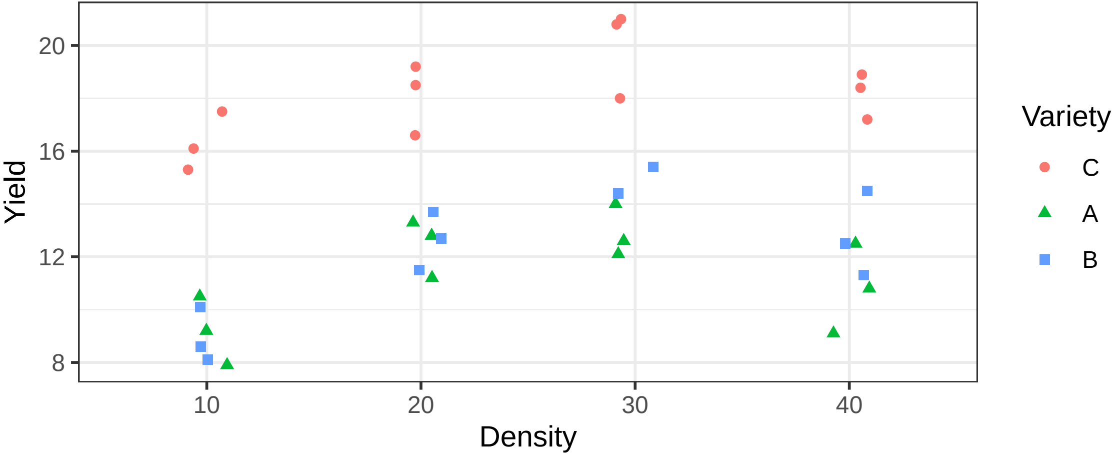
```
$emmeans
 Variety Density emmean    SE df lower.CL upper.CL
 C       10       16.30 0.727 24    14.80     17.8
 A       10        9.20 0.727 24     7.70     10.7
 B       10        8.93 0.727 24     7.43     10.4
 C       20       18.10 0.727 24    16.60     19.6
 A       20       12.43 0.727 24    10.93     13.9
 B       20       12.63 0.727 24    11.13     14.1
 C       30       19.93 0.727 24    18.43     21.4
 A       30       12.90 0.727 24    11.40     14.4
 B       30       14.50 0.727 24    13.00     16.0
 C       40       18.17 0.727 24    16.67     19.7
 A       40       10.80 0.727 24     9.30     12.3
 B       40       12.77 0.727 24    11.27     14.3

Confidence level used: 0.95

$contrasts
 contrast                  estimate   SE df  lower.CL upper.CL
 C Density10 - A Density10   7.1000 1.03 24   3.39362 10.80638
 C Density10 - B Density10   7.3667 1.03 24   3.66029 11.07305
 C Density10 - C Density20  -1.8000 1.03 24  -5.50638  1.90638
 C Density10 - A Density20   3.8667 1.03 24   0.16029  7.57305
 C Density10 - B Density20   3.6667 1.03 24  -0.03971  7.37305
 C Density10 - C Density30  -3.6333 1.03 24  -7.33971  0.07305
 C Density10 - A Density30   3.4000 1.03 24  -0.30638  7.10638
 C Density10 - B Density30   1.8000 1.03 24  -1.90638  5.50638
 C Density10 - C Density40  -1.8667 1.03 24  -5.57305  1.83971
 C Density10 - A Density40   5.5000 1.03 24   1.79362  9.20638
```

Summary

- Use `emmeans` to answer questions of scientific interest.
- Check model assumptions
- Consider alternative models, e.g. treating density as continuous

Unbalanced design

Suppose for some reason that a variety B, density 30 sample was contaminated. Although you started with a balanced design, the data is now unbalanced. Fortunately, we can still use the tools we have used previously.


Yield
20
16
12
8
10
20
30
40
Density
Variety
C
A
B

Summary statistics

```
# A tibble: 12 x 5
# Groups:   Variety [3]
   Variety Density     n  mean    sd
   <fct>   <fct>   <int> <dbl> <dbl>
 1 C       10          3 16.3  1.11 
 2 C       20          3 18.1  1.35 
 3 C       30          3 19.9  1.68 
 4 C       40          3 18.2  0.874
 5 A       10          3  9.2  1.3  
 6 A       20          3 12.4  1.10 
 7 A       30          3 12.9  0.985
 8 A       40          3 10.8  1.7  
 9 B       10          3  8.93 1.04 
10 B       20          3 12.6  1.10 
11 B       30          2 14.9  0.707
12 B       40          3 12.8  1.62 
```

Two-way ANOVA in R

```
m = lm(Yield ~ Variety * Density, data = tomato_unbalanced)
anova(m)

Analysis of Variance Table

Response: Yield
                Df Sum Sq Mean Sq F value    Pr(>F)    
Variety          2 329.99 164.994 102.343 3.552e-12 ***
Density          3  84.45  28.150  17.461 3.947e-06 ***
Variety:Density  6   8.80   1.467   0.910    0.5052    
Residuals       23  37.08   1.612                      
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Variety comparison

```
em <- emmeans(m, pairwise ~ Variety)
confint(em)

$emmeans
 Variety emmean    SE df lower.CL upper.CL
 C         18.1 0.367 23     17.4     18.9
 A         11.3 0.367 23     10.6     12.1
 B         12.3 0.389 23     11.5     13.1

Results are averaged over the levels of: Density
Confidence level used: 0.95

$contrasts
 contrast estimate    SE df lower.CL upper.CL
 C - A       6.792 0.518 23     5.49    8.090
 C - B       5.817 0.534 23     4.48    7.155
 A - B      -0.975 0.534 23    -2.31    0.363

Results are averaged over the levels of: Density
Confidence level used: 0.95
Conf-level adjustment: tukey method for comparing a family of 3 estimates
```

Density comparison

```
em <- emmeans(m, pairwise ~ Density)
confint(em)


$emmeans
 Density emmean    SE df lower.CL upper.CL
 10        11.5 0.423 23     10.6     12.4
 20        14.4 0.423 23     13.5     15.3
 30        15.9 0.457 23     15.0     16.9
 40        13.9 0.423 23     13.0     14.8

Results are averaged over the levels of: Variety
Confidence level used: 0.95

$contrasts
 contrast              estimate    SE df lower.CL upper.CL
 Density10 - Density20   -2.911 0.599 23   -4.567   -1.255
 Density10 - Density30   -4.433 0.623 23   -6.157   -2.709
 Density10 - Density40   -2.433 0.599 23   -4.090   -0.777
 Density20 - Density30   -1.522 0.623 23   -3.246    0.202
 Density20 - Density40    0.478 0.599 23   -1.179    2.134
 Density30 - Density40    2.000 0.623 23    0.276    3.724

Results are averaged over the levels of: Variety
Confidence level used: 0.95
Conf-level adjustment: tukey method for comparing a family of 4 estimates
```

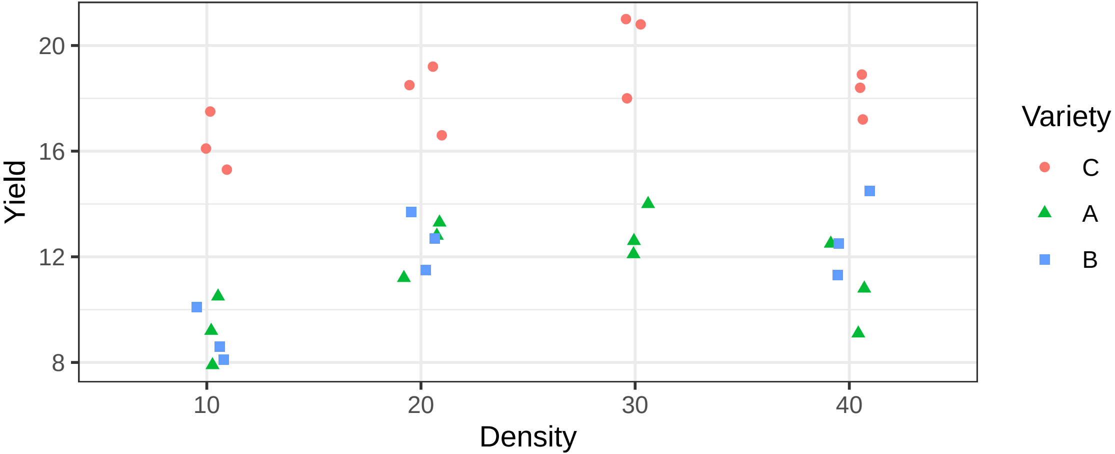
```
em <- emmeans(m, pairwise ~ Variety * Density)
confint(em)

$emmeans
 Variety Density emmean    SE df lower.CL upper.CL
 C       10       16.30 0.733 23    14.78     17.8
 A       10        9.20 0.733 23     7.68     10.7
 B       10        8.93 0.733 23     7.42     10.4
 C       20       18.10 0.733 23    16.58     19.6
 A       20       12.43 0.733 23    10.92     13.9
 B       20       12.63 0.733 23    11.12     14.1
 C       30       19.93 0.733 23    18.42     21.4
 A       30       12.90 0.733 23    11.38     14.4
 B       30       14.90 0.898 23    13.04     16.8
 C       40       18.17 0.733 23    16.65     19.7
 A       40       10.80 0.733 23     9.28     12.3
 B       40       12.77 0.733 23    11.25     14.3

Confidence level used: 0.95

$contrasts
 contrast                  estimate   SE df lower.CL upper.CL
 C Density10 - A Density10   7.1000 1.04 23   3.3462  10.8538
 C Density10 - B Density10   7.3667 1.04 23   3.6128  11.1205
 C Density10 - C Density20  -1.8000 1.04 23  -5.5538   1.9538
 C Density10 - A Density20   3.8667 1.04 23   0.1128   7.6205
 C Density10 - B Density20   3.6667 1.04 23  -0.0872   7.4205
 C Density10 - C Density30  -3.6333 1.04 23  -7.3872   0.1205
 C Density10 - A Density30   3.4000 1.04 23  -0.3538   7.1538
 C Density10 - B Density30   1.4000 1.16 23  -2.7969   5.5969
 C Density10 - C Density40  -1.8667 1.04 23  -5.6205   1.8872
 C Density10 - A Density40   5.5000 1.04 23   1.7462   9.2538
```

Unbalanced Summary

The analysis can be completed just like the balanced design using `emmeans` to answer scientific questions of interest.

Incomplete design

Suppose none of the samples from variety B, density 30 were obtained. Now the analysis becomes more complicated.


Yield
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16
12
8
10
20
30
40
Density
Variety
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Summary statistics

```
# A tibble: 11 x 5
# Groups:   Variety [3]
   Variety Density     n  mean    sd
   <fct>   <fct>   <int> <dbl> <dbl>
 1 C       10          3 16.3  1.11
 2 C       20          3 18.1  1.35
 3 C       30          3 19.9  1.68
 4 C       40          3 18.2  0.874
 5 A       10          3  9.2  1.3
 6 A       20          3 12.4  1.10
 7 A       30          3 12.9  0.985
 8 A       40          3 10.8  1.7
 9 B       10          3  8.93 1.04
10 B       20          3 12.6  1.10
11 B       40          3 12.8  1.62
```

Treat as a One-way ANOVA

When the design is incomplete, use a one-way ANOVA combined with contrasts to answer questions of interest. For example, to compare the average difference between B and C, we want to only compare at densities 10, 20, and 40.

	10	20	30	40
A	$\mu_{A,10}$	$\mu_{A,20}$	$\mu_{A,30}$	$\mu_{A,40}$
B	$\mu_{B,10}$	$\mu_{B,20}$		$\mu_{B,40}$
C	$\mu_{B,10}$	$\mu_{C,20}$	$\mu_{C,30}$	$\mu_{C,40}$

Thus, the contrast is

$$\begin{aligned}\gamma &= \tfrac{1}{3}(\mu_{C,10} + \mu_{C,20} + \mu_{C,40}) - \tfrac{1}{3}(\mu_{B,10} + \mu_{B,20} + \mu_{B,40}) \\ &= \left[(\mu_{C,10} - \mu_{B,10}) + (\mu_{C,20} - \mu_{B,20}) + (\mu_{C,40} - \mu_{B,40})\right]/3 \\ &= (\mu_{C,10} + \mu_{C,20} + \mu_{C,40} - \mu_{B,10} - \mu_{B,20} - \mu_{B,40})/3\end{aligned}$$

The Regression model

The regression model here considers variety-density combination as a single explanatory variable with 11 levels: A10, A20, A30, A40, B10, B20, B40, C10, C20, C30, and C40. Let C40 be the reference level. For observation i, let

- Y_i be the yield
- V_i be the variety
- D_i be the density

The model is then $Y_i \overset{ind}{\sim} N(\mu_i, \sigma^2)$ and

$$\begin{aligned}\mu_i = \beta_0 & \\ &+\beta_1 \mathrm{I}(V_i = A, D_i = 10) + \beta_2 \mathrm{I}(V_i = A, D_i = 20) + \beta_3 \mathrm{I}(V_i = A, D_i = 30) + \beta_4 \mathrm{I}(V_i = A, D_i = 40) \\ &+\beta_5 \mathrm{I}(V_i = B, D_i = 10) + \beta_6 \mathrm{I}(V_i = B, D_i = 20) + \beta_7 \mathrm{I}(V_i = B, D_i = 40) \\ &+\beta_8 \mathrm{I}(V_i = C, D_i = 10) + \beta_9 \mathrm{I}(V_i = C, D_i = 20) + \beta_{10} \mathrm{I}(V_i = C, D_i = 30)\end{aligned}$$

Two-way ANOVA in R

```
m <- lm(Yield ~ Variety * Density, data = tomato_incomplete)
anova(m)

Analysis of Variance Table

Response: Yield
                Df Sum Sq Mean Sq F value    Pr(>F)    
Variety          2 347.38 173.691 104.462 5.868e-12 ***
Density          3  66.65  22.218  13.362 3.514e-05 ***
Variety:Density  5   7.06   1.412   0.849      0.53    
Residuals       22  36.58   1.663                      
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How can you tell the design is not complete?

One-way ANOVA in R

```
m <- lm(Yield ~ Variety:Density, data = tomato_incomplete)
anova(m)

Analysis of Variance Table

Response: Yield
                Df Sum Sq Mean Sq F value    Pr(>F)
Variety:Density 10 421.09  42.109  25.326 8.563e-10 ***
Residuals       22  36.58   1.663
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Contrasts

```
m <- lm(Yield ~ VarietyDensity, tomato_incomplete)
em <- emmeans(m, ~ VarietyDensity)
contrast(em, method = list(
#         A10 A20 A30 A40 B10 B20     B40 C10 C20 C30 C40
"C-B" = c(  0,  0,  0,  0, -1, -1,     -1,  1,  1,  0,  1)/3,
"C-A" = c( -1, -1, -1, -1,  0,  0,      0,  1,  1,  1,  1)/4,
"B-A" = c( -1, -1,  0, -1,  1,  1,      1,  0,  0,  0,  0)/3)) |>
  confint()

 contrast estimate    SE df lower.CL upper.CL
 C-B         6.078 0.608 22    4.817     7.34
 C-A         6.792 0.526 22    5.700     7.88
 B-A         0.633 0.608 22   -0.627     1.89

Confidence level used: 0.95
```

```
m <- lm(Yield ~ VarietyDensity, data = tomato_incomplete)
em <- emmeans(m, pairwise ~ VarietyDensity) # Variety:Density produces nonEst
confint(em)
```

```
$emmeans
 VarietyDensity emmean    SE df lower.CL upper.CL
 A10              9.20 0.744 22     7.66     10.7
 A20             12.43 0.744 22    10.89     14.0
 A30             12.90 0.744 22    11.36     14.4
 A40             10.80 0.744 22     9.26     12.3
 B10              8.93 0.744 22     7.39     10.5
 B20             12.63 0.744 22    11.09     14.2
 B40             12.77 0.744 22    11.22     14.3
 C10             16.30 0.744 22    14.76     17.8
 C20             18.10 0.744 22    16.56     19.6
 C30             19.93 0.744 22    18.39     21.5
 C40             18.17 0.744 22    16.62     19.7

Confidence level used: 0.95

$contrasts
 contrast  estimate   SE df lower.CL upper.CL
 A10 - A20  -3.2333 1.05 22   -6.997   0.5304
 A10 - A30  -3.7000 1.05 22   -7.464   0.0637
 A10 - A40  -1.6000 1.05 22   -5.364   2.1637
 A10 - B10   0.2667 1.05 22   -3.497   4.0304
 A10 - B20  -3.4333 1.05 22   -7.197   0.3304
 A10 - B40  -3.5667 1.05 22   -7.330   0.1971
 A10 - C10  -7.1000 1.05 22  -10.864  -3.3363
 A10 - C20  -8.9000 1.05 22  -12.664  -5.1363
 A10 - C30 -10.7333 1.05 22  -14.497  -6.9696
 A10 - C40  -8.9667 1.05 22  -12.730  -5.2029
```

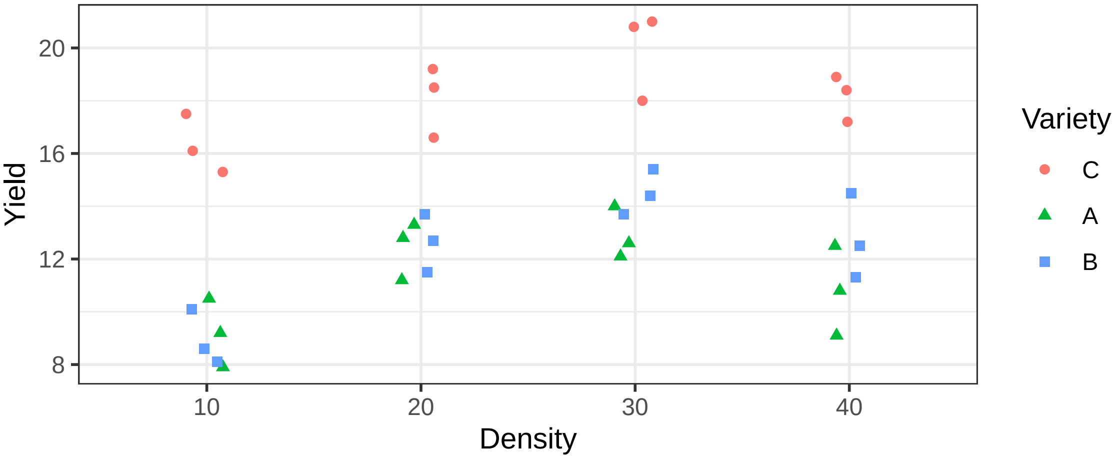
Summary

When dealing with an incomplete design, it is often easier to treat the analysis as a one-way ANOVA and use contrasts to answer scientific questions of interest.

Optimal yield

Now suppose you have the same data set, but your scientific question is different. Specifically, you are interested in choosing a variety-density combination that provides the optimal yield.

You can use the ANOVA analysis to choose from amongst the 3 varieties and one of the 4 densities, but there is no reason to believe that the optimal density will be one of those 4.


Yield
20
16
12
8
10
20
30
40
Density
Variety
C
A
B

Modeling

Considering a single variety, if we assume a linear relationship between Yield (Y_i) and Density (D_i) then the maximum Yield will occur at either $-\infty$ or $+\infty$ which is unreasonable. The easiest way to have a maximum (or minimum) is to assume a quadratic relationship, e.g.

$$E[Y_i] = \mu_i = \beta_0 + \beta_1 D_i + \beta_2 D_i^2$$

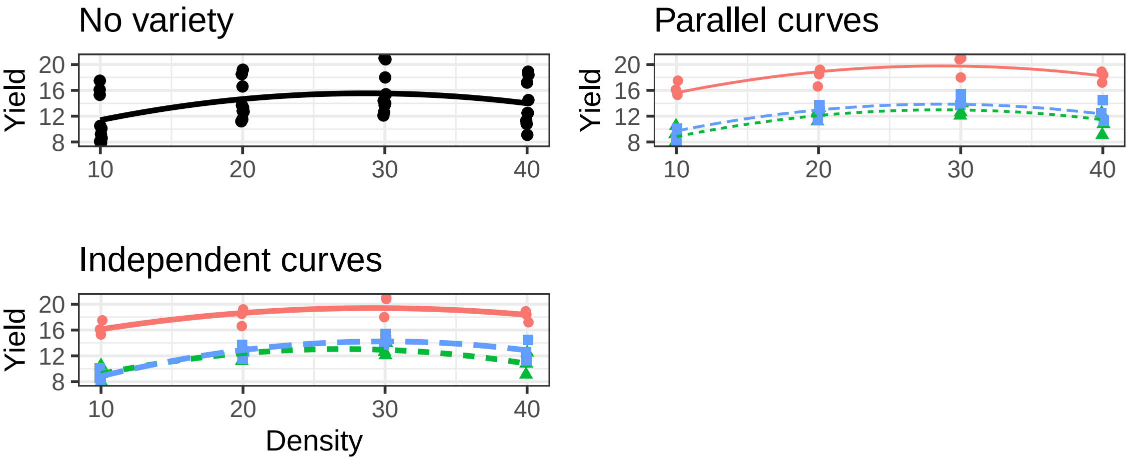
Now we can incorporate Variety (V_i) in many ways. Two options are parallel curves or completely independent curves.

Parallel curves:

$$\begin{aligned} \mu_i = \quad & \beta_0 + \beta_1 D_i + \beta_2 D_i^2 \\ & + \beta_3 \mathrm{I}(V_i = A) + \beta_4 \mathrm{I}(V_i = B) \end{aligned}$$

Independent curves:

$$\begin{aligned} \mu_i = \quad & \beta_0 + \beta_1 D_i + \beta_2 D_i^2 \\ & + \beta_3 \mathrm{I}(V_i = A) + \beta_4 \mathrm{I}(V_i = B) \\ & + \beta_5 \mathrm{I}(V_i = A) D_i + \beta_6 \mathrm{I}(V_i = B) D_i \\ & + \beta_7 \mathrm{I}(V_i = A) D_i^2 + \beta_8 \mathrm{I}(V_i = B) D_i^2 \end{aligned}$$


No variety
Parallel curves
Independent curves
Yield
20
16
12
8
10
20
30
40
Density

Finding the maximum

For a particular variety, there will be an equation like

$$E[Y_i] = \mu_i = \beta_0 + \beta_1 D_i + \beta_2 D_i^2$$

where these β_1 and β_2 need not correspond to any particular β_1 and β_2 we have discussed thus far.

If $\beta_2 < 0$, then the quadratic curve has a maximum and it occurs at $-\beta_1/2\beta_2$.

No variety

```
summary(m_noV <- lm(Yield ~ Density + I(Density^2), data = tomato))

Call:
lm(formula = Yield ~ Density + I(Density^2), data = tomato)

Residuals:
   Min     1Q Median     3Q    Max 
-4.898 -2.721 -1.320  3.364  6.109 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)  
(Intercept)   5.744444   3.128242   1.836   0.0753 .
Density       0.684111   0.285384   2.397   0.0223 *
I(Density^2) -0.011944   0.005618  -2.126   0.0411 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.371 on 33 degrees of freedom
Multiple R-squared:  0.1854,Adjusted R-squared:  0.136 
F-statistic: 3.755 on 2 and 33 DF,  p-value: 0.03395
```

Parallel curves

```
summary(m_V <- lm(Yield ~ Density + I(Density^2) + Variety, data = tomato))

Call:
lm(formula = Yield ~ Density + I(Density^2) + Variety, data = tomato)

Residuals:
    Min      1Q  Median      3Q     Max 
-2.3422 -0.9039  0.1744  0.8082  2.1828 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)   9.980556   1.184193   8.428 1.61e-09 ***
Density       0.684111   0.104707   6.534 2.71e-07 ***
I(Density^2) -0.011944   0.002061  -5.794 2.21e-06 ***
VarietyA     -6.791667   0.504942 -13.450 1.76e-14 ***
VarietyB     -5.916667   0.504942 -11.718 6.39e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.237 on 31 degrees of freedom
Multiple R-squared:  0.897,Adjusted R-squared:  0.8837 
F-statistic: 67.48 on 4 and 31 DF,  p-value: 7.469e-15
```

Independent curves

```
summary(m_DV <- lm(Yield ~ Density * Variety + I(Density^2) * Variety, data = tomato))


Call:
lm(formula = Yield ~ Density * Variety + I(Density^2) * Variety,
    data = tomato)

Residuals:
     Min       1Q   Median       3Q      Max 
-2.04500 -0.82125 -0.01417  0.94000  1.71000 

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)    
(Intercept)           11.808333   1.968364   5.999 2.12e-06 ***
Density                0.520167   0.179570   2.897  0.00739 ** 
VarietyA              -8.458333   2.783687  -3.039  0.00523 ** 
VarietyB              -9.733333   2.783687  -3.497  0.00165 ** 
I(Density^2)          -0.008917   0.003535  -2.522  0.01787 *  
Density:VarietyA       0.199167   0.253951   0.784  0.43971    
Density:VarietyB       0.292667   0.253951   1.152  0.25924    
VarietyA:I(Density^2) -0.004417   0.005000  -0.883  0.38482    
VarietyB:I(Density^2) -0.004667   0.005000  -0.933  0.35889    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.225 on 27 degrees of freedom
Multiple R-squared:  0.912,Adjusted R-squared:  0.886 
F-statistic: 34.99 on 8 and 27 DF,  p-value: 2.678e-12
```

F-test comparisons

```
anova(m_noV, m_V, m_DV)


Analysis of Variance Table

Model 1: Yield ~ Density + I(Density^2)
Model 2: Yield ~ Density + I(Density^2) + Variety
Model 3: Yield ~ Density * Variety + I(Density^2) * Variety
  Res.Df    RSS Df Sum of Sq        F    Pr(>F)
1     33 375.02
2     31  47.42  2    327.60 109.2144 1.147e-13 ***
3     27  40.49  4      6.93   1.1551    0.3524
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Completely randomized design (CRD)

This semester, we have assumed a completely randomized design. As an example, consider 36 plots and we are randomly assigning our variety-density combinations to the plots such that we have 3 reps of each combination. The result may look something like this

A20	A10	A20	B10	B10	A30
C10	C30	C30	C10	C20	A10
B30	B10	B20	B30	B40	B40
C40	B20	A10	C20	B30	A40
C30	B40	A30	C40	B20	C40
C10	C20	A40	A30	A20	A40

Complete randomized block design (RBD)

A randomized block design is appropriate when there is a nuisance factor that you want to control for. In our example, imagine you had 12 plots at 3 different locations and you expect these locations would have impact on yield. A randomized block design might look like this.

B10	B40
C30	A30
C40	C10
A20	B20
B30	A40
A10	C20

Block 1

C20	B40
C30	A30
C10	B10
A10	A20
B20	C40
B30	A40

Block 2

A20	B30
C10	A30
A10	C30
B20	C40
B40	A40
C20	B10

Block 3

RBD Analysis

Generally, you will want to model a randomized block design using an additive model for the treatment and blocking factor. If you have the replication, you should test for an interaction. Let's compute the degrees of freedom for the ANOVA tables for this current design considering the variety-density combination as the treatment.

V+D+B		T+B		Cell-means	
Factor	df	Factor	df	Factor	df
Variety	2				
Density	3	Treatment	11	Treatment	11
Block	2	Block	2	Block	2
				Treatment x Block	22
Error	28	Error	22	Error	0
Total	35	Total	35	Total	35

The cell-means model does not have enough degrees of freedom to estimate the interaction because there is no replication of the treatment within a block.

Why block?

Consider a simple experiment with 2 blocks each with 3 experimental units and 3 treatments (A, B, C).

Blocked

Block 1	Block 2
A	C
B	B
A	C

Unblocked

Block 1	Block 2
A	C
B	B
C	A

Let's consider 3 possible analyses:

- Blocked experiment using an additive model for treatment and block (RBD)
- Unblocked experiment using only treatment (CRD)

Why block?

Now suppose, the true model is

$$\mu_{ij} = \mu + T_i + B_j$$

where $T_1 = T_2 = T_3$ and $B_1 = 0$ and $B_2 = \delta$.

In the Blocked experiment using an additive model for treatment and block, the expected treatment differences to all be zero.

In the Unblocked design using only treatment, the expected difference between treatments is

$$\mu_C - \mu_B = \delta \qquad \text{and} \qquad \mu_C - \mu_A = \delta/2.$$

In the Unblocked design using an additive model for treatment and block, we would have an unbalanced design and it would be impossible to compare B and C.

Summary

Block what you can control; randomize what you cannot.