# R09 - Two-way ANOVA

STAT 401 (Engineering) - Iowa State University

April 19, 2018

# Two factors

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

- Balanced, complete design
- Unbalanced, complete
- Incomplete
- Optimization

# 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.

There is an expectation that planting density will have a different effect depending on the variety. Therefore a balanced, complete, randomized design was used.

- complete: each treatment (variety $\times$ density) is represented in the experiment
- balanced: each treatment in the experiment has the same number of replications
- randomized: treatment was randomly assigned to the plot

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

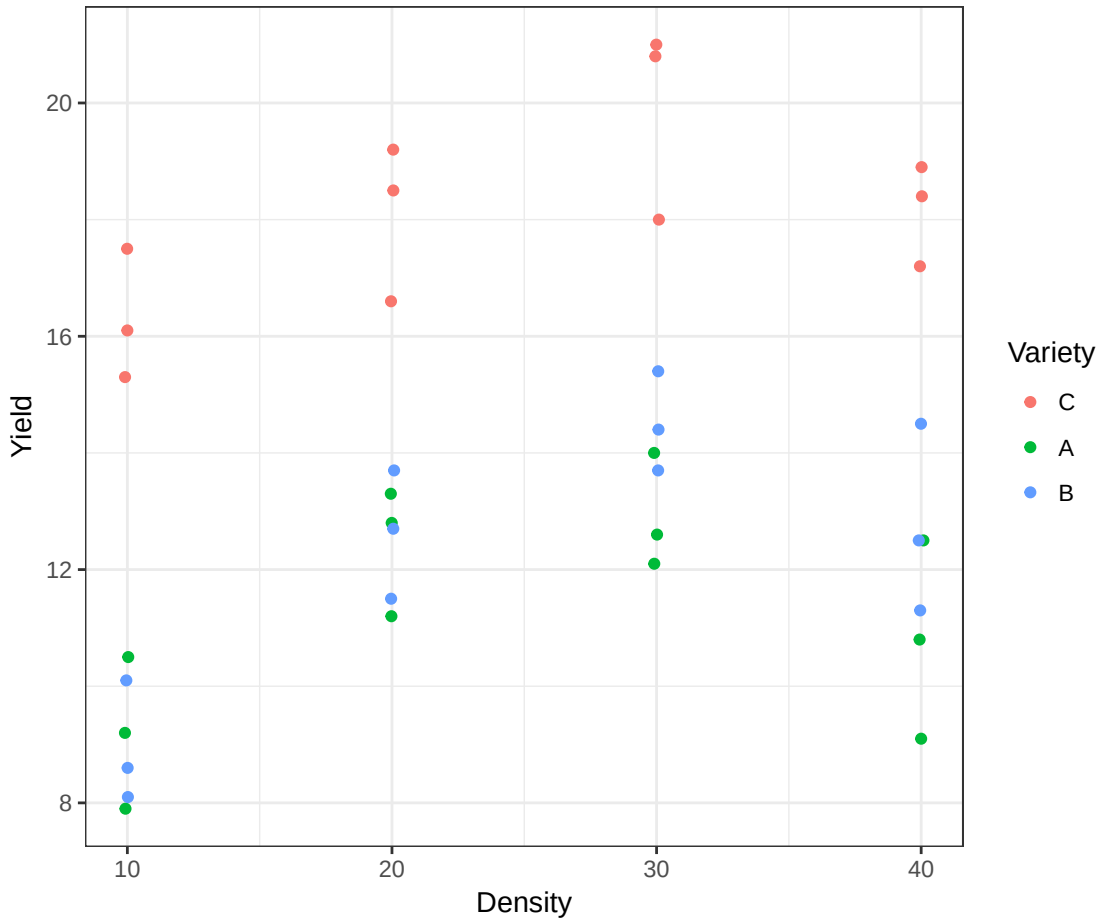
# Hypotheses

- 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 nature 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

```
sm = tomato %>%
  group_by(Variety, Density) %>%
  summarize(n    = n(),
            mean = mean(Yield),
            sd   = sd(Yield))
sm
```

```
# A tibble: 12 x 5
# Groups:   Variety [?]
   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  9.20 1.30
 6 A            20     3 12.4  1.10
 7 A            30     3 12.9  0.985
 8 A            40     3 10.8  1.70
 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
- Model:

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

where $Y_{ijk}$ is the

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

Consider the models:

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

| | 10 | 20 | 30 | 40 |
|---|---|---|---|---|
| A | $\mu_{11}$ | $\mu_{12}$ | $\mu_{13}$ | $\mu_{14}$ |
| B | $\mu_{21}$ | $\mu_{22}$ | $\mu_{23}$ | $\mu_{24}$ |
| C | $\mu_{31}$ | $\mu_{32}$ | $\mu_{33}$ | $\mu_{34}$ |

# 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 model:

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

   $\beta_1$ is the expected difference in yield between varieties A and C at any fixed density

5. The cell-means model:

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

   $\beta_1$ is the expected difference in yield between varieties A and C at a density of 40

# ANOVA Table

## ANOVA Table - Additive 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 | |
|---|---|---|---|---|
| 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 | | |

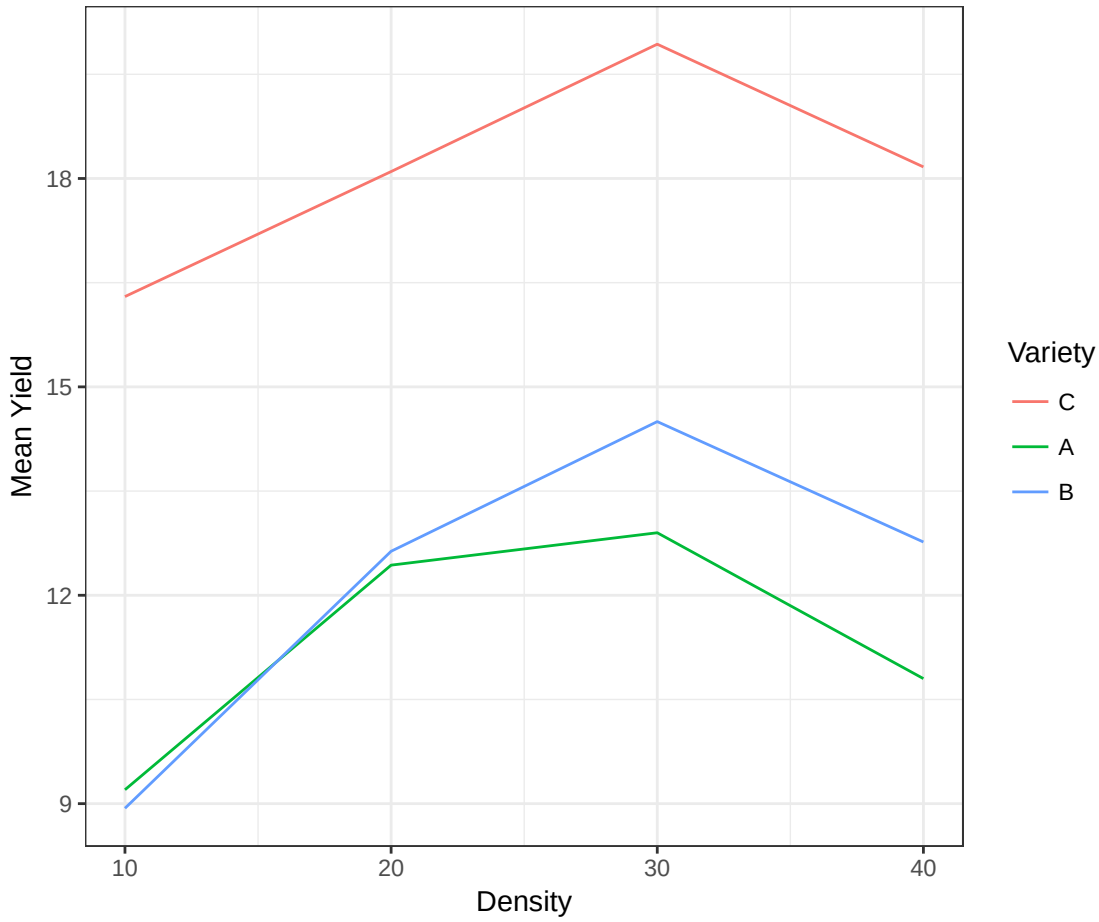
# Additive vs cell-means

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 | Complicated |
| Estimate of $\sigma^2$ | Biased | Unbiased |

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

```
ggplot(sm, aes(x=Density, y=mean, col=Variety)) + geom_line() + labs(y="Mean Yield") + theme_bw()
```



# 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)

Warning:  package 'emmeans' was built under R version 3.4.4

emmeans(m, pairwise~Variety)

$emmeans
 Variety   emmean        SE df lower.CL upper.CL
 C       18.12500 0.3634327 24 17.37491 18.87509
 A       11.33333 0.3634327 24 10.58325 12.08342
 B       12.20833 0.3634327 24 11.45825 12.95842

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

$contrasts
 contrast  estimate        SE df t.ratio p.value
 C - A     6.791667 0.5139715 24  13.214  <.0001
 C - B     5.916667 0.5139715 24  11.512  <.0001
 A - B    -0.875000 0.5139715 24  -1.702  0.2249

Results are averaged over the levels of: Density
P value adjustment: tukey method for comparing a family of 3 estimates
```

# Density comparison

```
emmeans(m, pairwise~Density)


$emmeans
 Density   emmean        SE df lower.CL upper.CL
 10      11.47778 0.4196559 24 10.61165 12.34391
 20      14.38889 0.4196559 24 13.52276 15.25502
 30      15.77778 0.4196559 24 14.91165 16.64391
 40      13.91111 0.4196559 24 13.04498 14.77724

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

$contrasts
 contrast   estimate        SE df t.ratio p.value
 10 - 20  -2.9111111 0.5934831 24  -4.905  0.0003
 10 - 30  -4.3000000 0.5934831 24  -7.245  <.0001
 10 - 40  -2.4333333 0.5934831 24  -4.100  0.0022
 20 - 30  -1.3888889 0.5934831 24  -2.340  0.1169
 20 - 40   0.4777778 0.5934831 24   0.805  0.8514
 30 - 40   1.8666667 0.5934831 24   3.145  0.0213

Results are averaged over the levels of: Variety
P value adjustment: tukey method for comparing a family of 4 estimates
```

```
emmeans(m, pairwise~Variety*Density)


$emmeans
 Variety Density    emmean        SE df  lower.CL upper.CL
 C       10      16.300000 0.7268654 24 14.799824 17.80018
 A       10       9.200000 0.7268654 24  7.699824 10.70018
 B       10       8.933333 0.7268654 24  7.433157 10.43351
 C       20      18.100000 0.7268654 24 16.599824 19.60018
 A       20      12.433333 0.7268654 24 10.933157 13.93351
 B       20      12.633333 0.7268654 24 11.133157 14.13351
 C       30      19.933333 0.7268654 24 18.433157 21.43351
 A       30      12.900000 0.7268654 24 11.399824 14.40018
 B       30      14.500000 0.7268654 24 12.999824 16.00018
 C       40      18.166667 0.7268654 24 16.666490 19.66684
 A       40      10.800000 0.7268654 24  9.299824 12.30018
 B       40      12.766667 0.7268654 24 11.266490 14.26684

Confidence level used: 0.95

$contrasts
 contrast        estimate       SE df t.ratio p.value
 C,10 - A,10   7.10000000 1.027943 24   6.907  <.0001
 C,10 - B,10   7.36666667 1.027943 24   7.166  <.0001
 C,10 - C,20  -1.80000000 1.027943 24  -1.751  0.8276
 C,10 - A,20   3.86666667 1.027943 24   3.762  0.0356
 C,10 - B,20   3.66666667 1.027943 24   3.567  0.0543
 C,10 - C,30  -3.63333333 1.027943 24  -3.535  0.0582
 C,10 - A,30   3.40000000 1.027943 24   3.308  0.0932
 C,10 - B,30   1.80000000 1.027943 24   1.751  0.8276
 C,10 - C,40  -1.86666667 1.027943 24  -1.816  0.7947
 C,10 - A,40   5.50000000 1.027943 24   5.350  0.0008
 C,10 - B,40   3.53333333 1.027943 24   3.437  0.0714
 A,10 - B,10   0.26666667 1.027943 24   0.259  1.0000
 A,10 - C,20  -8.90000000 1.027943 24  -8.658  <.0001
 A,10 - A,20  -3.23333333 1.027943 24  -3.145  0.1284
```

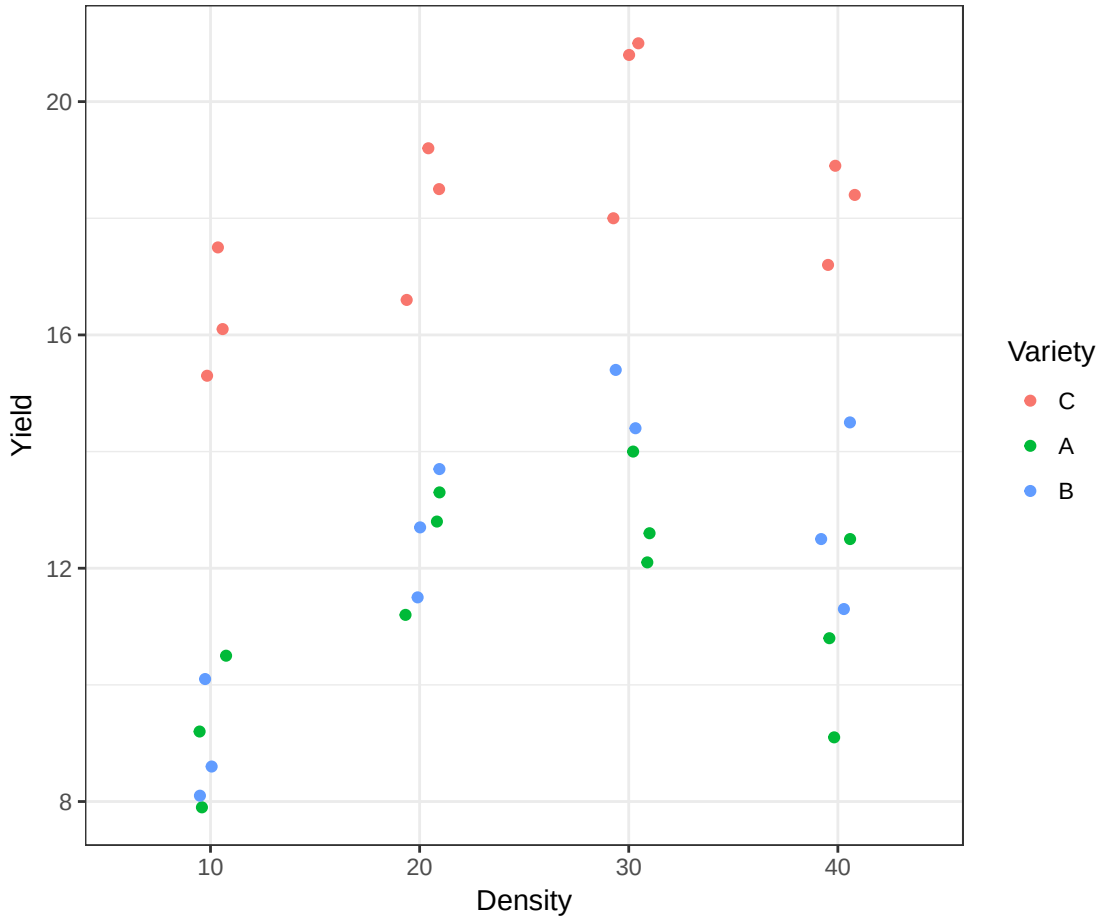
# Summary

- 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.

```
tomato_unbalanced = tomato[-19,]
ggplot(tomato_unbalanced, aes(x=Density, y=Yield, color=Variety)) +  geom_jitter(height=0, width=0.1) + theme_b
```



# Summary statistics

```
sm_unbalanced = tomato_unbalanced %>%
  group_by(Variety, Density) %>%
  summarize(n    = n(),
            mean = mean(Yield),
            sd   = sd(Yield))
sm_unbalanced
```

```
# A tibble: 12 x 5
# Groups:   Variety [?]
   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  9.20 1.30
 6 A       20          3 12.4  1.10
 7 A       30          3 12.9  0.985
 8 A       40          3 10.8  1.70
 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, 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

```
emmeans(m, pairwise~Variety)


$emmeans
 Variety   emmean        SE df lower.CL upper.CL
 C       18.12500 0.3665349 23 17.36676 18.88324
 A       11.33333 0.3665349 23 10.57510 12.09157
 B       12.30833 0.3887690 23 11.50410 13.11256

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

$contrasts
 contrast  estimate        SE df t.ratio p.value
 C - A     6.791667 0.5183586 23  13.102  <.0001
 C - B     5.816667 0.5343118 23  10.886  <.0001
 A - B    -0.975000 0.5343118 23  -1.825  0.1839

Results are averaged over the levels of: Density
P value adjustment: tukey method for comparing a family of 3 estimates
```

# Density comparison

```
emmeans(m, pairwise~Density)


$emmeans
 Density   emmean        SE df lower.CL upper.CL
 10      11.47778 0.4232380 23 10.60224 12.35331
 20      14.38889 0.4232380 23 13.51335 15.26442
 30      15.91111 0.4571493 23 14.96543 16.85680
 40      13.91111 0.4232380 23 13.03558 14.78665

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

$contrasts
 contrast   estimate        SE df t.ratio p.value
 10 - 20  -2.9111111 0.5985490 23  -4.864  0.0004
 10 - 30  -4.4333333 0.6229895 23  -7.116  <.0001
 10 - 40  -2.4333333 0.5985490 23  -4.065  0.0025
 20 - 30  -1.5222222 0.6229895 23  -2.443  0.0967
 20 - 40   0.4777778 0.5985490 23   0.798  0.8545
 30 - 40   2.0000000 0.6229895 23   3.210  0.0189

Results are averaged over the levels of: Variety
P value adjustment: tukey method for comparing a family of 4 estimates
```

```
emmeans(m, pairwise~Variety*Density)


$emmeans
 Variety Density    emmean        SE df  lower.CL upper.CL
 C       10      16.300000 0.7330698 23 14.783530 17.81647
 A       10       9.200000 0.7330698 23  7.683530 10.71647
 B       10       8.933333 0.7330698 23  7.416863 10.44980
 C       20      18.100000 0.7330698 23 16.583530 19.61647
 A       20      12.433333 0.7330698 23 10.916863 13.94980
 B       20      12.633333 0.7330698 23 11.116863 14.14980
 C       30      19.933333 0.7330698 23 18.416863 21.44980
 A       30      12.900000 0.7330698 23 11.383530 14.41647
 B       30      14.900000 0.8978235 23 13.042711 16.75729
 C       40      18.166667 0.7330698 23 16.650196 19.68314
 A       40      10.800000 0.7330698 23  9.283530 12.31647
 B       40      12.766667 0.7330698 23 11.250196 14.28314

Confidence level used: 0.95

$contrasts
 contrast        estimate       SE df t.ratio p.value
 C,10 - A,10   7.10000000 1.036717 23   6.849  <.0001
 C,10 - B,10   7.36666667 1.036717 23   7.106  <.0001
 C,10 - C,20  -1.80000000 1.036717 23  -1.736  0.8341
 C,10 - A,20   3.86666667 1.036717 23   3.730  0.0396
 C,10 - B,20   3.66666667 1.036717 23   3.537  0.0597
 C,10 - C,30  -3.63333333 1.036717 23  -3.505  0.0638
 C,10 - A,30   3.40000000 1.036717 23   3.280  0.1008
 C,10 - B,30   1.40000000 1.159085 23   1.208  0.9828
 C,10 - C,40  -1.86666667 1.036717 23  -1.801  0.8022
 C,10 - A,40   5.50000000 1.036717 23   5.305  0.0011
 C,10 - B,40   3.53333333 1.036717 23   3.408  0.0778
 A,10 - B,10   0.26666667 1.036717 23   0.257  1.0000
 A,10 - C,20  -8.90000000 1.036717 23  -8.585  <.0001
 A,10 - A,20  -3.23333333 1.036717 23  -3.119  0.1375
```

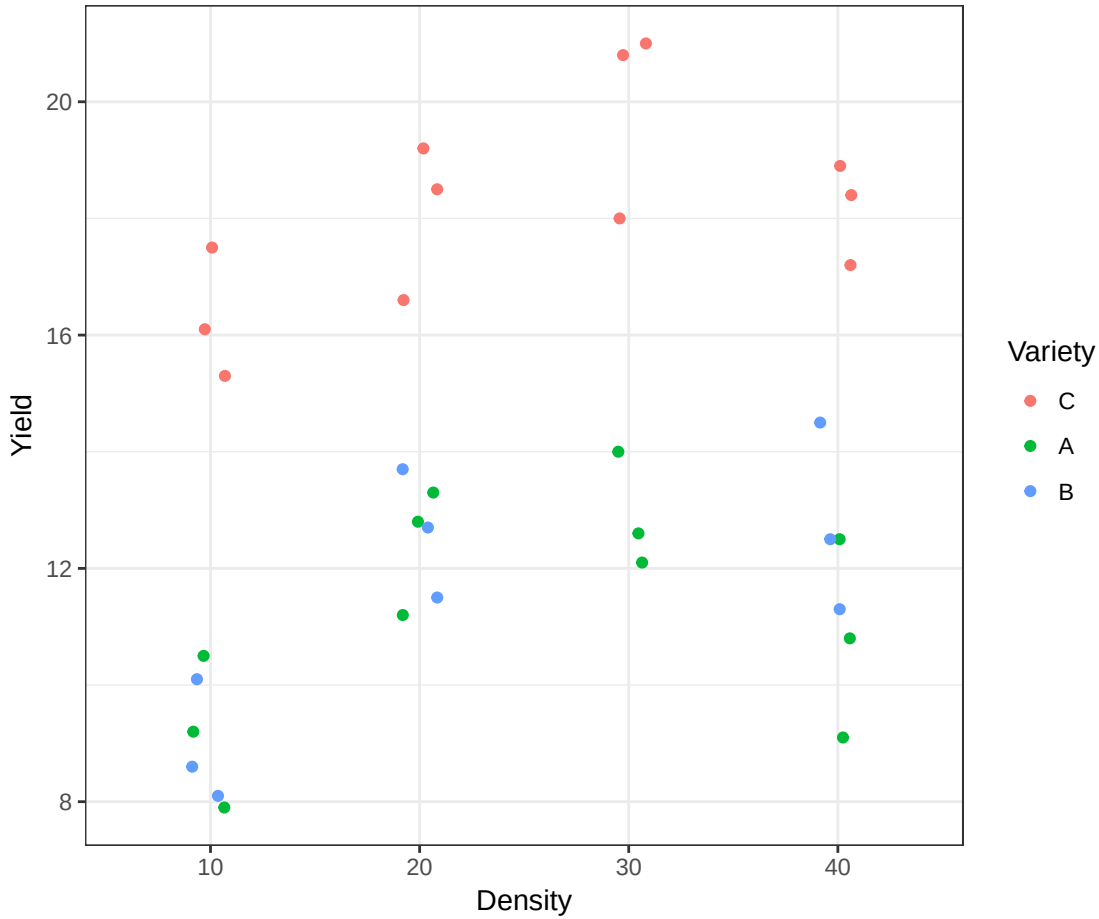
# Summary

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.

```
tomato_incomplete = tomato %>%
  filter(!(Variety == "B" & Density == 30)) %>%
  mutate(VarietyDensity = paste0(Variety,Density))
ggplot(tomato_incomplete, aes(x=Density, y=Yield, color=Variety)) + geom_jitter(height=0, width=0.1) + theme_bw
```



# Summary statistics

```
sm_incomplete = tomato_incomplete %>%
  group_by(Variety, Density) %>%
  summarize(n    = n(),
            mean = mean(Yield),
            sd   = sd(Yield))
sm_incomplete
```

```
# A tibble: 11 x 5
# Groups:   Variety [?]
   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  9.20 1.30
 6 A       20          3 12.4  1.10
 7 A       30          3 12.9  0.985
 8 A       40          3 10.8  1.70
 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 | $\mu_{11}$ | $\mu_{12}$ | $\mu_{13}$ | $\mu_{14}$ |
| B | $\mu_{21}$ | $\mu_{22}$ | $\mu_{23}$ | $\mu_{24}$ |
| C | $\mu_{31}$ | $\mu_{32}$ | $\mu_{33}$ | $\mu_{34}$ |

Thus, the contrast is

$$\begin{aligned}\gamma &= \frac{1}{3}(\mu_{31}+\mu_{32}+\mu_{34}) - \frac{1}{3}(\mu_{21}+\mu_{22}+\mu_{24}) \\ &= \frac{1}{3}(\mu_{31}+\mu_{32}+\mu_{34}-\mu_{21}-\mu_{22}-\mu_{24})\end{aligned}$$

# 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

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

# 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, 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

```
# Note the -1 in order to construct the contrast
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      6.0777778 0.607861 22  4.8171513 7.338404
 C-A      6.7916667 0.526423 22  5.6999321 7.883401
 B-A      0.6333333 0.607861 22 -0.6272931 1.893960

Confidence level used: 0.95
```

```
m = lm(Yield~Variety:Density, tomato_incomplete)
emmeans(m, pairwise~Variety:Density)
```

```
$emmeans
 Variety Density    emmean        SE df  lower.CL upper.CL
 C       10      16.300000 0.7444746 22 14.756054 17.84395
 A       10       9.200000 0.7444746 22  7.656054 10.74395
 B       10       8.933333 0.7444746 22  7.389388 10.47728
 C       20      18.100000 0.7444746 22 16.556054 19.64395
 A       20      12.433333 0.7444746 22 10.889388 13.97728
 B       20      12.633333 0.7444746 22 11.089388 14.17728
 C       30      19.933333 0.7444746 22 18.389388 21.47728
 A       30      12.900000 0.7444746 22 11.356054 14.44395
 B       30         nonEst        NA NA        NA       NA
 C       40      18.166667 0.7444746 22 16.622721 19.71061
 A       40      10.800000 0.7444746 22  9.256054 12.34395
 B       40      12.766667 0.7444746 22 11.222721 14.31061

Confidence level used: 0.95

$contrasts
 contrast        estimate       SE df t.ratio p.value
 C,10 - A,10   7.10000000 1.052846 22   6.744  <.0001
 C,10 - B,10   7.36666667 1.052846 22   6.997  <.0001
 C,10 - C,20  -1.80000000 1.052846 22  -1.710  0.8458
 C,10 - A,20   3.86666667 1.052846 22   3.673  0.0465
 C,10 - B,20   3.66666667 1.052846 22   3.483  0.0688
 C,10 - C,30  -3.63333333 1.052846 22  -3.451  0.0734
 C,10 - A,30   3.40000000 1.052846 22   3.229  0.1136
 C,10 - B,30       nonEst       NA NA      NA      NA
 C,10 - C,40  -1.86666667 1.052846 22  -1.773  0.8156
 C,10 - A,40   5.50000000 1.052846 22   5.224  0.0014
 C,10 - B,40   3.53333333 1.052846 22   3.356  0.0887
 A,10 - B,10   0.26666667 1.052846 22   0.253  1.0000
 A,10 - C,20  -8.90000000 1.052846 22  -8.453  <.0001
```

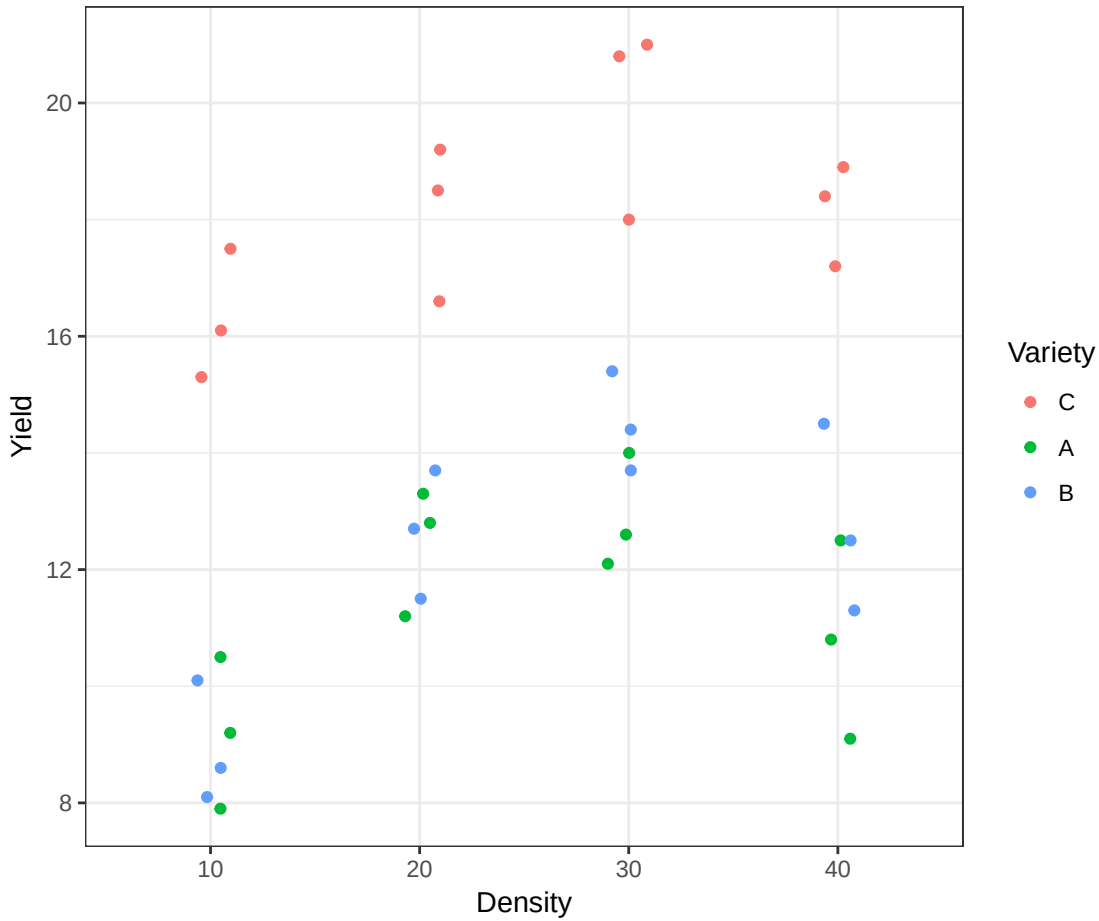
# Summary

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.

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

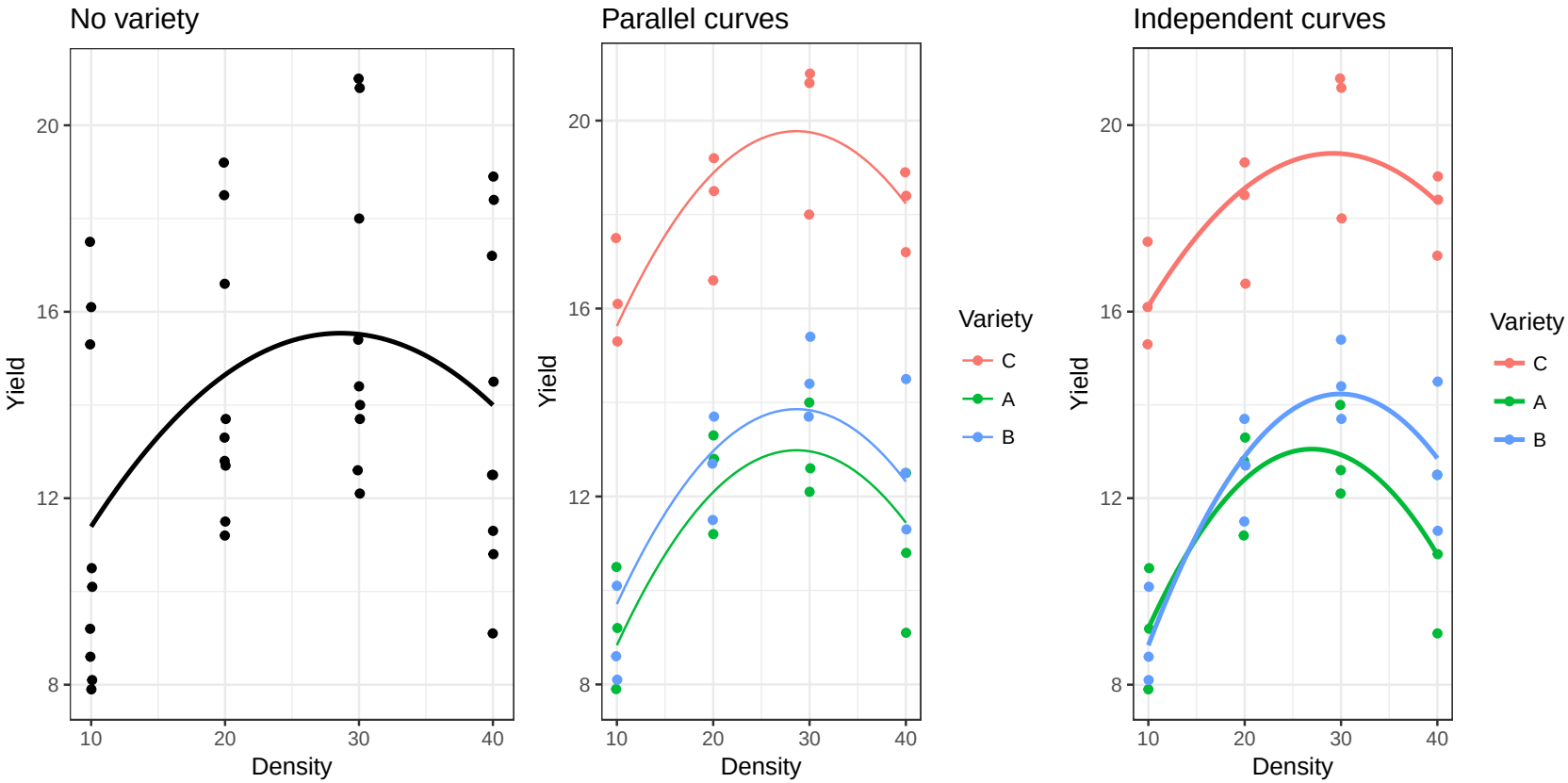
Now we can incorporate Variety ($V_i$) in many ways. Two options are parallel curves or completely independent curves.

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

# 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 $\beta_1$ and $\beta_2$ need not correspond to any particular $\beta_1$ and $\beta_2$ 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(lm(Yield~Density+I(Density^2), 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(lm(Yield~Density+I(Density^2) + Variety, 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(lm(Yield~Density*Variety+I(Density^2)*Variety, 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
```

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

# 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.

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

Block 1

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

Block 2

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

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 interacion 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

| | |
|---|---|
| B | C |
| A | B |
| C | A |

Block 1 Block 2

Unblocked

| | |
|---|---|
| B | C |
| A | C |
| B | A |

Block 1 Block 2

Let's consider 3 possible analyses:

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

# 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.