Analysis of Variance

Description of Data

- Data from a Latin Square designs testing the effect of feeds (A, B, C, D, E) on milk yield
- Two blocking factors

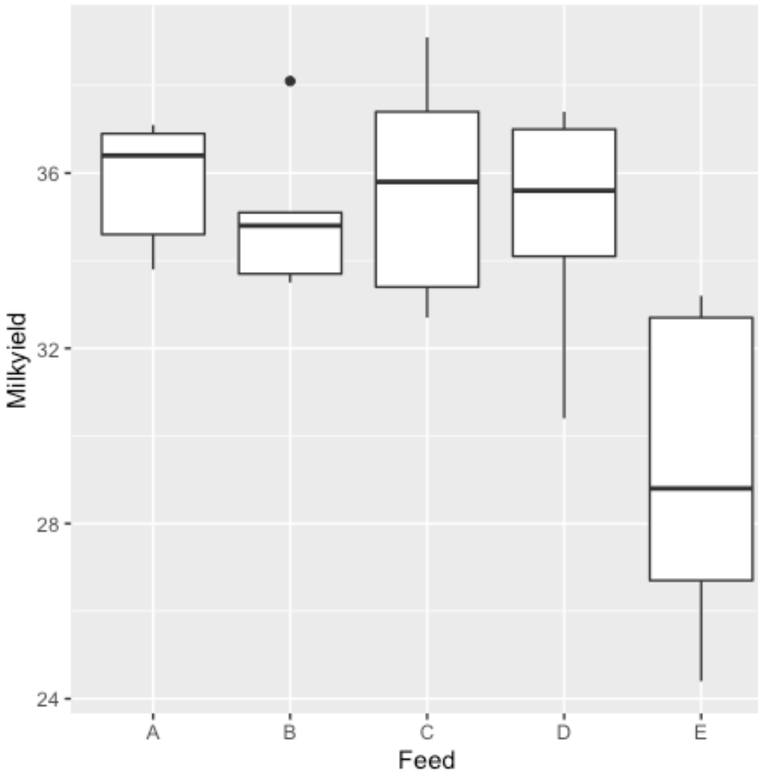
  1) Animals (each animal has some uniqueness)

  2) Milkmen (each milkman has some uniqueness)

	Milkman 1	Milkman 2	Milkman 3	Milkman 4	Milkman 5
	A (33.8)	B (33.7)	D (30.4)	C (32.7)	E (24.4)
	D(37.0)	E(28.8)	B(33.5)	A(34.6)	C(33.4)
	C(35.8)	D(35.6)	A(36.9)	E(26.7)	B(35.1)
	E(33.2)	A(37.1)	C(37.4)	B(38.1)	D(34.1)
	B(34.8)	C(39.1)	E(32.7)	D(37.4)	A(36.4)

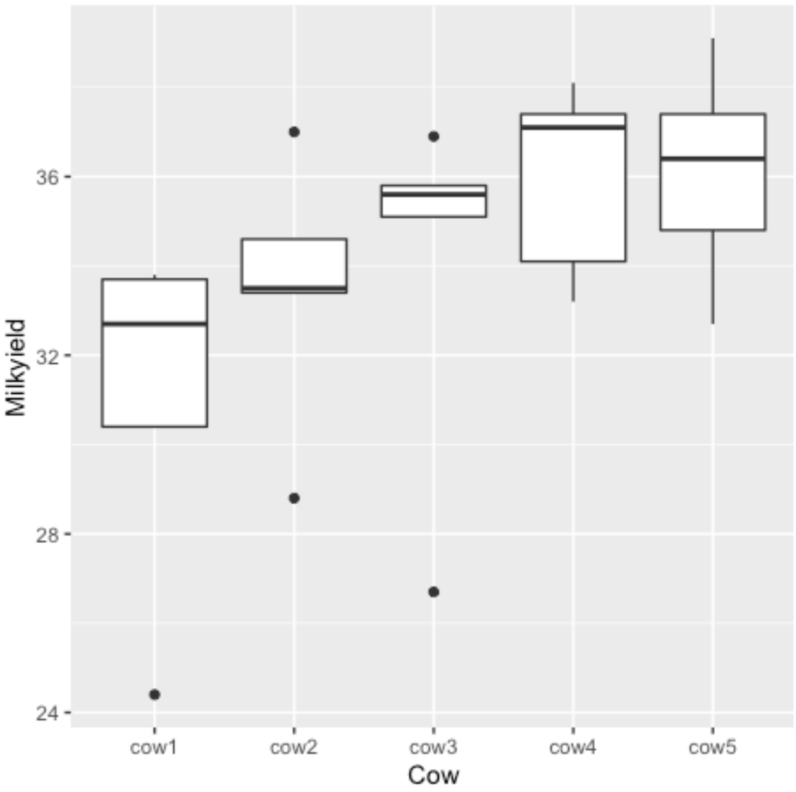
Data exploration

ggplot(latinsquare,aes(x=Feed,y= Milkyield) +geom_boxplot()



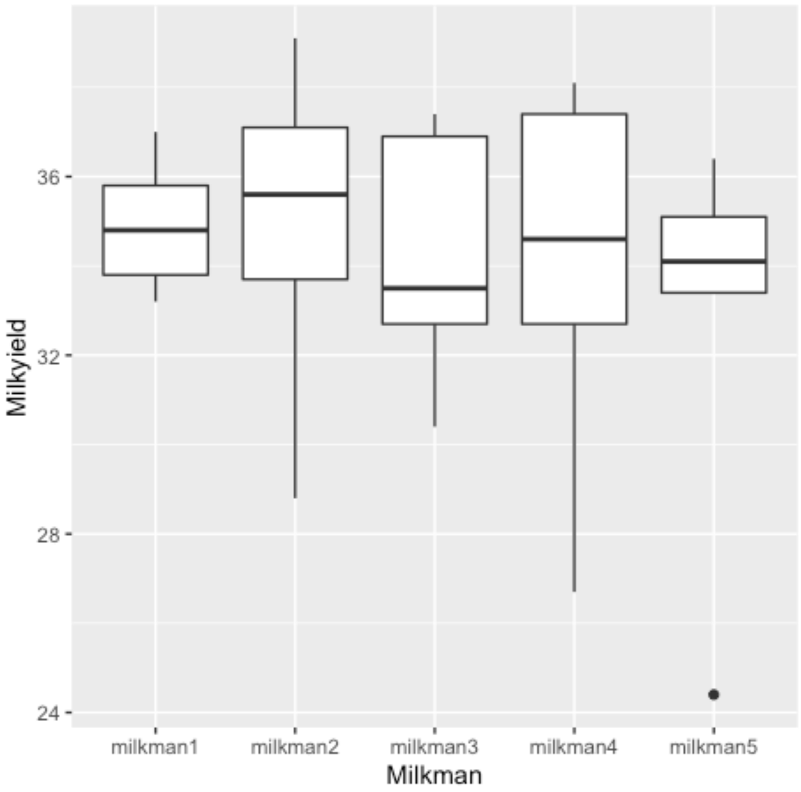
Feed E produces least amount of milk

ggplot(latinsquare,aes(x=Cow, y= Milkyield) +geom_boxplot()



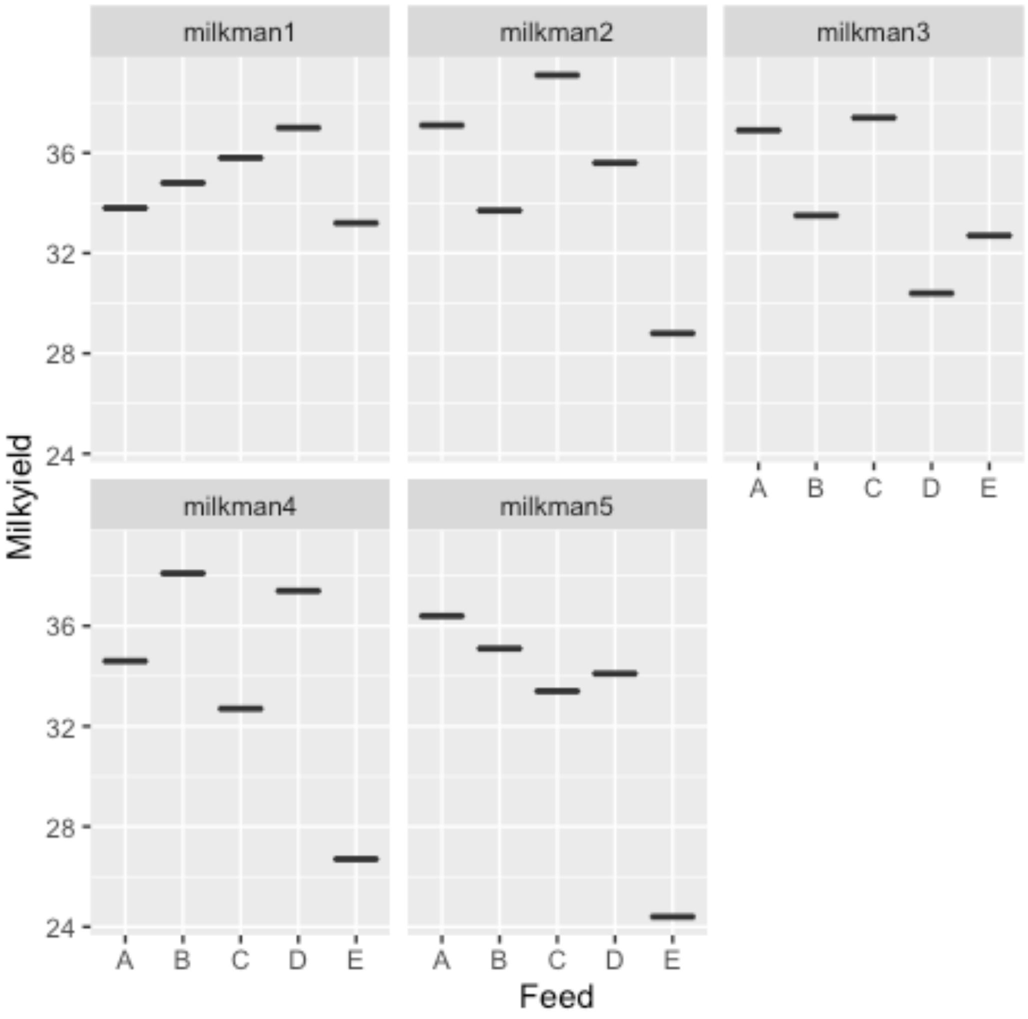
Differences exist among cows – could affect feeds comparison

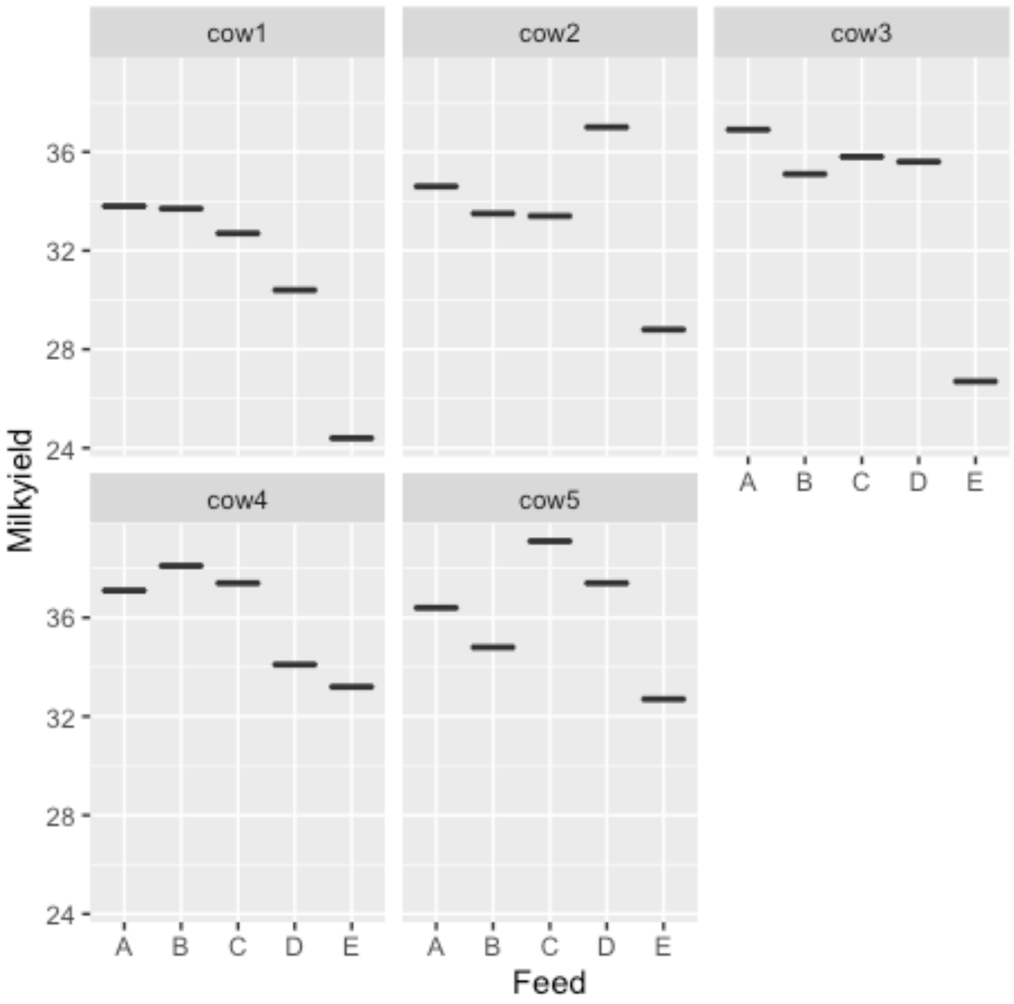
ggplot(latinsquare,aes(x=Milkman, y= Milkyield) +geom_boxplot()



No much differences among milkmen

Data exploration





Analysis of Variance

Model : Design + Treatment + Random error

Full Model - Latin Square Model

Milk yield** = **Effect feed** + **Effect cow + Milkman Effect** + **Error

Null model (No design effect, No treatment effect)

Milk yield = General mean + Error

We can have three other models between the null and full models

	Milkman 1	Milkman 2	Milkman 3	Milkman 4	Milkman 5
	A (33.8)	B (33.7)	D (30.4)	C (32.7)	E (24.4)
	D(37.0)	E(28.8)	B(33.5)	A(34.6)	C(33.4)
	C(35.8)	D(35.6)	A(36.9)	E(26.7)	B(35.1)
	E(33.2)	A(37.1)	C(37.4)	B(38.1)	D(34.1)
	B(34.8)	C(39.1)	E(32.7)	D(37.4)	A(36.4)

Analysis of Variance

1) Null model

Milk yield = General mean + Error

2) CRD model (ignore cow and milkman effects)

Milk yield** = **Effect feed** + **Error

3) RCBD with cow effects as blocking factor (ignore milkman effect)

Milk yield** = **Effect feed** + **Effect cow** + **Error

4) RCBD with milkman as blocking factor (ignore cow effect)

Milk yield** = **Effect feed** + **Milkman Effect** + **Error

5) Full model with two blocking factors

Milk yield** = **Effect feed** + **Effect cow + Milkman Effect** + **Error

	Milkman 1	Milkman 2	Milkman 3	Milkman 4	Milkman 5
	A (33.8)	B (33.7)	D (30.4)	C (32.7)	E (24.4)
	D(37.0)	E(28.8)	B(33.5)	A(34.6)	C(33.4)
	C(35.8)	D(35.6)	A(36.9)	E(26.7)	B(35.1)
	E(33.2)	A(37.1)	C(37.4)	B(38.1)	D(34.1)
	B(34.8)	C(39.1)	E(32.7)	D(37.4)	A(36.4)

Analysis of Variance

1) Null model (all effects are in the error term)

Analysis of Variance Table
Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Residuals	24	296.66	12.361		

2) CRD model (ignore cow and milkman effects)

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.89	38.974	5.5374	0.003619	**
Residuals	**20**	**140.76**	**7.038**			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

	Milkman 1	Milkman 2	Milkman 3	Milkman 4	Milkman 5
	A (33.8)	B (33.7)	D (30.4)	C (32.7)	E (24.4)
	D(37.0)	E(28.8)	B(33.5)	A(34.6)	C(33.4)
	C(35.8)	D(35.6)	A(36.9)	E(26.7)	B(35.1)
	E(33.2)	A(37.1)	C(37.4)	B(38.1)	D(34.1)
	B(34.8)	C(39.1)	E(32.7)	D(37.4)	A(36.4)

Residuals MS = 12.361 (Null model)
Residuals MS = 7.038 (CRD Model)

Analysis of Variance

2) CRD model (ignore cow and milkman effects)

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.89	38.974	5.5374	0.003619	**
Residuals	**20**	**140.76**	**7.038**			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

3) RBCD model with cows block

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.894	38.974	11.6859	0.0001245	***
Cow	4	87.402	21.851	6.5517	0.0025449	**
Residuals	**16**	**53.362**	**3.335**			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

	Milkman 1	Milkman 2	Milkman 3	Milkman 4	Milkman 5
	A (33.8)	B (33.7)	D (30.4)	C (32.7)	E (24.4)
	D(37.0)	E(28.8)	B(33.5)	A(34.6)	C(33.4)
	C(35.8)	D(35.6)	A(36.9)	E(26.7)	B(35.1)
	E(33.2)	A(37.1)	C(37.4)	B(38.1)	D(34.1)
	B(34.8)	C(39.1)	E(32.7)	D(37.4)	A(36.4)

Residuals MS = 12.361 (Null model)

Residuals MS = 7.038 (CRD Model)

Residuals MS = 3.335 (RCBD –cow)

Analysis of Variance

2) CRD model (ignore cow and milkman effects)

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.89	38.974	5.5374	0.003619	**
Residuals	**20**	**140.76**	**7.038**			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

4) RBCD model with Milkman as block

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.894	38.974	5.0207	0.00815	**
Milkman	4	16.562	4.141	0.5334	0.71314	
Residuals	**16**	**124.202**	**7.763**			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

	Milkman 1	Milkman 2	Milkman 3	Milkman 4	Milkman 5
	A (33.8)	B (33.7)	D (30.4)	C (32.7)	E (24.4)
	D(37.0)	E(28.8)	B(33.5)	A(34.6)	C(33.4)
	C(35.8)	D(35.6)	A(36.9)	E(26.7)	B(35.1)
	E(33.2)	A(37.1)	C(37.4)	B(38.1)	D(34.1)
	B(34.8)	C(39.1)	E(32.7)	D(37.4)	A(36.4)

Residuals MS = 12.361 (Null model)

Residuals MS = 7.038 (CRD Model)

Residuals MS = 3.335 (RCBD –cow)

Residuals MS = 7.763 (RCBD – Milkman)

Analysis of Variance

<u>2) CRD model (ignore cow and milkman effects)</u>

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.89	38.974	5.5374	0.003619	**
Residuals	**20**	**140.76**	**7.038**			

<u>4) RBCD model with Milkman as block</u>

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.894	38.974	12.7091	0.000284	***
Cow	4	87.402	21.851	7.1254	0.003533	**
Milkman	4	16.562	4.141	1.3502	0.307872	
Residuals	12	36.799	3.067			

	Milkman 1	Milkman 2	Milkman 3	Milkman 4	Milkman 5
	A (33.8)	B (33.7)	D (30.4)	C (32.7)	E (24.4)
	D(37.0)	E(28.8)	B(33.5)	A(34.6)	C(33.4)
	C(35.8)	D(35.6)	A(36.9)	E(26.7)	B(35.1)
	E(33.2)	A(37.1)	C(37.4)	B(38.1)	D(34.1)
	B(34.8)	C(39.1)	E(32.7)	D(37.4)	A(36.4)

Residuals MS = 12.361 (Null model)

Residuals MS = 7.038 (CRD Model)

Residuals MS = 3.335 (RCBD –cow)

Residuals MS = 7.763 (RCBD – Milkman)

Residuals MS = 3.067 (Latin Square – Cow & Milkman)

Assumptions of the ANOVA

- Statistical models for the different experimental designs

CRD $$y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$

RCBD $$y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

Latin Square $$y_{ijk} = \mu + \tau_i + C_j + R_k + \varepsilon_{ijk}$$

Error terms

Assumptions of ANOVA

CRD model: ***Milk yield*** = ***Effect feed*** + ***Error***

$$y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$

> model1<-aov(Milkyield~Feed, latinsquare) #analysis as CRD

> anova(model1)

Analysis of Variance Table

Response: Milkyield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Feed	4	155.89	38.974	5.5374	0.003619	**
Residuals	20	140.76	7.038			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Assumptions of ANOVA

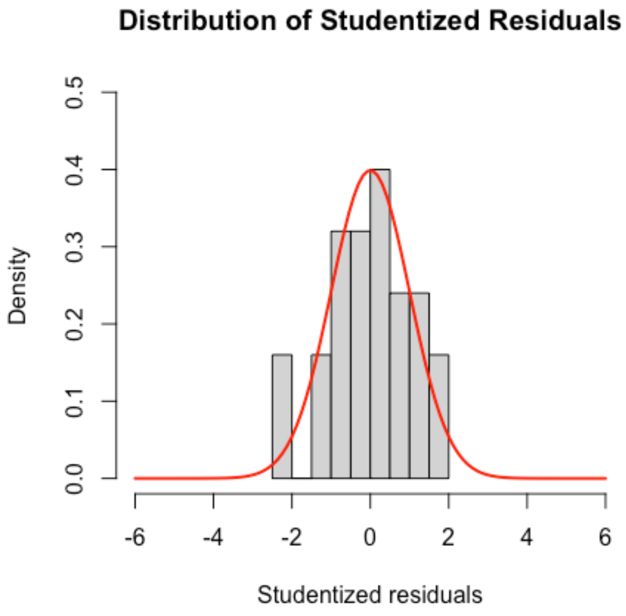
$$y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$

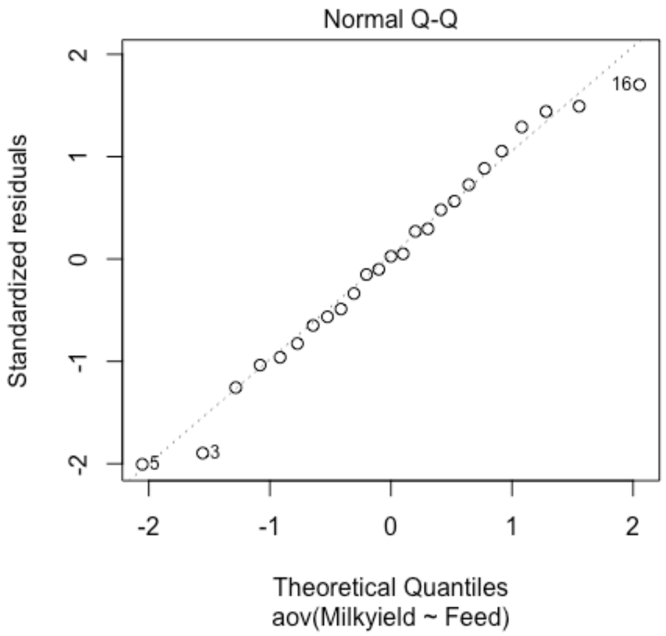
> model1$residuals

Datapoint	Observed Milk yeild	Fitted Milk yield	Residual
1	33.8	35.76	-1.96
2	33.7	35.04	-1.34
3	30.4	34.9	-4.5
4	32.7	35.68	-2.98
5	24.4	29.16	-4.76
6	37	34.9	2.1
7	28.8	29.16	-0.36
8	33.5	35.04	-1.54
9	34.6	35.76	-1.16
10	33.4	35.68	-2.28
11	35.8	35.68	0.12
12	35.6	34.9	0.7
13	36.9	35.76	1.14
14	26.7	29.16	-2.46
15	35.1	35.04	0.06
16	33.2	29.16	4.04
17	37.1	35.76	1.34
18	37.4	35.68	1.72
19	38.1	35.04	3.06
20	34.1	34.9	-0.8
21	34.8	35.04	-0.24
22	39.1	35.68	3.42
23	32.7	29.16	3.54
24	37.4	34.9	2.5
25	36.4	35.76	0.64

Assumptions of ANOVA

$$y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$



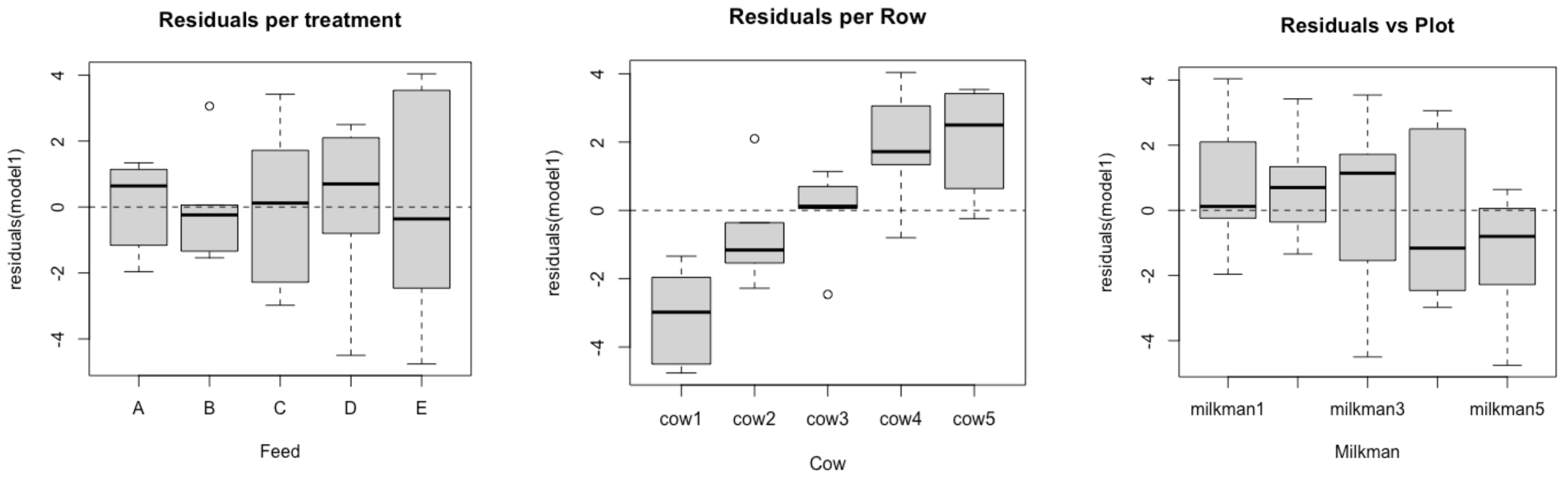


Residuals
-1.96
-1.34
-4.5
-2.98
-4.76
2.1
-0.36
-1.54
-1.16
-2.28
0.12
0.7
1.14
-2.46
0.06
4.04
1.34
1.72
3.06
-0.8
-0.24
3.42
3.54
2.5
0.64

Normally distributed with mean of zero

Assumptions of ANOVA

CRD model: ***Milk yield*** = ***feed effect*** + ***Error***



Residuals
-1.96
-1.34
-4.5
-2.98
-4.76
2.1
-0.36
-1.54
-1.16
-2.28
0.12
0.7
1.14
-2.46
0.06
4.04
1.34
1.72
3.06
-0.8
-0.24
3.42
3.54
2.5
0.64

More variation in Feed type E
Less variation in Feed type B

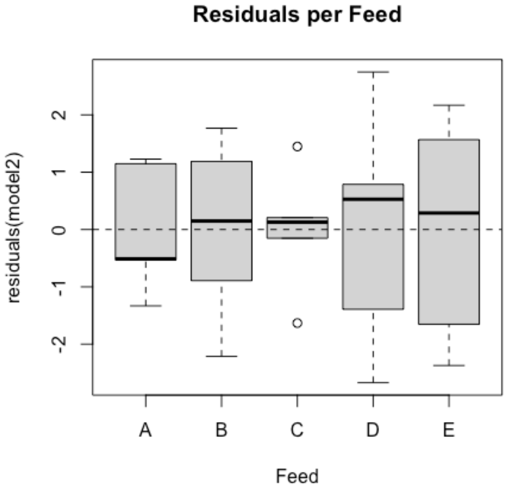
Errors for cow 1 & 2 mostly negative
Errors for cow4 and 5 mostly positive

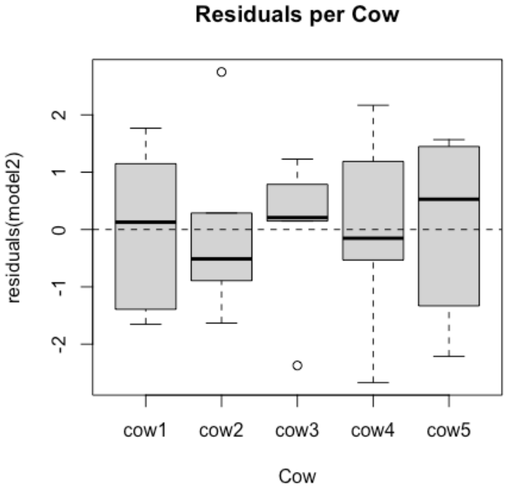
Patterns appear more random
More variations for milkman 4

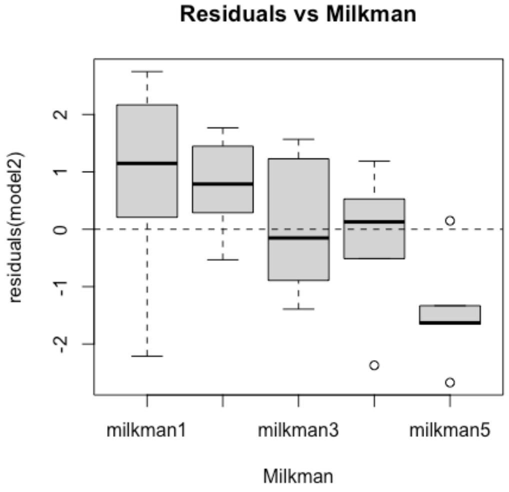
Error terms are randomly & independent, constant variance

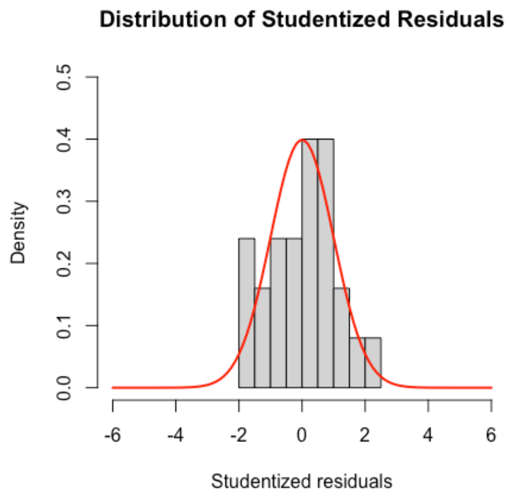
Assumptions of ANOVA

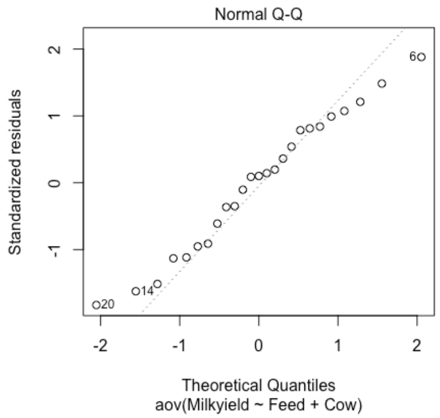
RCBD model: ***Milk yield*** = ***feed effect*** + *Cow effect* + ***Error***







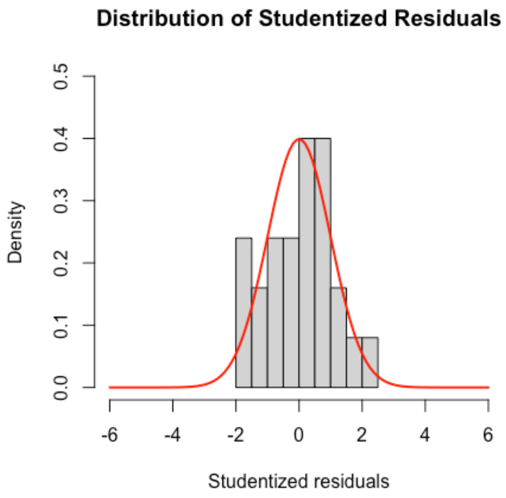


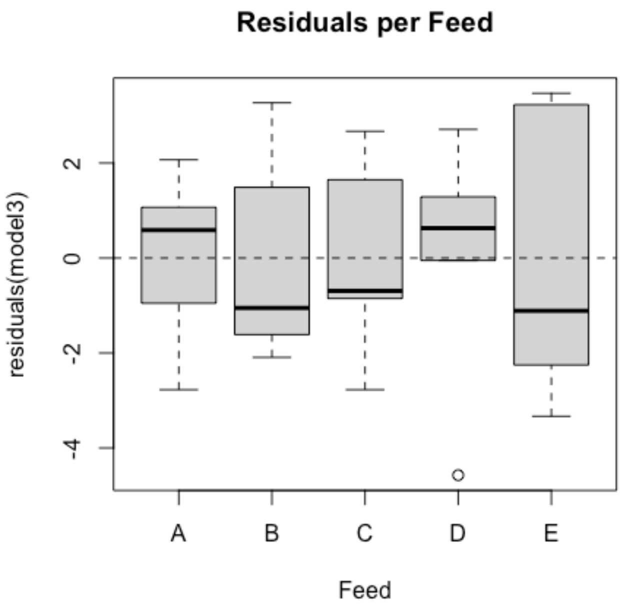


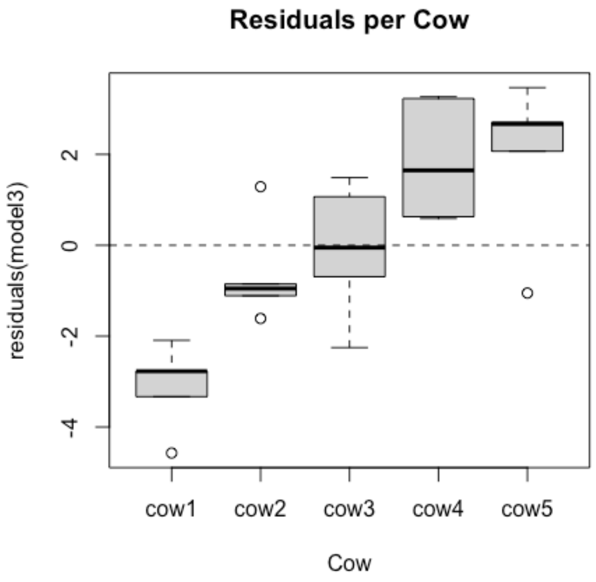
Error terms are randomly & independent, normally distributed with constant variance

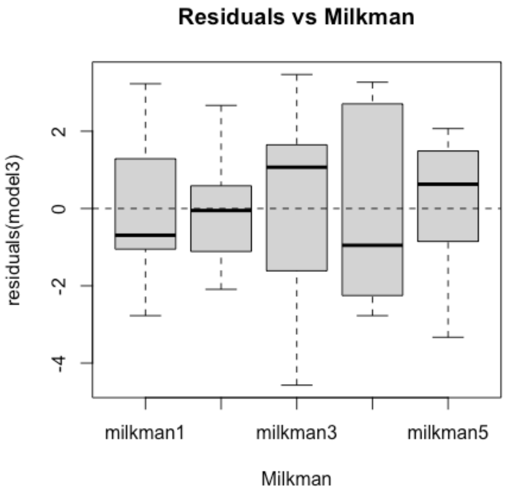
Assumptions of ANOVA

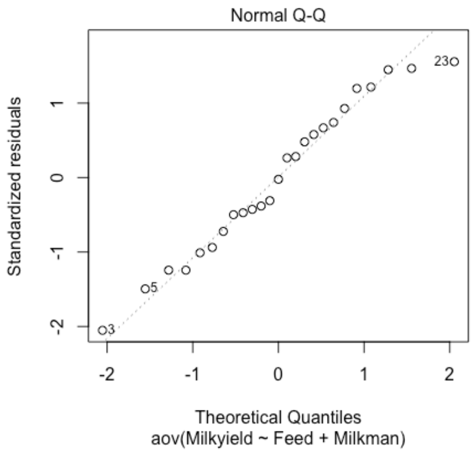
RCBD model: ***Milk yield*** = ***feed effect*** + ***Milkman effect*** + ***Error***







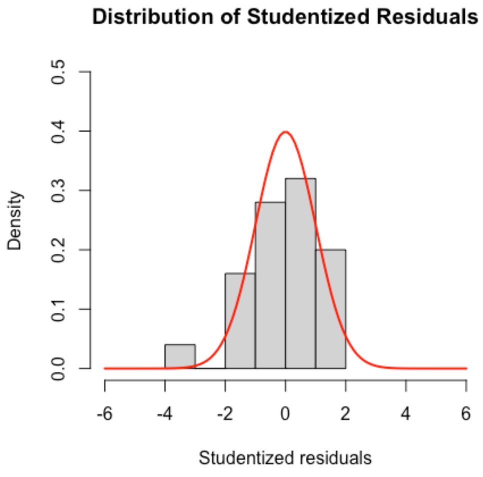


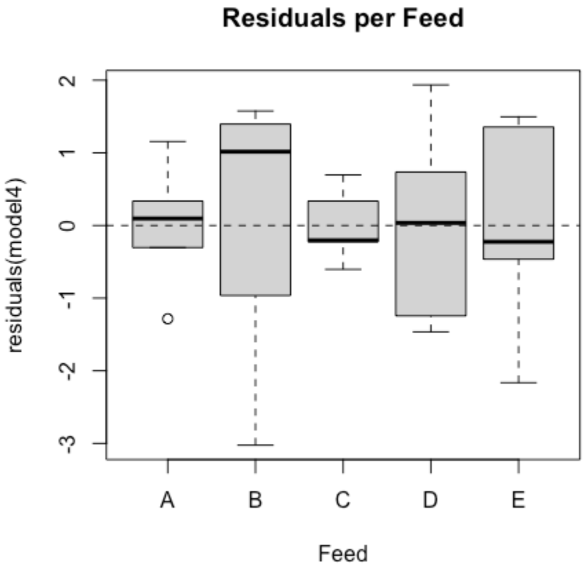


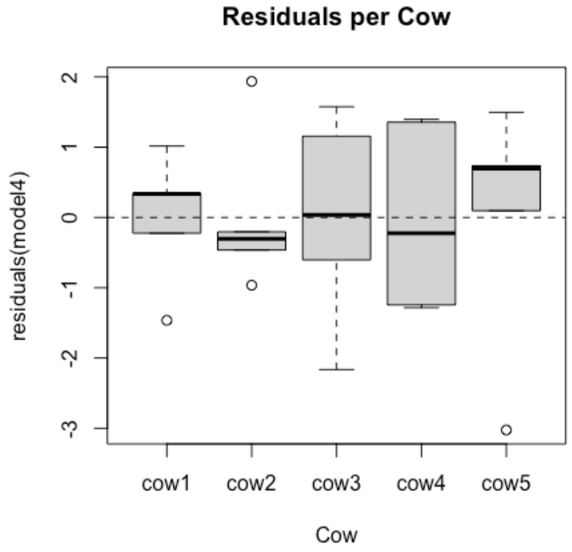
Error terms are randomly & independent, normally distributed with constant variance

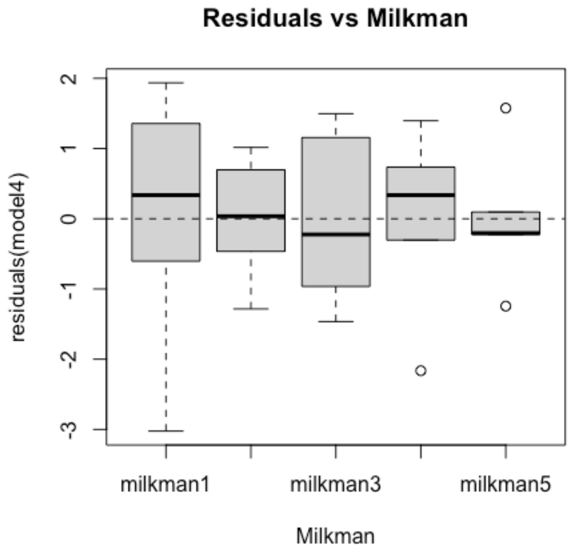
Assumptions of ANOVA

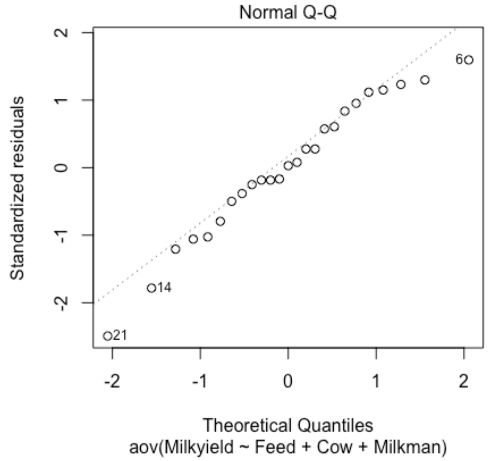
LSD model: ***Milk yield*** = ***feed effect*** + *cow effect* + ***Milkman effect*** + ***Error***











Error terms are randomly & independent, normally distributed with constant variance

Assumptions of Analysis of Variance

> shapiro.test(resid(model1))

Shapiro-Wilk normality test

data: resid(model1)

W = 0.97753, p-value = 0.8321

> shapiro.test(resid(model2))

Shapiro-Wilk normality test

data: resid(model2)

W = 0.97334, p-value = 0.7301

> shapiro.test(resid(model3))

Shapiro-Wilk normality test

data: resid(model3)

W = 0.96399, p-value = 0.4996

> shapiro.test(resid(model4))

Shapiro-Wilk normality test

data: resid(model4)

W = 0.96669, p-value = 0.5629

Assumptions of Analysis of Variance

> anova(lm((resid(lm(Milkyield~Feed, latinsquare))^2)~Feed, latinsquare))

Analysis of Variance Table

Response: (resid(lm(Milkyield ~ Feed, latinsquare))^2)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Feed	4	295.75	73.938	2.0426	**0.1269**
Residuals	20	723.95	36.198		

> anova(lm((resid(lm(Milkyield~Feed + Cow, latinsquare))^2)~Feed, latinsquare))

Analysis of Variance Table

Response: (resid(lm(Milkyield ~ Feed + Cow, latinsquare))^2)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Feed	4	27.195	6.7987	1.4541	**0.2533**
Residuals	20	93.509	4.6755		

Assumptions of Analysis of Variance

```
> anova(lm((resid(lm(Milkyield~Feed + Milkman, latinsquare))^2)~Feed, latinsquare))
```

Analysis of Variance Table

Response: (resid(lm(Milkyield ~ Feed + Milkman, latinsquare))^2)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Feed	4	83.51	20.879	0.7728	0.5556
Residuals	20	540.32	27.016		

```
> anova(lm((resid(lm(Milkyield~Feed + Cow + Milkman, latinsquare))^2)~Feed, latinsquare))
```

Analysis of Variance Table

Response: (resid(lm(Milkyield ~ Feed + Cow + Milkman, latinsquare))^2)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Feed	4	25.425	6.3564	1.7526	0.1781
Residuals	20	72.535	3.6268		

Assumptions of Analysis of Variance

```
> leveneTest(latinsquare$Milkyield, latinsquare$Feed)
Levene's Test for Homogeneity of Variance (center = median)
        Df  F value  Pr(>F)
group  4    1.1808  0.3493
      20
```

```
> leveneTest(latinsquare$Milkyield, latinsquare$Cow)
Levene's Test for Homogeneity of Variance (center = median)
        Df F value  Pr(>F)
group  4  0.0909  0.9842
      20
```

```
> leveneTest(latinsquare$Milkyield, latinsquare$Milkman)
Levene's Test for Homogeneity of Variance (center = median)
        Df  F value Pr(>F)
group  4   0.4433 0.7759
      20
```

Assumptions of Analysis of Variance

```
> #Rule of thumb check ratio of maximum variance to minimum variance should not exceed 5
> max(by(latinsquare$Milkyield,latinsquare$Feed,sd))^2/min(by(latinsquare$Milkyield,latinsquare$Feed,sd))^2
[1] 6.637368
> max(by(latinsquare$Milkyield,latinsquare$Cow,sd))^2/min(by(latinsquare$Milkyield,latinsquare$Cow,sd))^2
[1] 3.610889
> max(by(latinsquare$Milkyield,latinsquare$Milkman,sd))^2/min(by(latinsquare$Milkyield,latinsquare$Milkman,sd))^2
[1] 9.732847
```

Analysis of Variance for Factorial Experiments

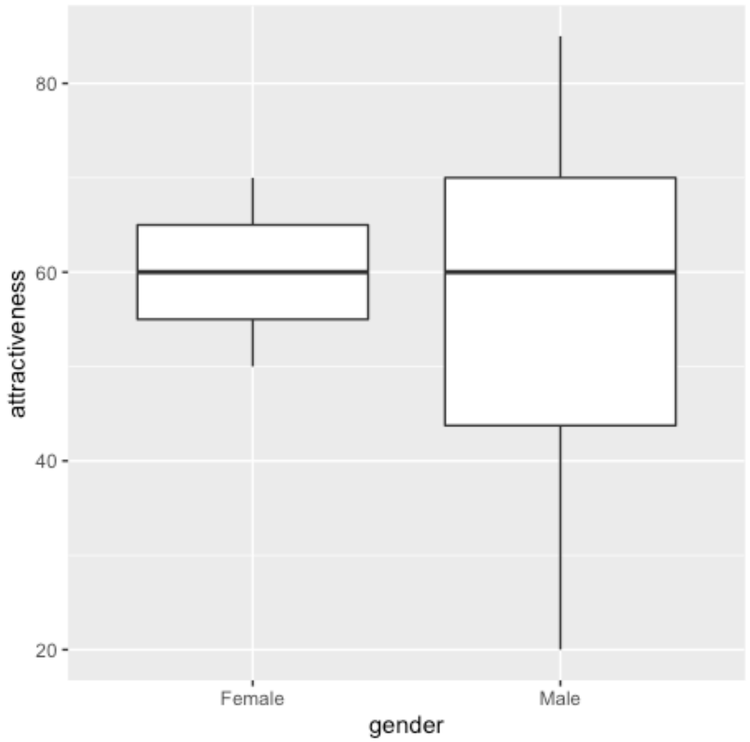
Example: Beer-goggle effects (adopted Discovering statistics using R)

Antropologist is interested in the effect beers on mate selection in a night club

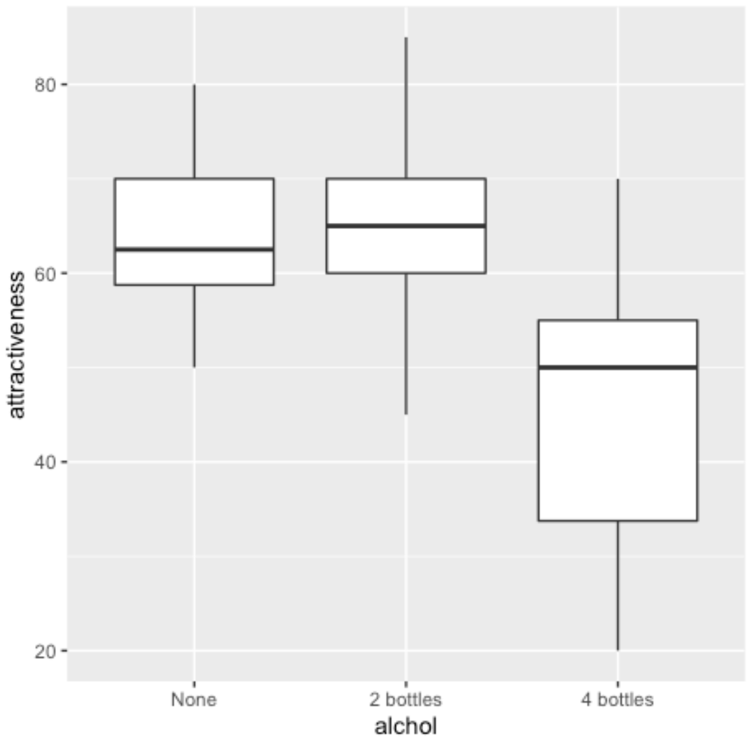
- **Rationale**: after alcohol consumption, subjective perceptions of physical attractiveness would become more inaccurate (the well-known beer-goggles effect).
- Does beer-goggles effect depend on sex?

Sex	Alcohol level	Number of participants	Variable measured
Female	0 (alcohol free lager)	6	*Take a photograph of the person that the participant was chatting up. She then got a pool of independent judges to assess the attractiveness of the person in each photograph (out of 100)*
Female	2 bottles of beer	6	
Female	4 bottles of beer	6	
Male	0 (alcohol free lager)	6	
Male	2 bottles of beer	6	
Male	4 bottles of beer	6	

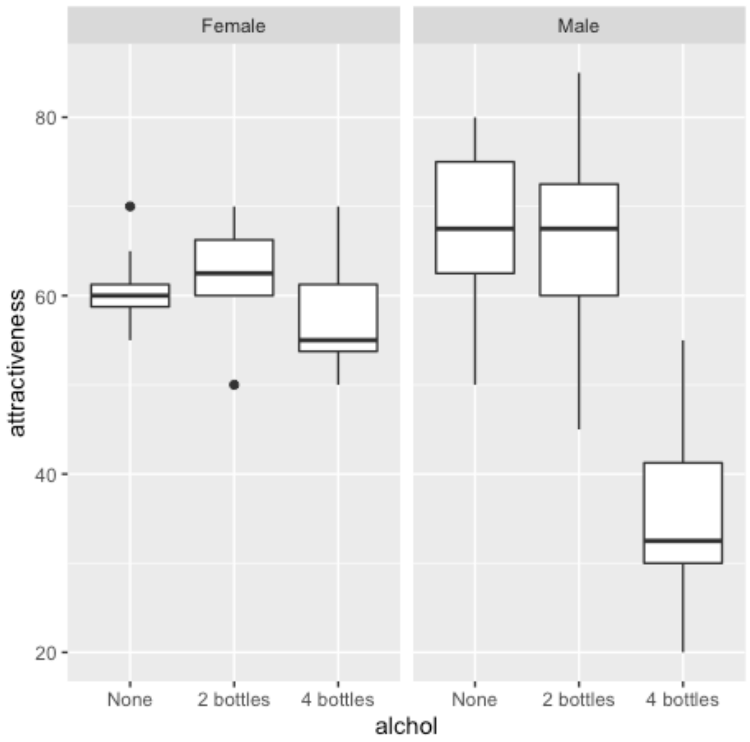
Data exploration



Gender ignoring alcohol effect



Alcohol ignoring gender effect



Considering both effects

Data exploration

```
> by(attracdata$attractiveness, attracdata$gender, summary) #summary by gender
attracdata$gender: Female
   Min.  1st Qu.  Median    Mean  3rd Qu.    Max.
  50.00   55.00   60.00    60.21   65.00    70.00
------------------------------------------------------------
attracdata$gender: Male
   Min.  1st Qu.  Median    Mean  3rd Qu.    Max.
  20.00   43.75   60.00    56.46   70.00    85.00
```

Data exploration

```
> by(attracdata$attractiveness, attracdata$alchol, summary) #summary by alcohol
attracdata$alchol: None
   Min.  1st Qu.  Median    Mean  3rd Qu.    Max.
  50.00   58.75    62.50     63.75    70.00     80.00
------------------------------------------------------------
attracdata$alchol: 2 bottles
   Min. 1st Qu.  Median    Mean   3rd Qu.    Max.
  45.00   60.00   65.00      64.69   70.00     85.00
------------------------------------------------------------
attracdata$alchol: 4 bottles
   Min.  1st Qu.  Median    Mean 3rd Qu.    Max.
  20.00   33.75    50.00     46.56   55.00   70.00
```

Data exploration

summary)#by gender & alcohol

: Female

: None

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
55.00	58.75	60.00	60.62	61.25	70.00

: Male

: None

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
50.00	62.50	67.50	66.88	75.00	80.00

----

summary)#by gender & alcohol

: Female

: 2 bottles

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
50.00	60.00	62.50	62.50	66.25	70.00

: Male

: 2 bottles

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
45.00	60.00	67.50	66.88	72.50	85.00

Data exploration

summary)#by gender & alcohol
: Female
: None

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
55.00	58.75	60.00	60.62	61.25	70.00

: Male
: None

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
50.00	62.50	67.50	66.88	75.00	80.00

----

summary)#by gender & alcohol
: Female
: 4 bottles

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
50.00	53.75	55.00	57.50	61.25	70.00

: Male
: 4 bottles

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
20.00	30.00	32.50	35.62	41.25	55.00

One-way ANOVA

> attractmodel1<-aov(attractiveness~gender, data=attracdata)

> anova(attractmodel1)

Analysis of Variance Table

Response: attractiveness

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gender	1	168.7	168.75	0.8823	**0.3525**
Residuals	46	8797.9	191.26		

> attractmodel2<-aov(attractiveness~alchol, data=attracdata)

> anova(attractmodel2)

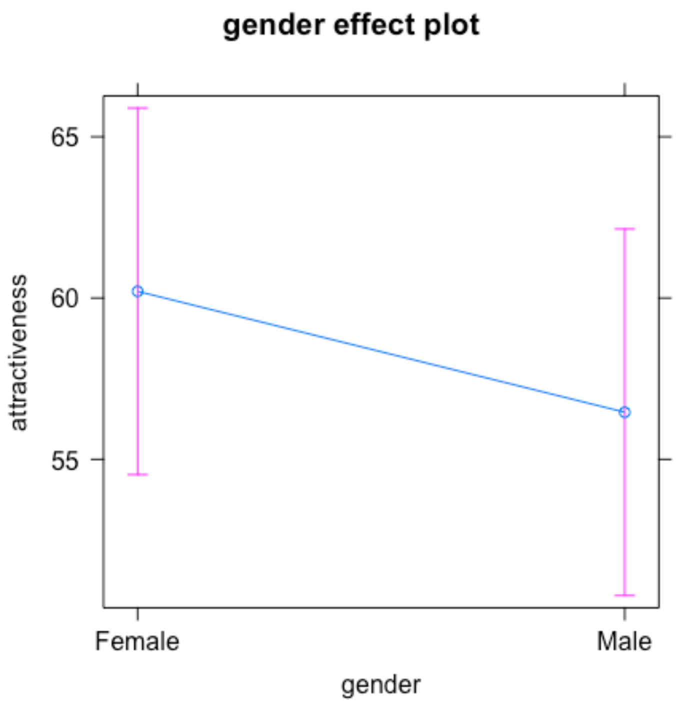
Analysis of Variance Table

Response: attractiveness

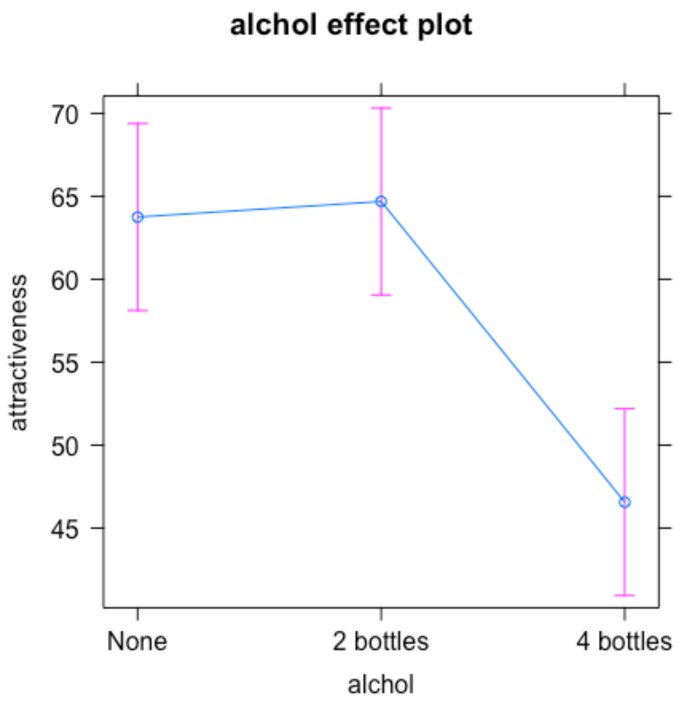
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
alchol	2	3332.3	1666.15	13.307	2.883e-05
Residuals	45	5634.4	125.21		

One-way ANOVA

> attractmodel1<-aov(attractiveness~gender, data=attracdata)



> attractmodel2<-aov(attractiveness~alchol, data=attracdata)



Two-way ANOVA

*> attractmodel3<-aov(attractiveness~gender*alchol, data=attracdata)*

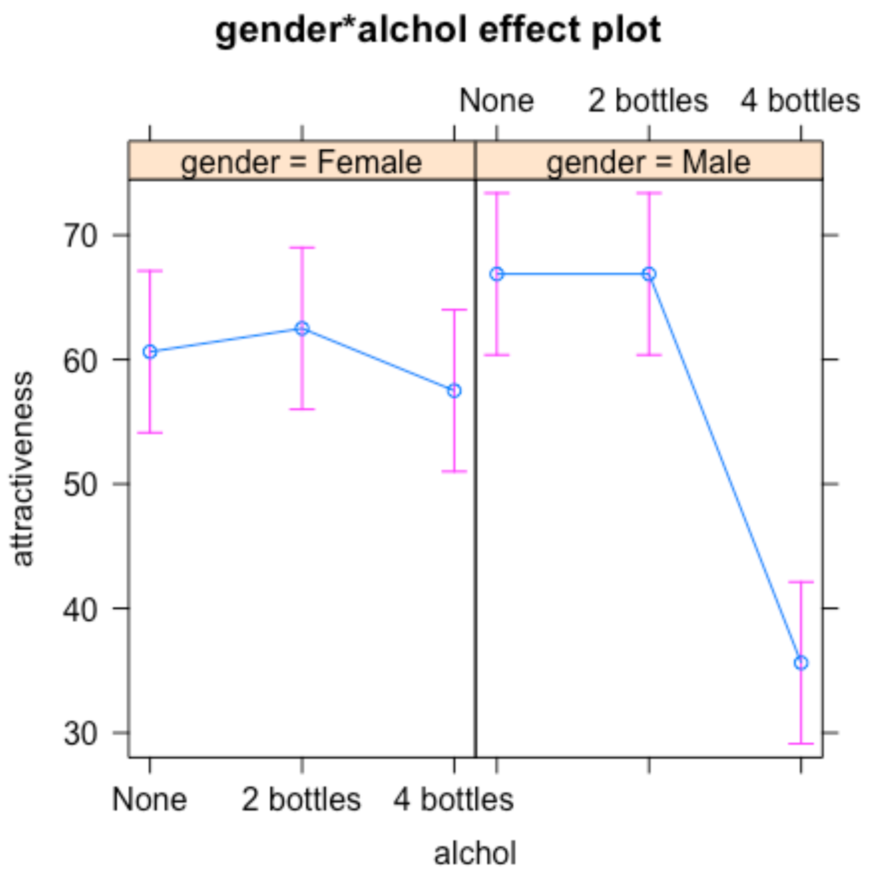
> anova(attractmodel3)

Analysis of Variance Table

Response: attractiveness

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
gender	1	168.7	168.75	2.0323	0.1614	
alchol	2	3332.3	1666.15	20.0654	7.649e-07	***
gender:alchol	2	1978.1	989.06	11.9113	7.987e-05	***
Residuals	42	3487.5	83.04			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1



Contrast and Posthoc Test

- Contrast are useful when comparing treatments with structure
- Instead of comparing individual treatments we compare groups of treatments
- Example

Contrast 1: No alcohol vs some alcohol (average 2 and 4 bottles)

Contrast 2: 2 bottles vs 4 bottles

Contrast 3: Male vs Female

Contrast and Posthoc Test

Use the commands below we can modify our data frame

contrasts(attracdata$alchol)<-cbind(c(-2, 1, 1), c(0, -1, 1))#creating contrast for alcohol

contrasts(attracdata$gender)<-c(-1, 1)#creating contrast for gender

```
……………………………………………………………………………
attr(,"contrasts")
          [,1] [,2]
None        -2    0
2 bottles    1   -1
4 bottles    1    1
Levels: None 2 bottles 4 bottles
```

Contrast and Posthoc Test

> anova(attractmodel4)

Analysis of Variance Table

Response: attractiveness

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gender	1	168.7	168.75	2.0323	0.1614
alchol	2	3332.3	1666.15	20.0654	7.649e-07
gender:alchol	2	1978.1	989.06	11.9113	7.987e-05
Residuals	42	3487.5	83.04		

> summary.lm(attractmodel4)

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	58.333	1.315	44.351	< 2e-16 ***
gender1	-1.875	1.315	-1.426	0.161382
alchol1	-2.708	0.930	-2.912	0.005727 **
alchol2	-9.062	1.611	-5.626	1.37e-06 ***
gender1:alchol1	-2.500	0.930	-2.688	0.010258 *
gender1:alchol2	-6.562	1.611	-4.074	0.000201 ***

Residual standard error: 9.112 on 42 degrees of freedom

Multiple R-squared: 0.6111, Adjusted R-squared: 0.5648

F-statistic: 13.2 on 5 and 42 DF, p-value: 9.609e-08

Simple effects

- Significant interaction between two factors – Implies the effects of the two factors cannot be interpreted independent of each other
- Simple effect: Comparing the level of one factor when holding the level of the other factor constant – ***Similar to one-way ANOVA***
- Example

  Compare male and female – at Zero alcohol level

  Compare male and female – at two bottle level
- ***Contrast can be constructed to test for simple effects***

Simple effects

Contrast for simple effects

> simple

		alcEffect1	alcEffect2	gender_none	gender_2bottles	gender_4bottles
Female_None	[1,]	-2	0	-1	0	0
Female_2bottles	[2,]	1	-1	0	-1	0
Female_4bottles	[3,]	1	1	0	0	-1
Male_None	[4,]	-2	0	1	0	0
Male_2bottles	[5,]	1	-1	0	1	0
Male_4bottles	[6,]	1	1	0	0	1

Simple effects

```
> model4<-aov(attractiveness ~ simple_effect, data = attracdata)
> summary.lm(model4)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	58.333	1.315	44.351	< 2e-16 ***
simple_effectalcEffect1	-2.708	0.930	-2.912	0.00573 **
simple_effectalcEffect2	-9.062	1.611	-5.626	1.37e-06 ***
simple_effectgender_none	3.125	2.278	1.372	**0.17742**
simple_effectgender_2bottles	2.188	2.278	0.960	**0.34243**
simple_effectgender_4bottles	-10.938	2.278	-4.801	2.02e-05 ***

Posthoc

> pairwise.t.test(attracdata$attractiveness, attracdata$alchol, p.adjust.method ="bonferroni")

Pairwise comparisons using t tests with pooled SD

data: attracdata$attractiveness and attracdata$alchol

	None	2 bottles
2 bottles	**1.00000**	-
4 bottles	0.00024	0.00011

P value adjustment method: bonferroni

Posthoc

> *summary(postHocs)*

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: aov(formula = attractiveness ~ gender * alchol, data = attracdata)

Linear Hypotheses:

	Estimate	Std. Error.	t value	Pr(>|t|)
2 bottles - None == 0	0.9375	3.2217	0.291	0.954
4 bottles - None == 0	-17.1875	3.2217	-5.335	<1e-04 ***
4 bottles - 2 bottles == 0	-18.1250	3.2217	-5.626	<1e-04 ***