

Analysis of Multifactor Experiments

Corresponds to Chapter 13
of Tamhane and Dunlop

Slides prepared by Elizabeth Newton (MIT),
with some slides by Jacqueline Telford
(Johns Hopkins University)

Analysis of Multifactor Experiments

(See Table 13.1 on page 505 of the course textbook.)

Model and estimates

$$y_{ijk} = \mu + \tau_i + \beta_j + (\tau\beta)_{ij} + \varepsilon_{ijk}$$

$$\hat{\mu} = \bar{y}_{...}$$

$$\hat{\tau}_i = \bar{y}_{i...} - \bar{y}_{...}$$

$$\hat{\beta}_j = \bar{y}_{\cdot j \cdot} - \bar{y}_{...}$$

$$(\tau\beta)_{ij} = \bar{y}_{ij\cdot} - \bar{y}_{i...} - \bar{y}_{\cdot j \cdot} + \bar{y}_{...}$$

$$\hat{y}_{ijk} = \bar{y}_{ij\cdot}$$

$$e_{ijk} = y_{ijk} - \hat{y}_{ijk} = y_{ijk} - \bar{y}_{ij\cdot}$$

For any model

y = vector of observed response values

\hat{y} = vector of fitted values

\bar{y} = vector of grand mean

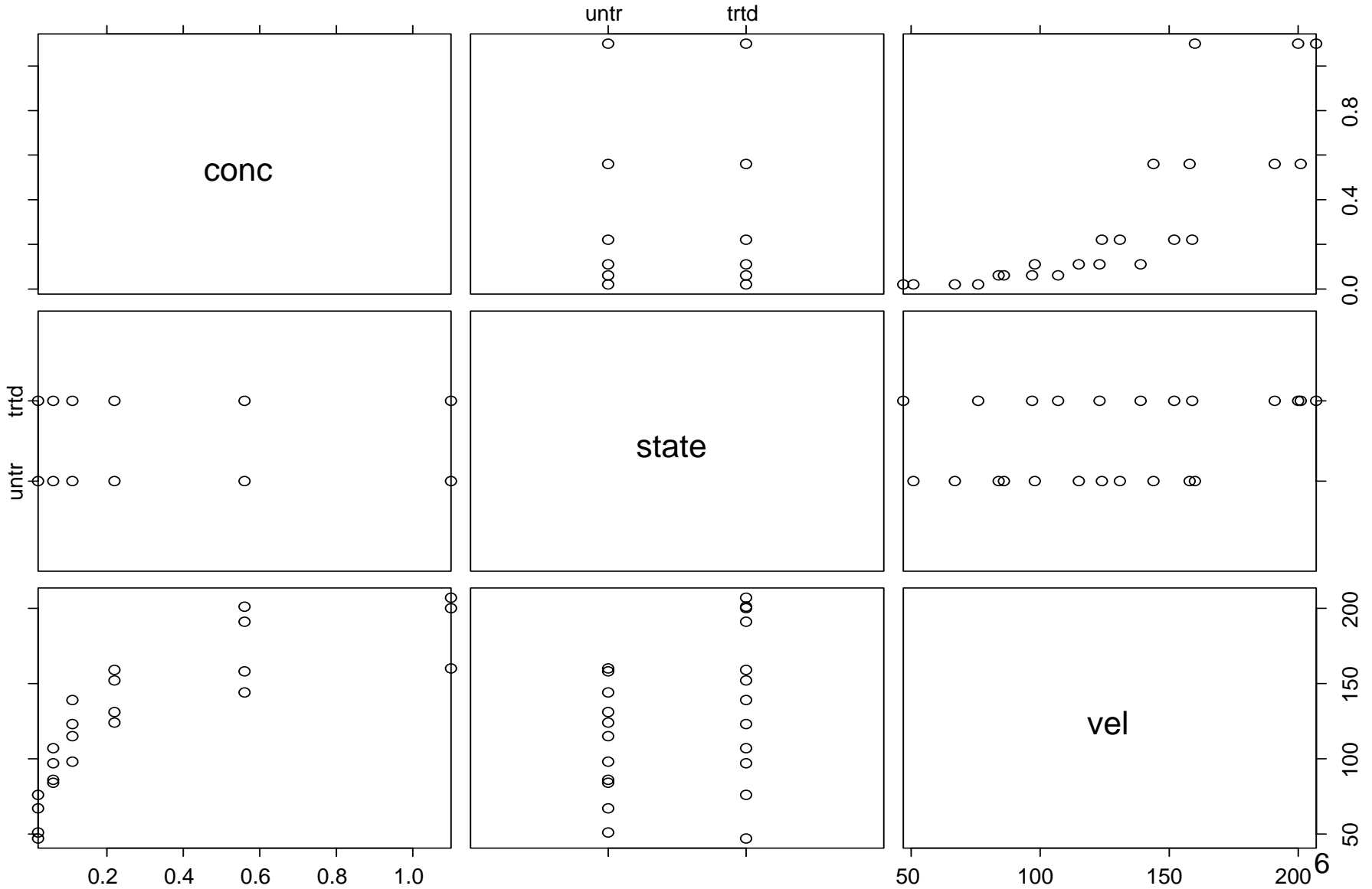
$$SST = SST_{\text{Total}} = (y - \bar{y})' (y - \bar{y})$$

$$SSM = SS_{\text{Model}} = (\hat{y} - \bar{y})' (\hat{y} - \bar{y})$$

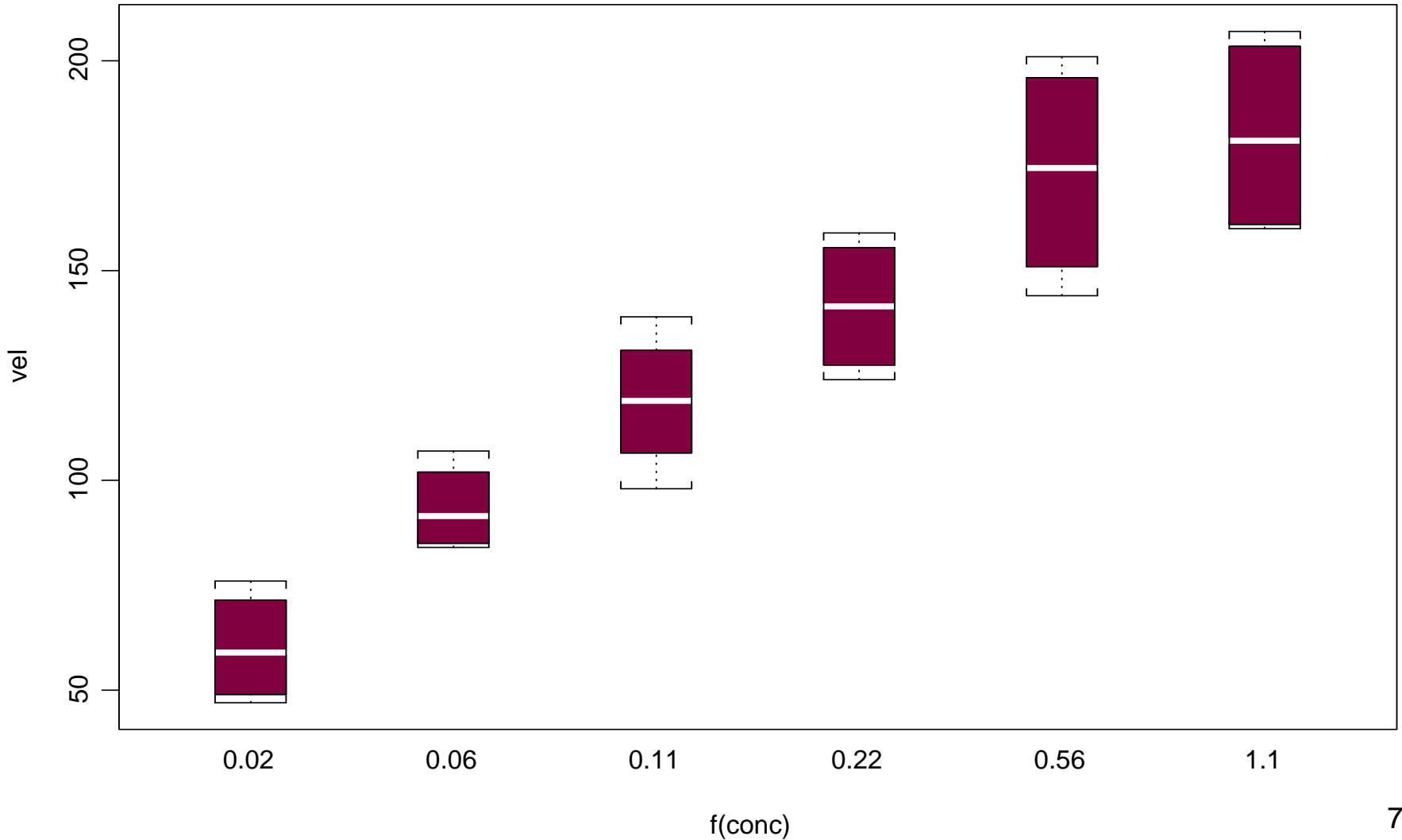
$$SSE = SS_{\text{Error}} = (y - \hat{y})' (y - \hat{y})$$

- **Biochemical Reactions of Cells Treated with Puromycin**
- **SUMMARY:**
- The “Balanced” Puromycin data frame has 24 rows representing the measurement of initial velocity of a biochemical reaction for 6 different concentrations of substrate and two different cell treatments. This data frame contains the following variables (columns):
- **ARGUMENTS:**
- **conc**
 - the concentration of the substrate.
- **vel**
 - the initial velocity of the reaction.
- **state**
 - a factor telling whether the cells involved were treated or untreated.

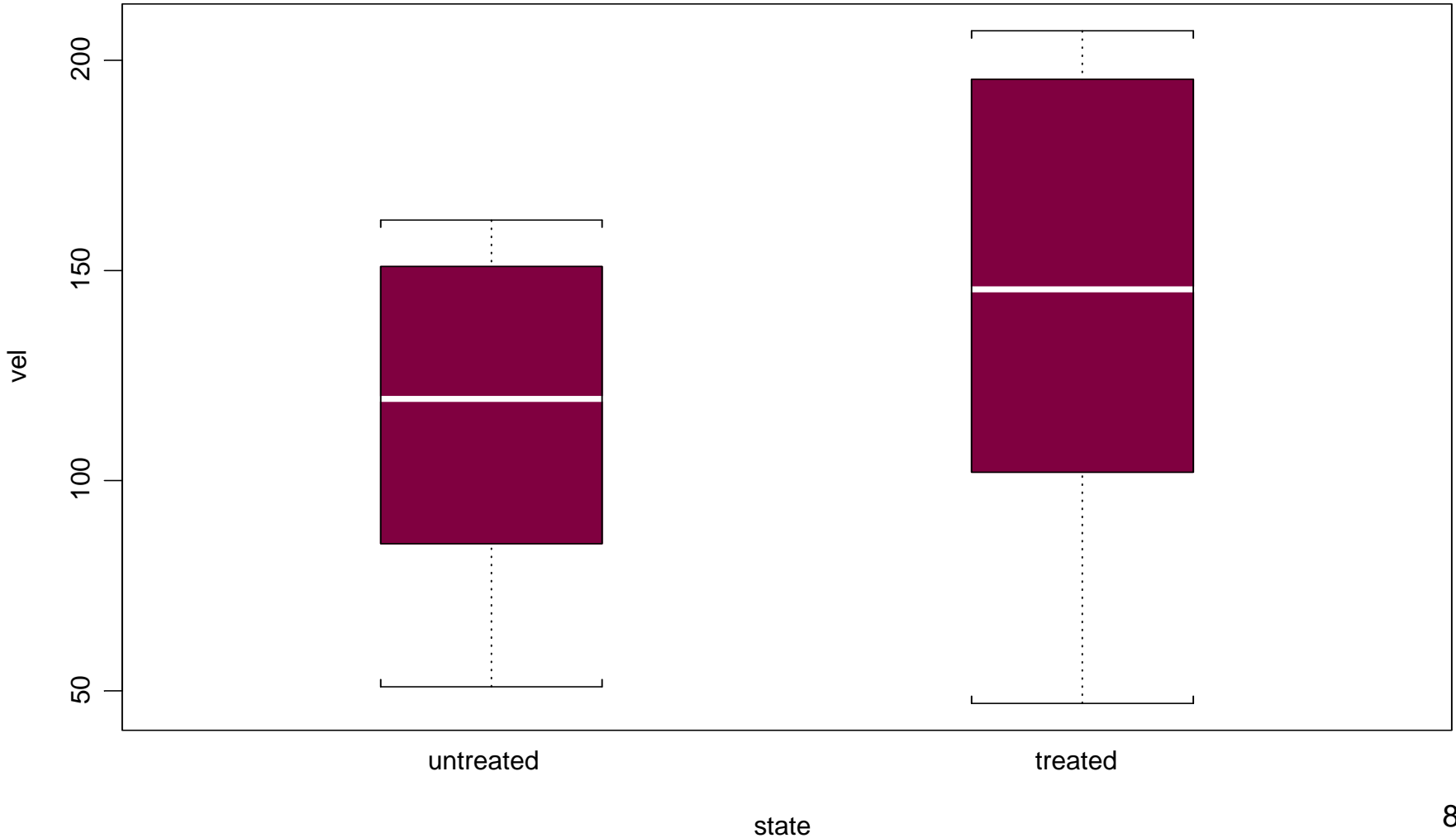
Scatterplot matrix for puromycin data set



plot.factor(conc,vel)



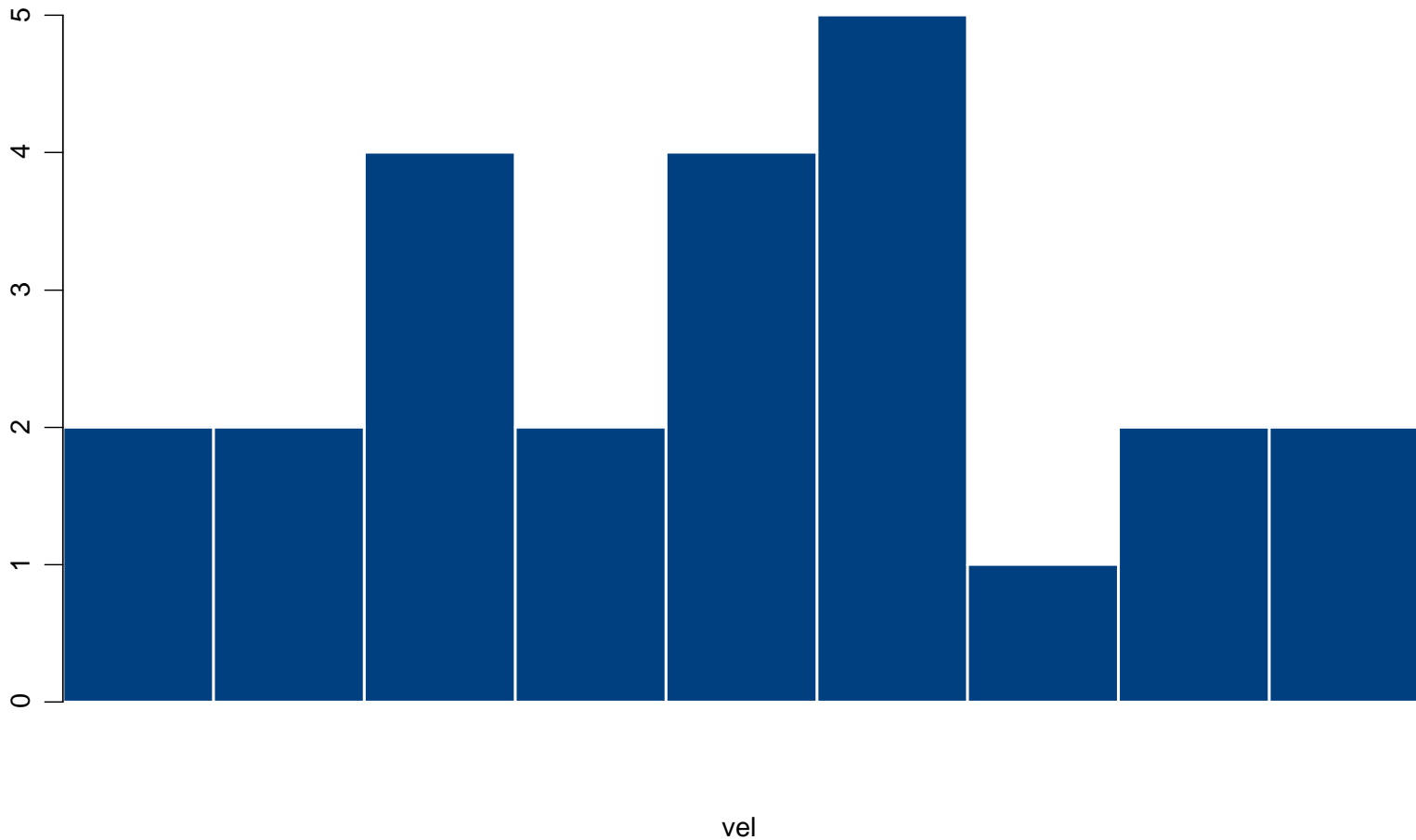
plot.factor(state, vel)



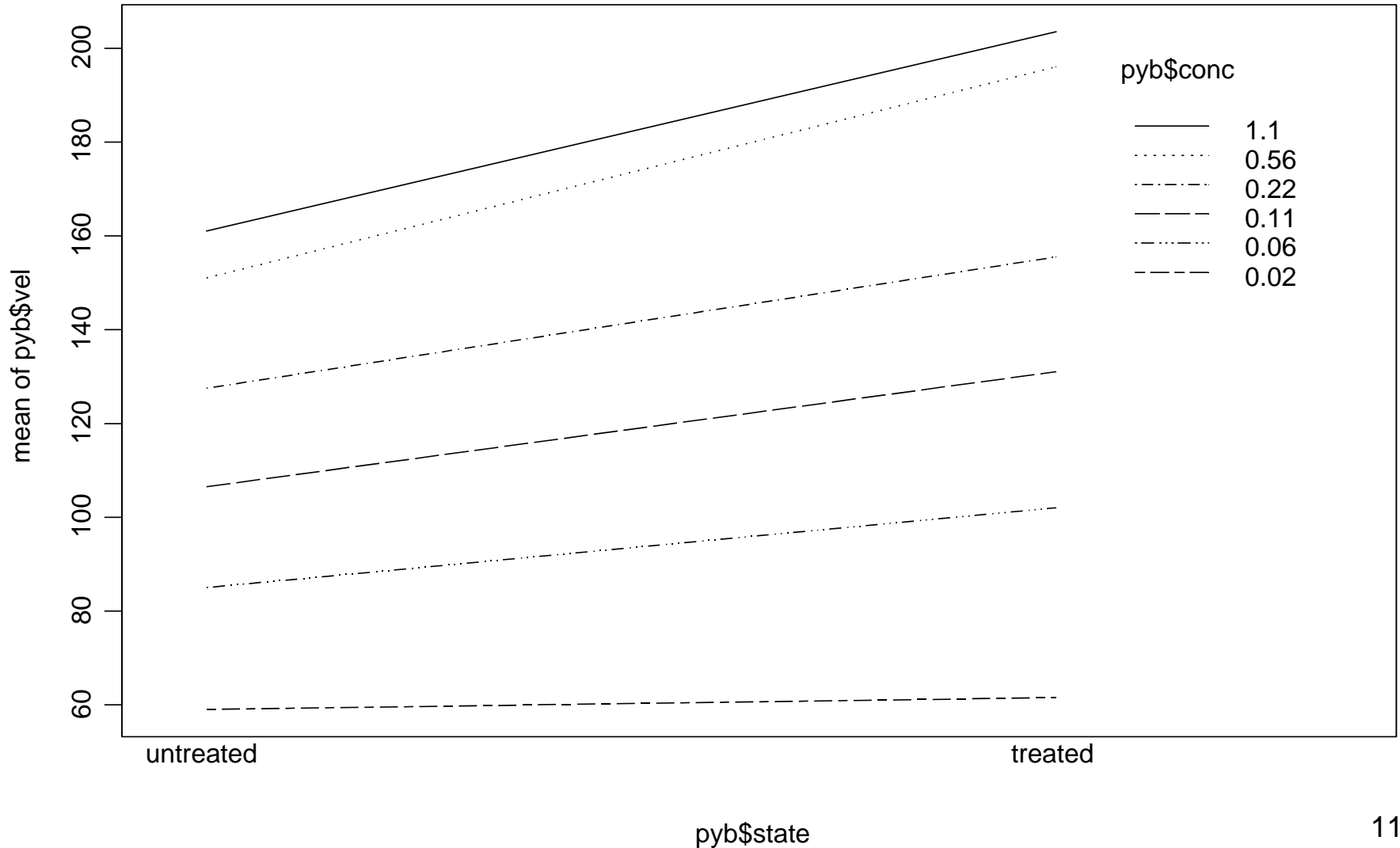
Velocity in “Balanced” puromycin data set

conc	treated		untreated	
0.02	76	47	67	51
0.06	97	107	84	86
0.11	123	139	98	115
0.22	159	152	131	124
0.56	191	201	144	158
1.10	207	200	160	162

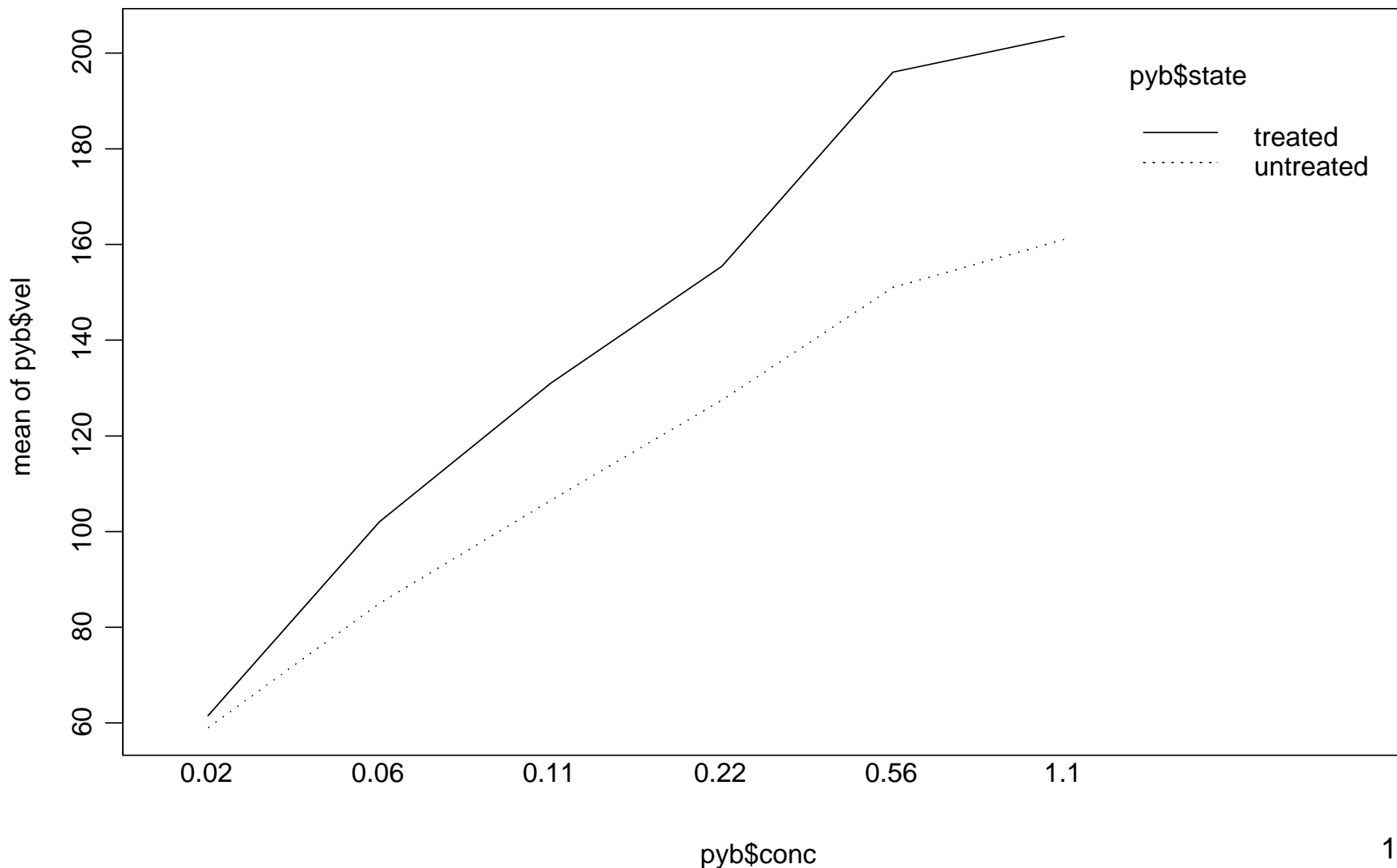
Histogram of velocity



```
interaction.plot(pyb$state,pyb$conc,pyb$vel)
```



interaction.plot(pyb\$conc,pyb\$state,pyb\$vel)



Summaries of puromycin model

Residuals:

Min	1Q	Median	3Q	Max
-14.5	-5	-4.441e-016	5	14.5

Residual standard error: 9.559 on 12 degrees of freedom

Multiple R-Squared: 0.9784

F-statistic: 49.5 on 11 and 12 degrees of freedom, the p-value is 2.919e-008

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
state	1	4240.04	4240.042	46.40264	0.00001871
conc	5	44243.71	8848.742	96.83985	0.00000000
state:conc	5	1270.71	254.142	2.78130	0.06803651
Residuals	12	1096.50	91.375		

Observed velocity and fitted values for puromycin model with interaction

	Observed				Fitted Values			
conc	treated		untreated		treated		untreated	
0.02	76	47	67	51	61.5	61.5	59.0	59.0
0.06	97	107	84	86	102.0	102.0	85.0	85.0
0.11	123	139	98	115	131.0	131.0	106.5	106.5
0.22	159	152	131	124	155.5	155.5	127.5	127.5
0.56	191	201	144	158	196.0	196.0	151.0	151.0
1.10	207	200	160	162	203.5	203.5	161.0	161.0

model.tables

Tables of means

Grand mean

128.29

state

untreated treated

115.00 141.58

conc

0.02 0.06 0.11 0.22 0.56 1.1

60.25 93.50 118.75 141.50 173.50 182.25

state:conc

Dim 1 : state

Dim 2 : conc

0.02 0.06 0.11 0.22 0.56 1.1

untreated 59.0 85.0 106.5 127.5 151.0 161.0

treated 61.5 102.0 131.0 155.5 196.0 203.5

multicomp(pyb.aov,focus="concf")

95 % simultaneous confidence intervals for specified
linear combinations, by the Tukey method

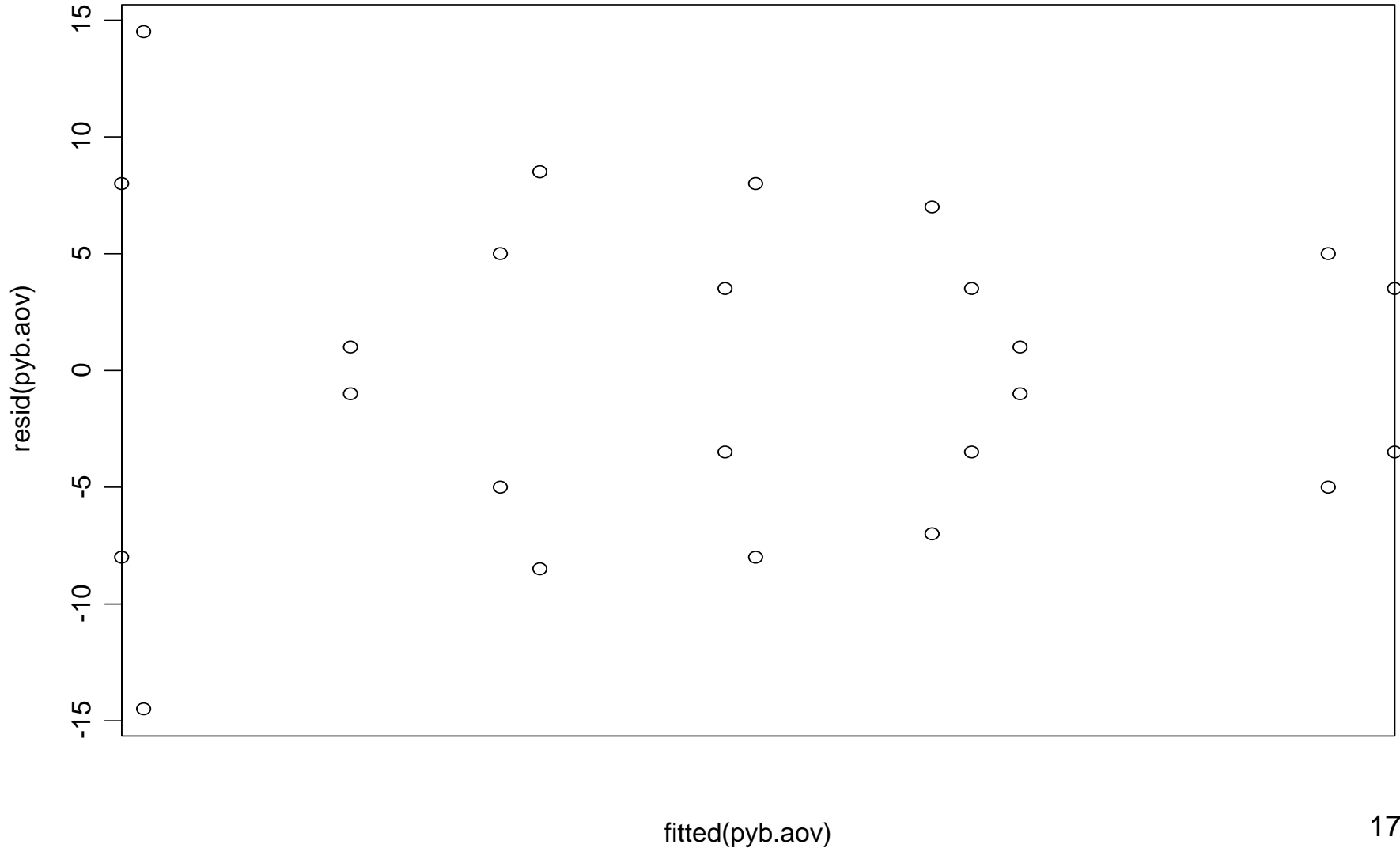
critical point: 3.3595

response variable: vel

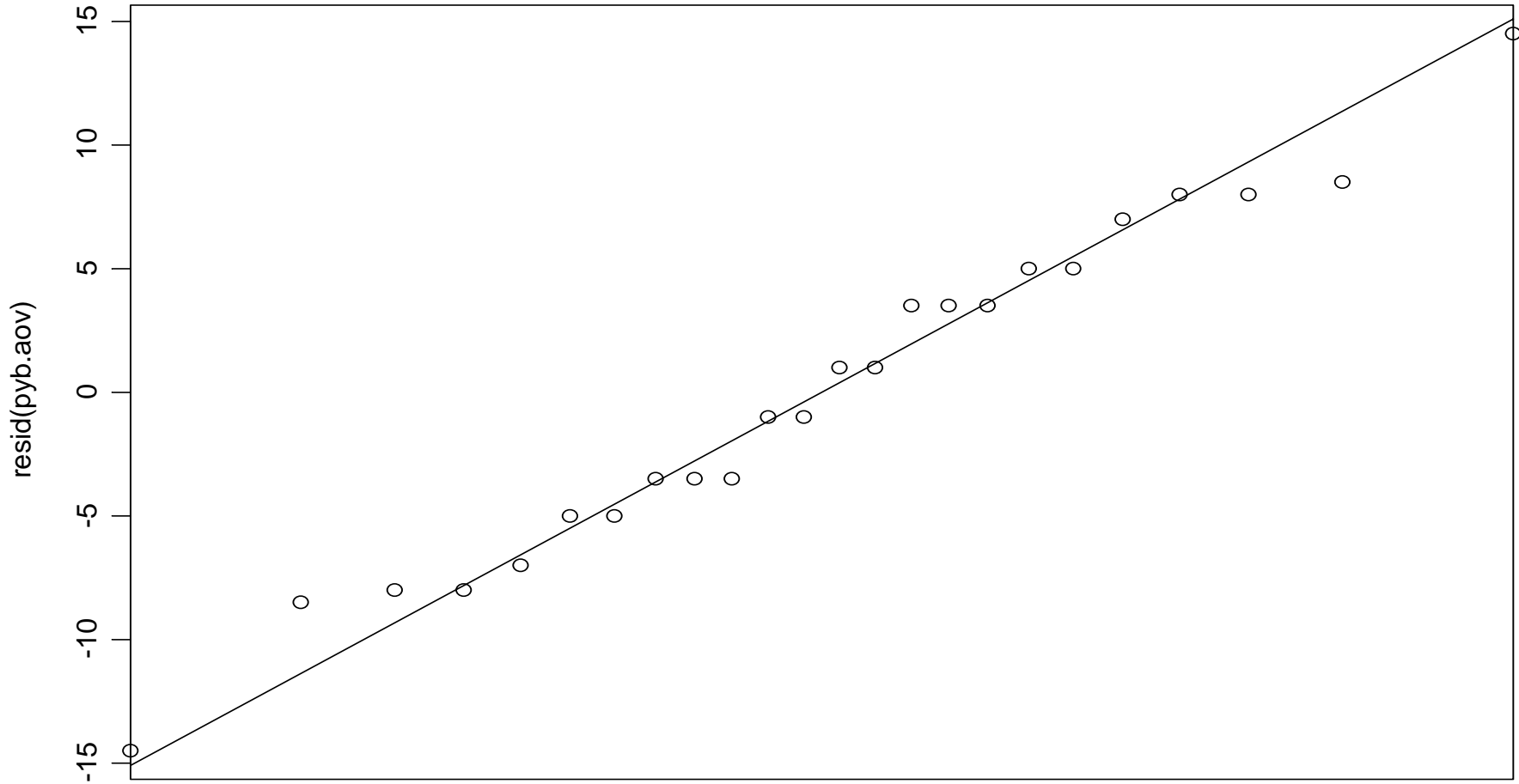
intervals excluding 0 are flagged by '****'

	Estimate	Std.Error	Lower Bound	Upper Bound	
0.02-0.06	-33.20	6.76	-56.0	-10.5000	****
0.02-0.11	-58.50	6.76	-81.2	-35.8000	****
0.02-0.22	-81.20	6.76	-104.0	-58.5000	****
0.02-0.56	-113.00	6.76	-136.0	-90.5000	****
0.02-1.1	-122.00	6.76	-145.0	-99.3000	****
0.06-0.11	-25.30	6.76	-48.0	-2.5400	****
0.06-0.22	-48.00	6.76	-70.7	-25.3000	****
0.06-0.56	-80.00	6.76	-103.0	-57.3000	****
0.06-1.1	-88.70	6.76	-111.0	-66.0000	****
0.11-0.22	-22.70	6.76	-45.5	-0.0425	****
0.11-0.56	-54.70	6.76	-77.5	-32.0000	****
0.11-1.1	-63.50	6.76	-86.2	-40.8000	****
0.22-0.56	-32.00	6.76	-54.7	-9.2900	****
0.22-1.1	-40.70	6.76	-63.5	-18.0000	****
0.56-1.1	-8.75	6.76	-31.5	14.0000	

Residual vs. fit for puromycin model



qqplot of residuals for puromycin model



Summaries of puromycin model without interaction

Residuals:

Min	1Q	Median	3Q	Max
-26.54	-7.083	2.625	4.792	20.04

Residual standard error: 11.8 on 17 degrees of freedom

Multiple R-Squared: 0.9534

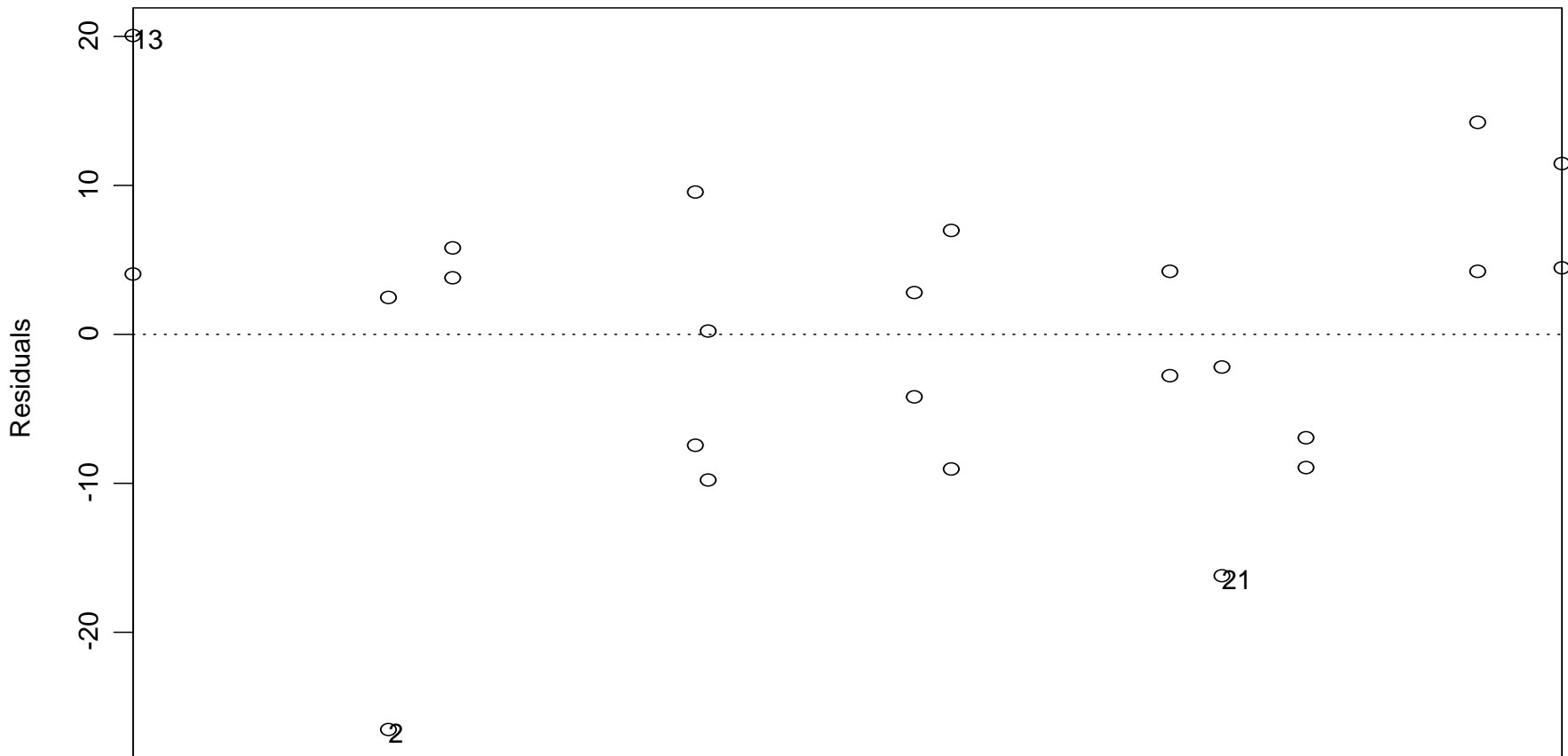
F-statistic: 58.03 on 6 and 17 degrees of freedom, the p-value is 2.18e-010

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
conc	5	44243.71	8848.742	63.54684	0.000000000021
state	1	4240.04	4240.042	30.44967	0.00003762498
Residuals	17	2367.21	139.248		

Observed velocity and fitted values for puromycin model without interaction

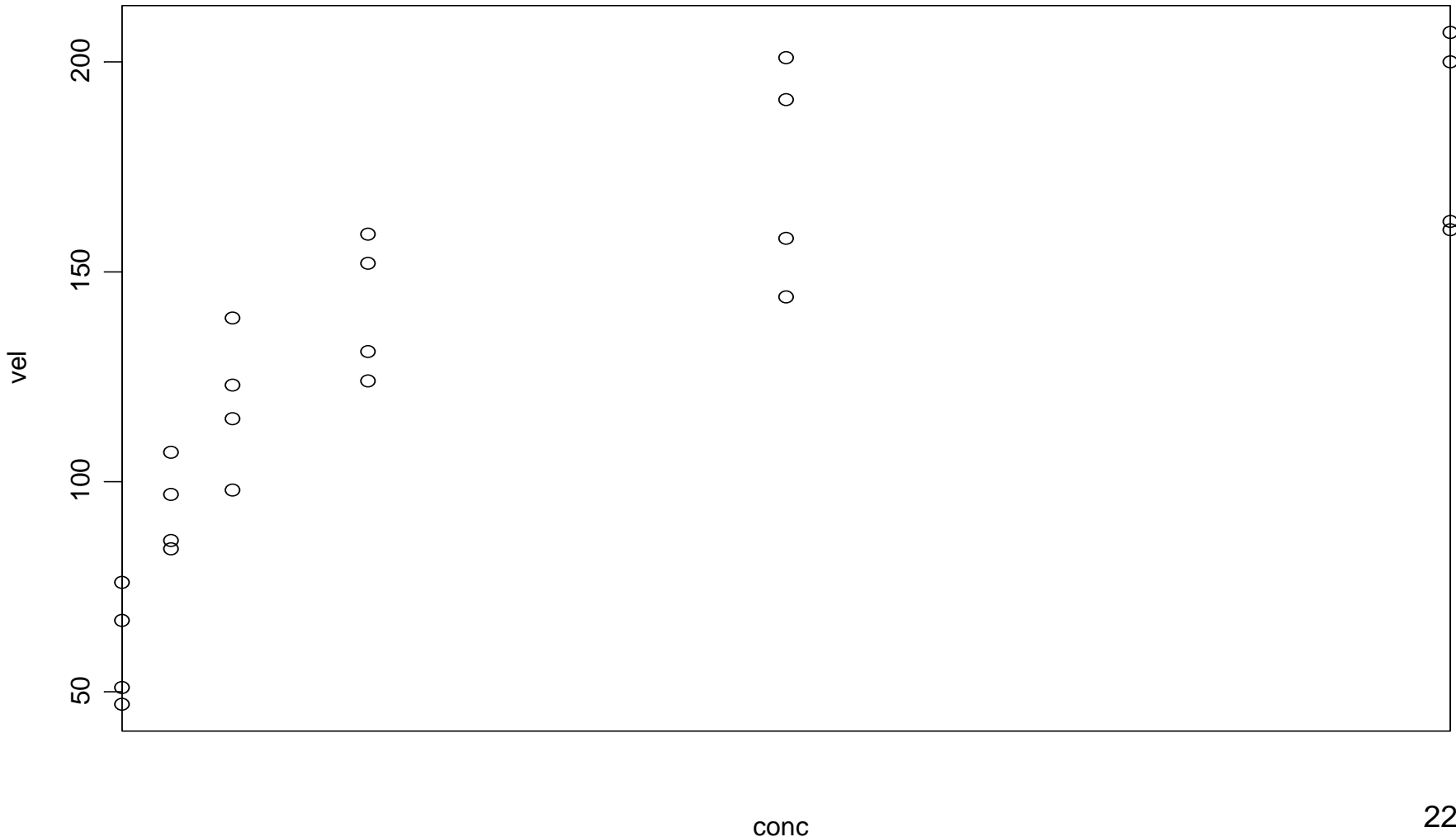
	Observed				Fitted			
conc	treated		untreated		treated		untreated	
0.02	76	47	67	51	73.542	73.542	46.958	46.958
0.06	97	107	84	86	106.792	106.792	80.208	80.208
0.11	123	139	98	115	132.042	132.042	105.458	105.458
0.22	159	152	131	124	154.792	154.792	128.208	128.208
0.56	191	201	144	158	186.792	186.792	160.208	160.208
1.10	207	200	160	162	195.542	195.542	168.958	168.958

Plot of residual vs. fit for puromycin model without interaction



Fitted : conc + state

Plot of velocity vs. concentration



```
Call: aov(formula = vel ~ conc + conc^2 + state)
```

```
Residuals:
```

Min	1Q	Median	3Q	Max
-45.4	-6.93	4.227	7.902	23.94

```
Coefficients:
```

	Value	Std. Error	t value	Pr(> t)
(Intercept)	73.0885	6.0136	12.1539	0.0000
conc	304.9581	37.3027	8.1752	0.0000
I(conc^2)	-188.9327	32.5953	-5.7963	0.0000
state	13.2917	3.4172	3.8897	0.0009

```
Residual standard error: 16.74 on 20 degrees of freedom
```

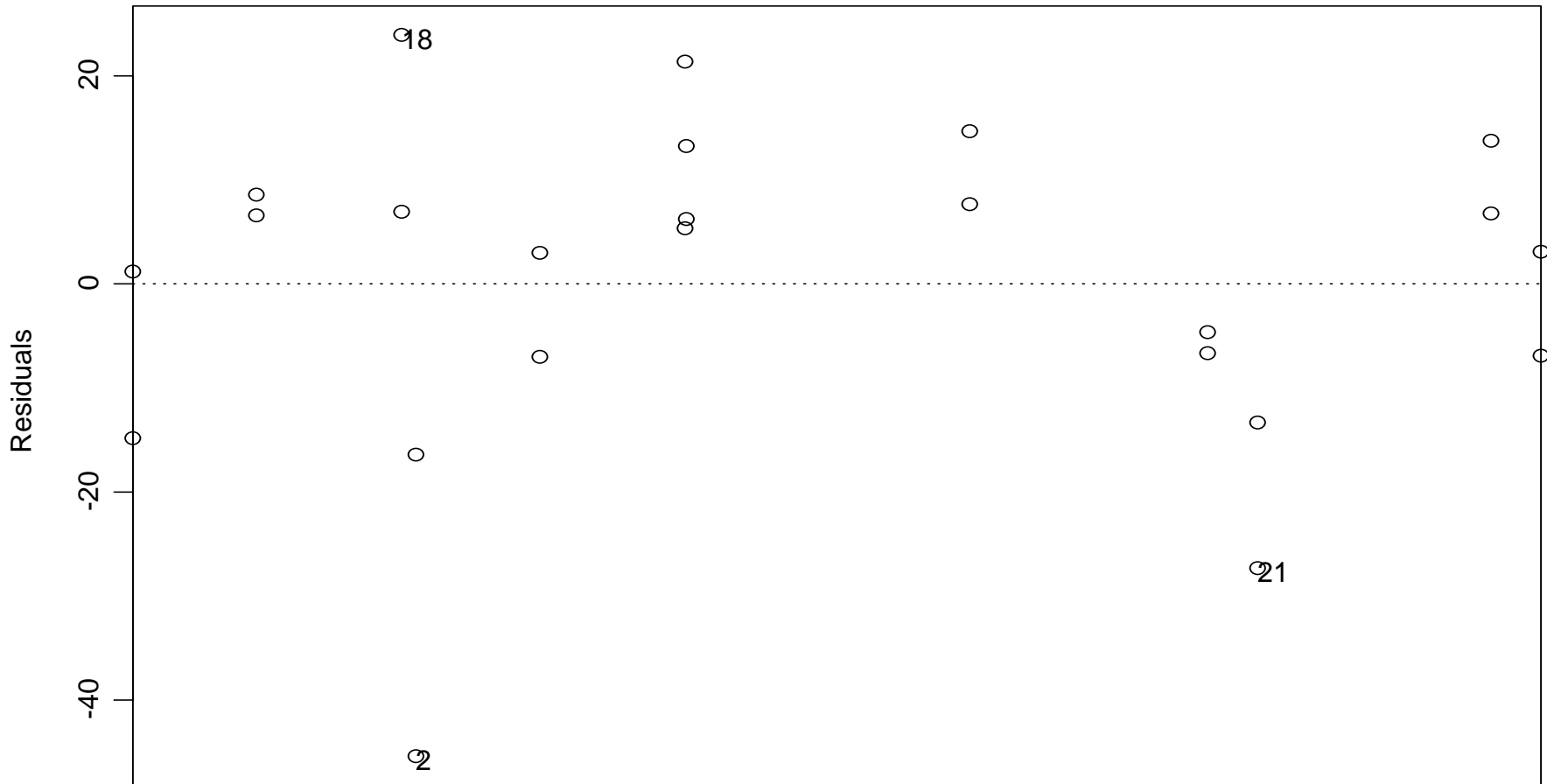
```
Multiple R-Squared: 0.8898
```

```
F-statistic: 53.82 on 3 and 20 degrees of freedom, the p-value is 9.291e-010
```

```
> summary(pyb2.aov)
```

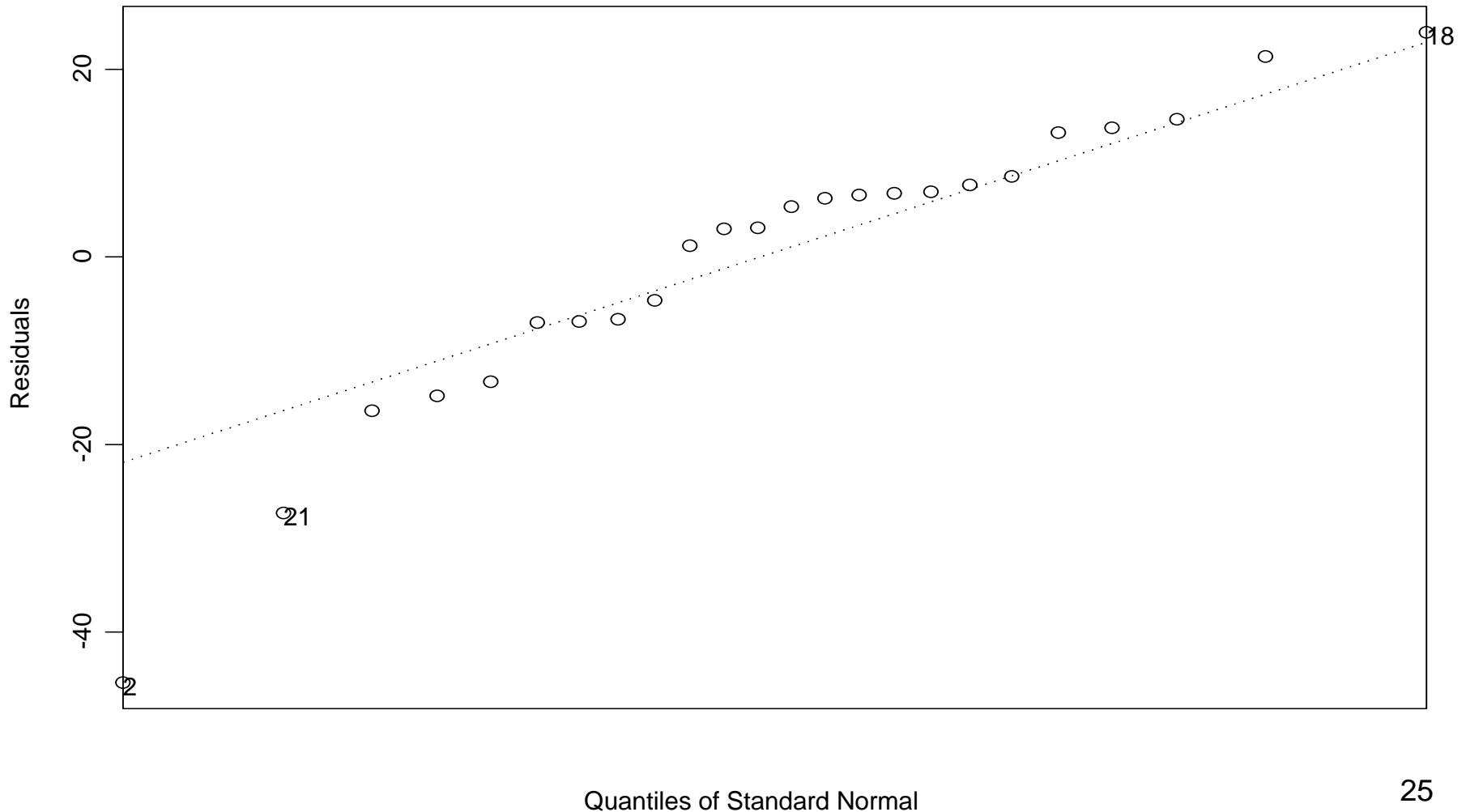
	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
conc	1	31590.27	31590.27	112.7215	0.0000000011
I(conc^2)	1	9415.64	9415.64	33.5972	0.0000113551
state	1	4240.04	4240.04	15.1295	0.0009104989
Residuals	20	5605.01	280.25		

Plot of residual vs. fit for pyb2.aov



Fitted : conc + conc² + state

qqplot of residuals for pyb2.aov



```
Call: aov(formula = vel ~ conc + conc^2 + conc^3 + conc^4
+ conc^5 + state)
```

```
Residuals:
```

Min	1Q	Median	3Q	Max
-26.54	-7.083	2.625	4.792	20.04

```
Coefficients:
```

```
Residual standard error: 11.8 on 17 degrees of freedom
```

```
Multiple R-Squared: 0.9534
```

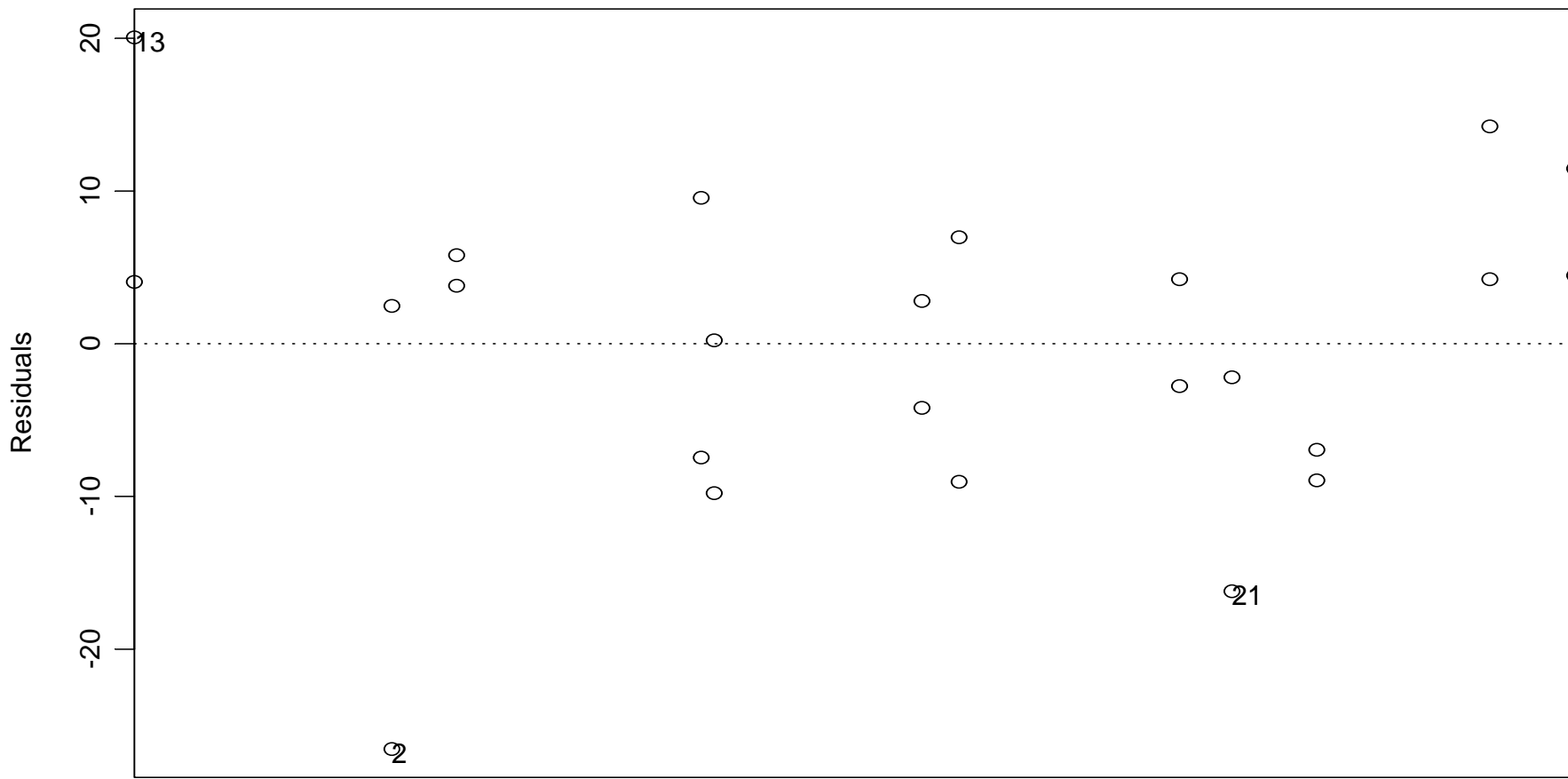
```
F-statistic: 58.03 on 6 and 17 degrees of freedom, the p-  
value is 2.18e-010
```

```
> summary(pyb5.aov)
```

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
conc	1	31590.27	31590.27	226.8641	0.0000000
I(conc^2)	1	9415.64	9415.64	67.6180	0.0000003
I(conc^3)	1	2603.71	2603.71	18.6984	0.0004604
I(conc^4)	1	631.13	631.13	4.5324	0.0481759
I(conc^5)	1	2.96	2.96	0.0213	0.8857934
state	1	4240.04	4240.04	30.4497	0.0000376
Residuals	17	2367.21	139.25		

```
>
```

Plot of residual vs. fit for pyb5.aov

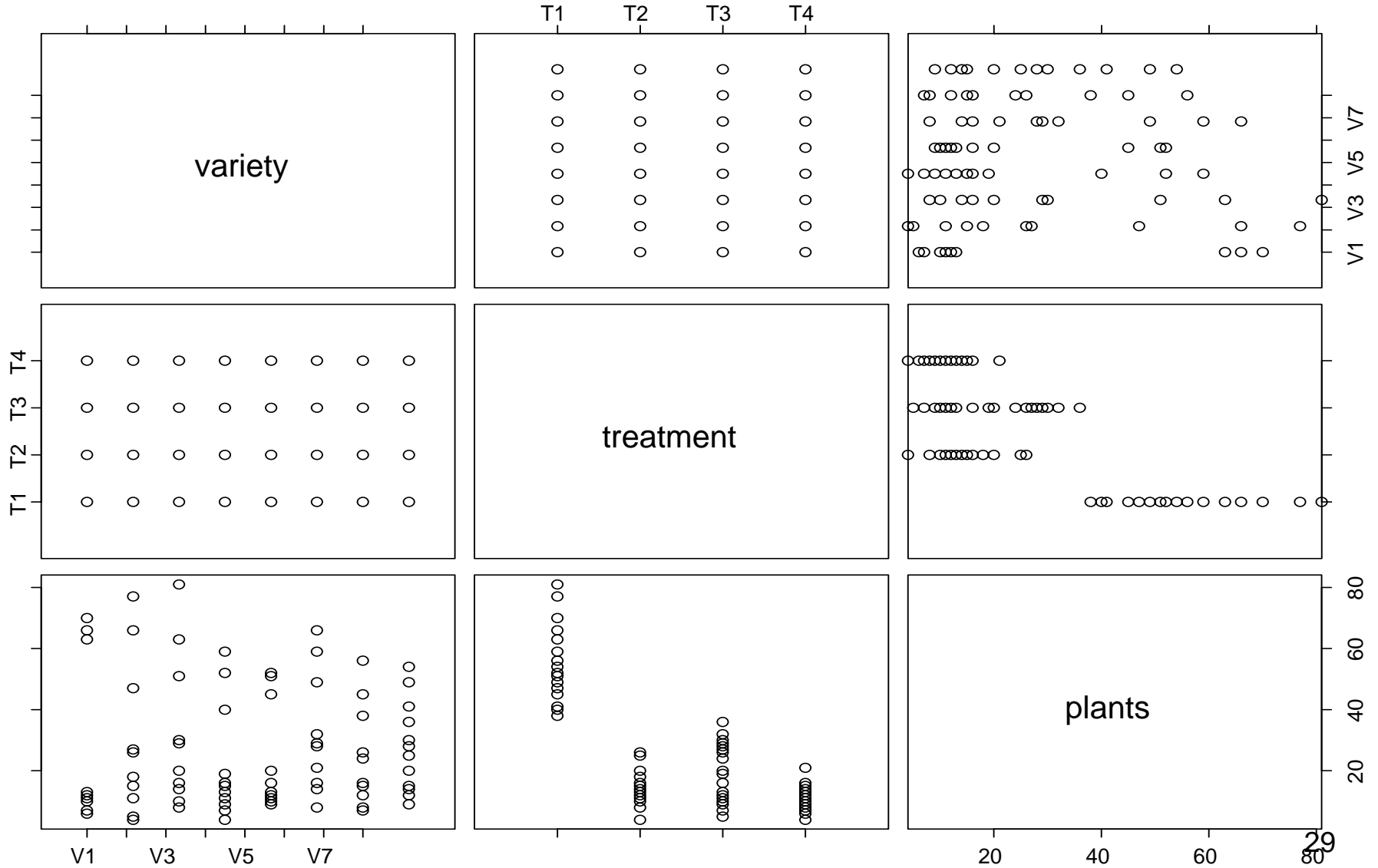


Fitted : conc + conc^2 + conc^3 + conc^4 + conc^5 + state

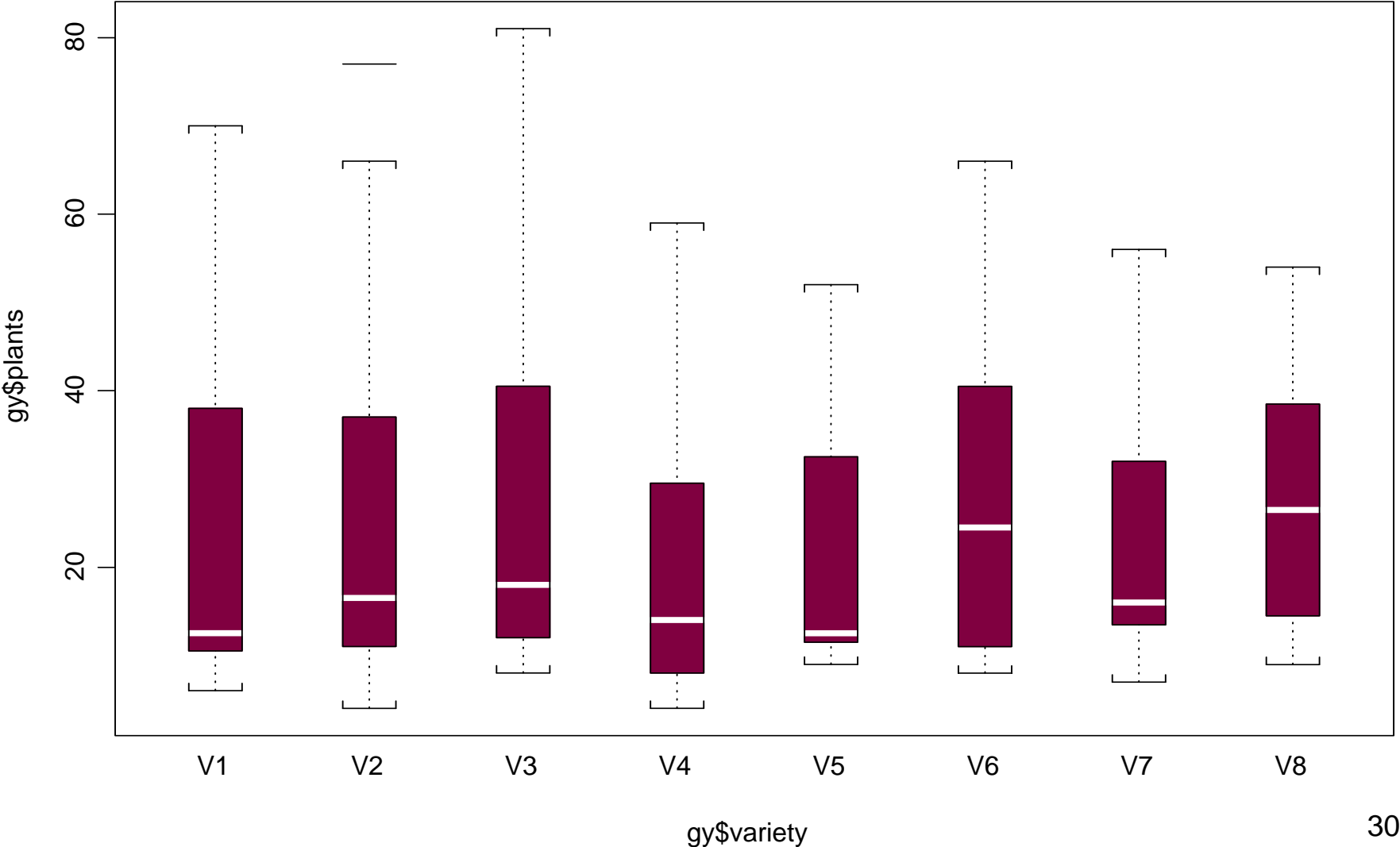
Guayule data set

- **Rate of Germination of Treated Guayule Seeds**
- **SUMMARY:**
- The guayule data frame, a design object, has 96 rows and 5 columns. The guayule is a Mexican plant from which rubber is manufactured. Batches of 100 seeds of eight varieties (`variety`) of guayule were given one of four treatments (`treatment`), and planted; the number of plants that came up in each batch (`plants`) was recorded.
- **ARGUMENTS:**
- **variety**
 - factor with levels V1 through V8 labeling the variety of guayule.
- **treatment**
 - factor with levels T1 through T4 labeling the treatment given to the seeds.
- **plants**
 - numeric vector giving the number seeds out of a batch of 100 that germinated.

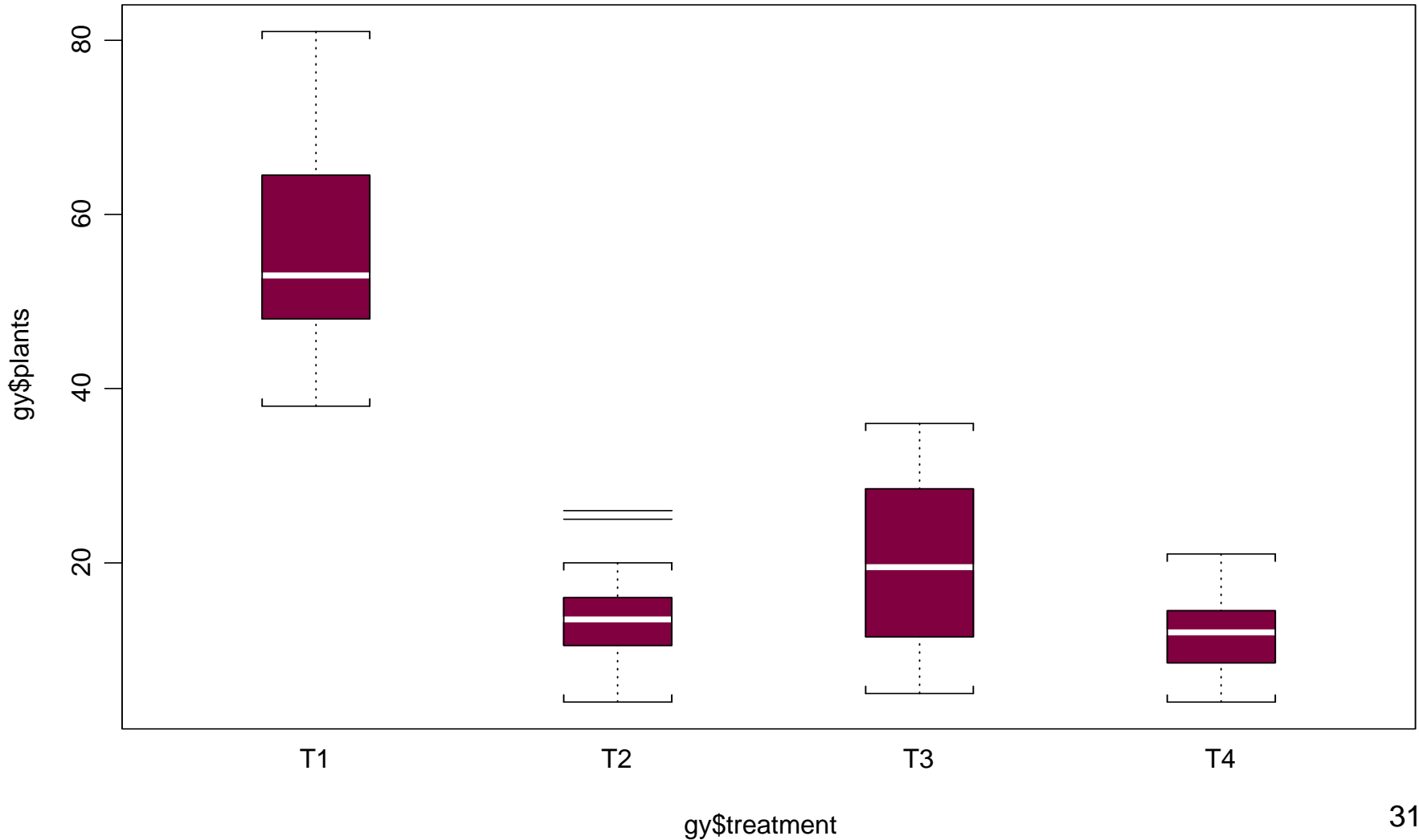
pairs(gy)



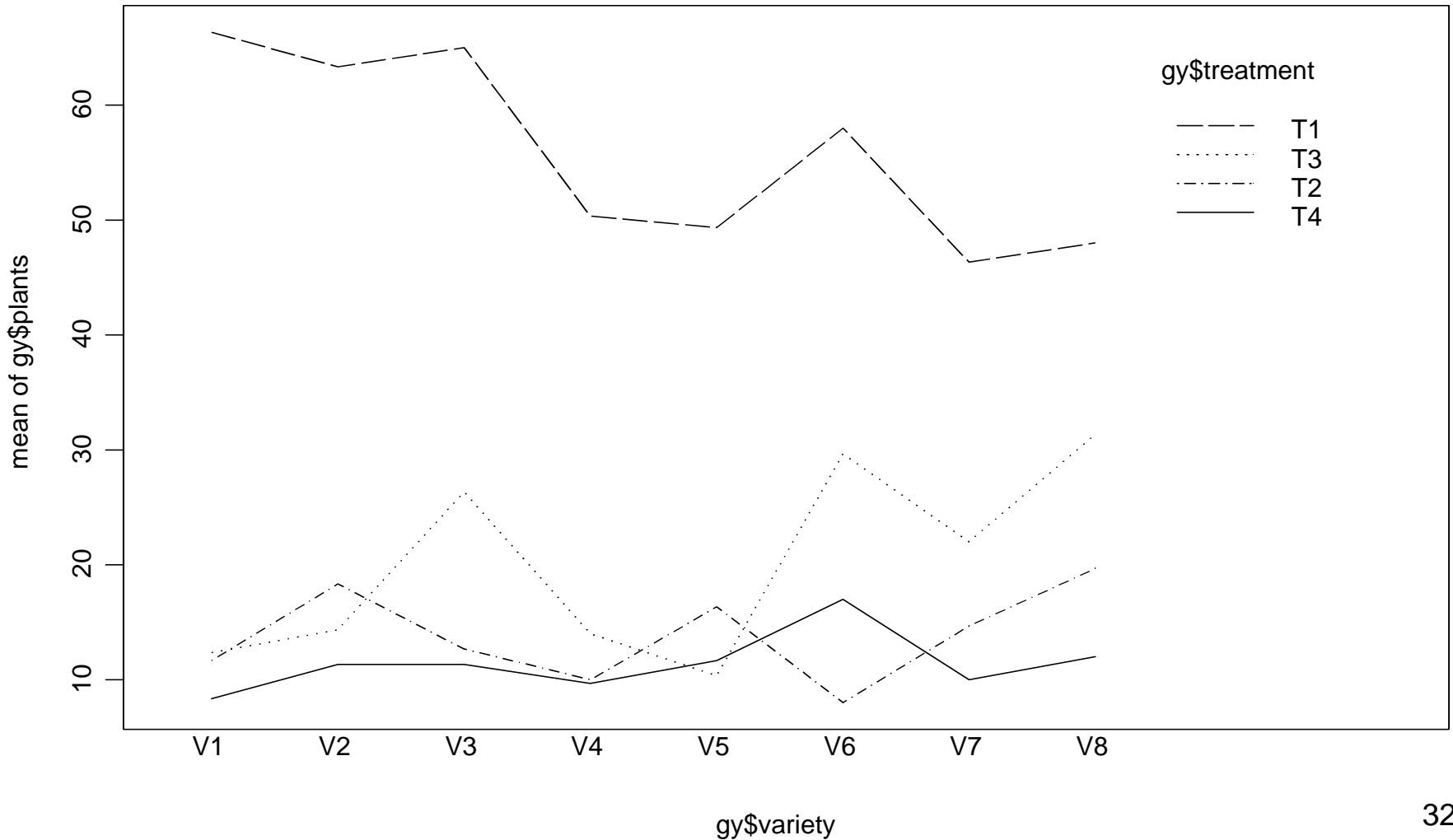
plot.factor(gy\$variety,gy\$plants)



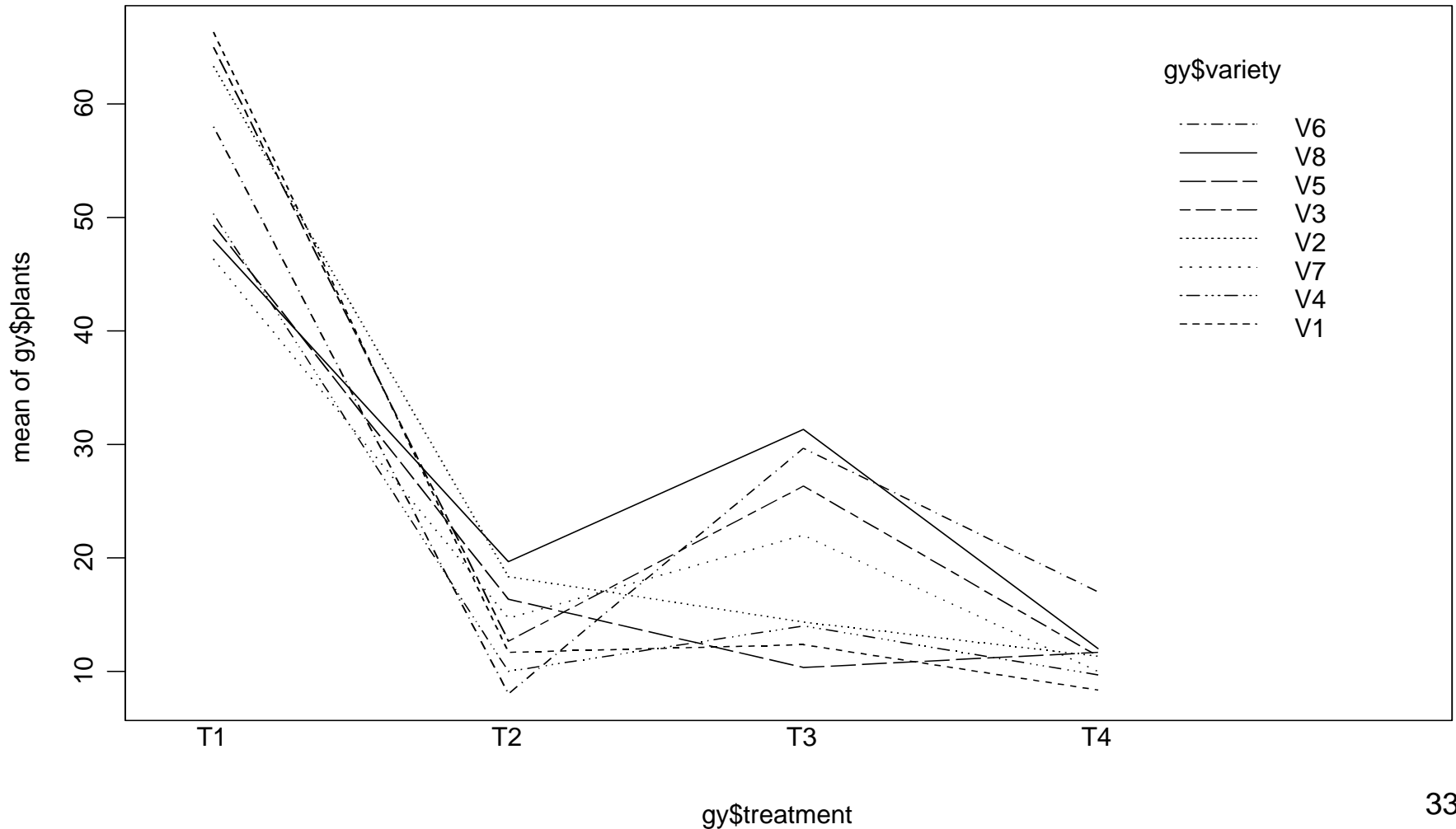
```
plot.factor(gy$treatment,gy$plants)
```



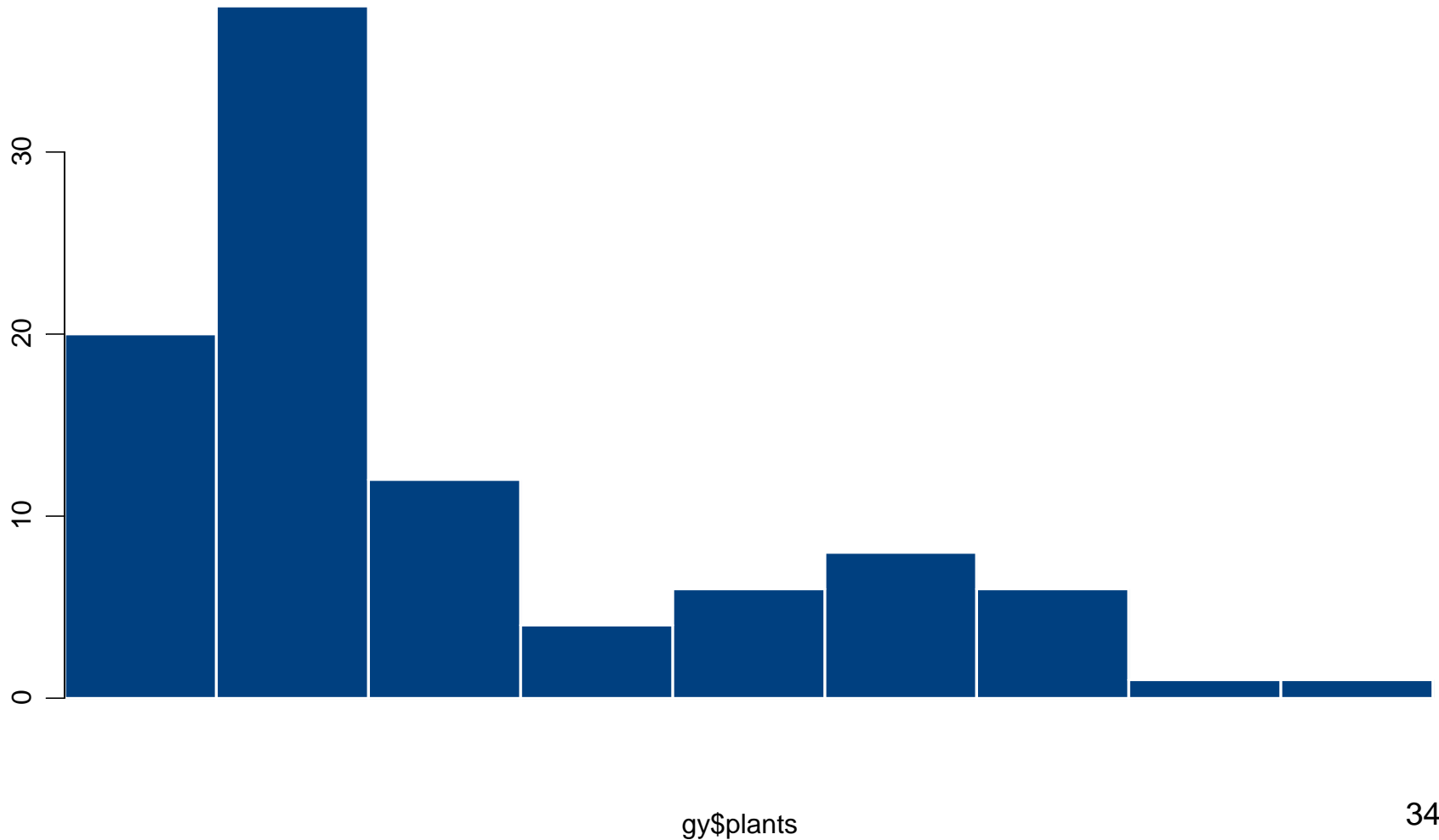
interaction.plot(gy\$variety,gy\$treatment,gy\$plants)




```
interaction.plot(gy$treatment,gy$variety,gy$plants)
```



hist(gy\$plants)



Summaries of gy.aov

```
Call: aov(formula = plants ~ variety * treatment, data = gy)
```

```
Residuals:
```

```
      Min      1Q      Median      3Q      Max
-16.33 -2.667 1.494e-015  2.75   16
```

```
Residual standard error: 6.348 on 64 degrees of freedom
```

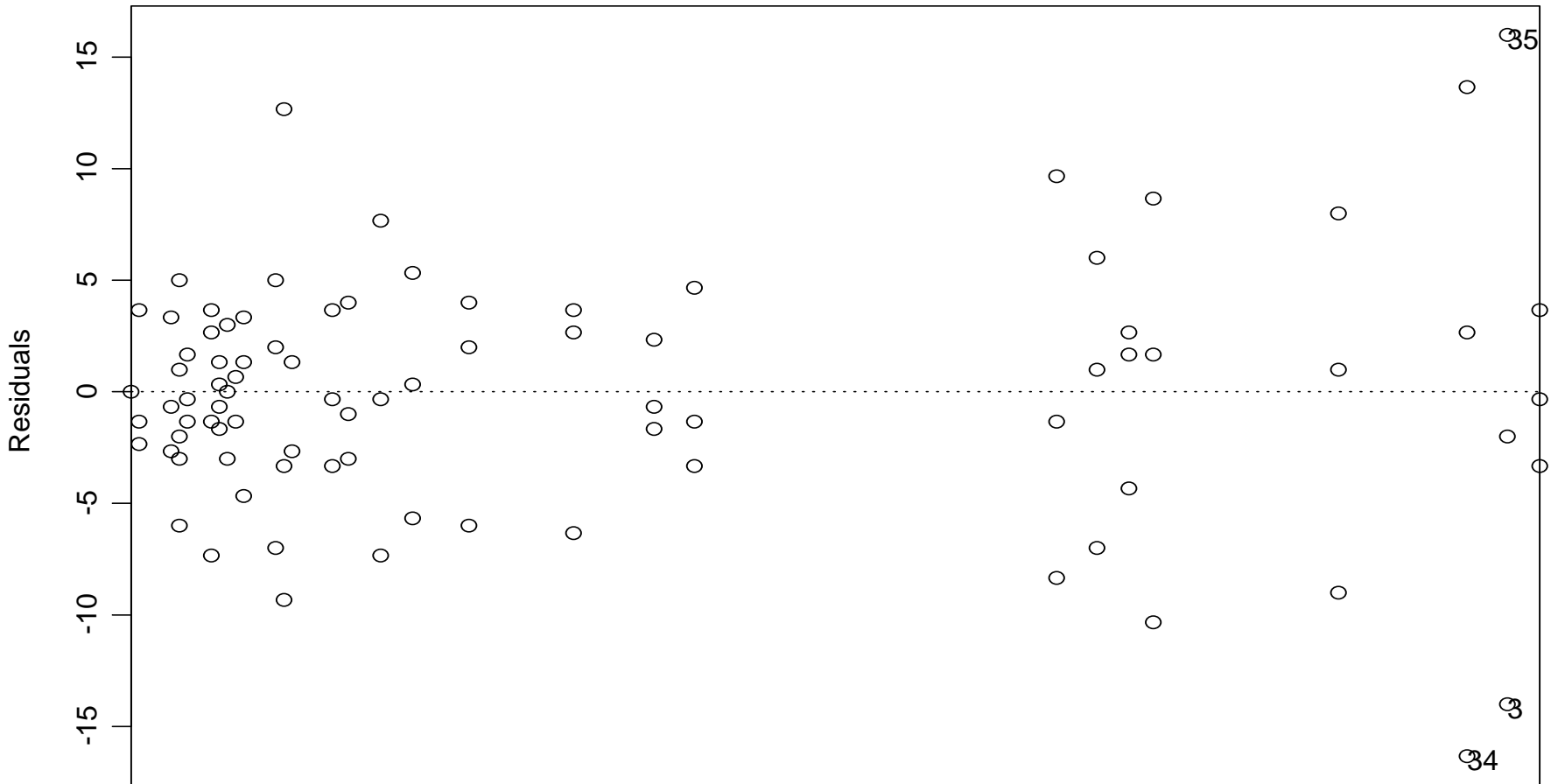
```
Multiple R-Squared: 0.9298
```

```
F-statistic: 27.35 on 31 and 64 degrees of freedom, the p-value is 0
```

```
> summary(gy.aov)
```

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
variety	7	763.16	109.02	2.7058	0.01604076
treatment	3	30774.28	10258.09	254.5959	0.00000000
variety:treatment	21	2620.14	124.77	3.0966	0.00026666
Residuals	64	2578.67	40.29		

Plot of residual vs. fit for gy data set



Fitted : variety * treatment

model.tables(gy.aov,type="mean")

Tables of means

Grand mean

25.302

variety

V1	V2	V3	V4	V5	V6	V7	V8
24.667	26.833	28.833	21.000	21.917	28.167	23.250	27.750

treatment

T1	T2	T3	T4
55.833	13.917	20.042	11.417

model.tables(gy.aov,type="mean")

```
variety:treatment
Dim 1 : variety
Dim 2 : treatment
      T1      T2      T3      T4
V1 66.333 11.667 12.333  8.333
V2 63.333 18.333 14.333 11.333
V3 65.000 12.667 26.333 11.333
V4 50.333 10.000 14.000  9.667
V5 49.333 16.333 10.333 11.667
V6 58.000  8.000 29.667 17.000
V7 46.333 14.667 22.000 10.000
V8 48.000 19.667 31.333 12.000
```

```
multicomp(gy.aov, focus="treatment")
```

95 % simultaneous confidence intervals for specified linear combinations, by the Tukey method

critical point: 2.6378

response variable: plants

intervals excluding 0 are flagged by '****'

	Estimate	Std.Error	Lower Bound	Upper Bound	
T1-T2	41.90	1.83	37.10	46.80	****
T1-T3	35.80	1.83	31.00	40.60	****
T1-T4	44.40	1.83	39.60	49.30	****
T2-T3	-6.12	1.83	-11.00	-1.29	****
T2-T4	2.50	1.83	-2.33	7.33	
T3-T4	8.62	1.83	3.79	13.50	****

Guayule ANOVA with variety random

```
> gyr.tab
```

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
treatment	3	30774.28	10258.09	82.21711	0.0000000
variety	7	763.16	109.02	0.87380	0.5428964
treatment:variety	21	2620.14	124.77	3.09663	0.0002667
Residuals	64	2578.67	40.29		

Random if:

- Not interested in those particular factor levels (e.g. batches)
- Levels of factor are randomly chosen from a larger population of factor levels (e.g. 10 universities selected from all universities in country).
- Want to generalize to a larger population of factor levels.

EMS for 2-factor models

(See Table 24.5 on page 981 of Neter et al. *Applied Linear Statistical Models*.)

Nested vs. Crossed Design

(See Figure 28.1 in Neter et al. *Applied Linear Statistical Models*.)

Nested Fixed Factors

(See Table 28.3 on page 1129 of Neter et al. *Applied Linear Statistical Models*.)

Nested Mixed Factors

(See Table 28.5 on page 1133 of Neter et al. *Applied Linear Statistical Models*.)

Cross-Nested Models

(See Table 28.11 on page 1151 of Neter et al. *Applied Linear Statistical Models*.)

Images of book covers:

Patrick O'Brian, *The Commodore*.

Patrick O'Brian, *The Fortune of War*.

Nested Factors

- **Speed of Firing Naval Guns**
- **SUMMARY:**
- The gun data frame, a design object, has 36 rows representing runs of a team of 3 men loading and firing naval guns attempting to get off as many rounds per minute as possible. The three predictor variables (columns) specify the team and the physique of the men on it and the loading method used; the outcome variable is the rounds fired per minute.
- **ARGUMENTS:**
- **Method**
 - factor giving one of two methods for loading rounds into Naval guns. Levels are M1 and M2 .
- **Physique**
 - an ordered factor giving the physique of the men: S for slight, A for average, and H for heavy.
- **Team**
 - factor with levels T1 , T2 or T3 . In fact there are nine teams, three of each physique, i.e. a slight T1 , an average T1 , and a heavy T1 , etc.
- **Rounds**
 - numeric vector giving the number of rounds per minute fired by a team.

gun

	Method	Physique	Team	Rounds
1	M1	S	T1	20.2
2	M2	S	T1	14.2
3	M1	A	T1	22.0
4	M2	A	T1	14.1
5	M1	H	T1	23.1
6	M2	H	T1	14.1
7	M1	S	T2	26.2
8	M2	S	T2	18.0
9	M1	A	T2	22.6
10	M2	A	T2	14.0
11	M1	H	T2	22.9
12	M2	H	T2	12.2
13	M1	S	T3	23.8
14	M2	S	T3	12.5
15	M1	A	T3	22.9
16	M2	A	T3	13.7
17	M1	H	T3	21.8
18	M2	H	T3	12.7
19	M1	S	T1	24.1
20	M2	S	T1	16.2

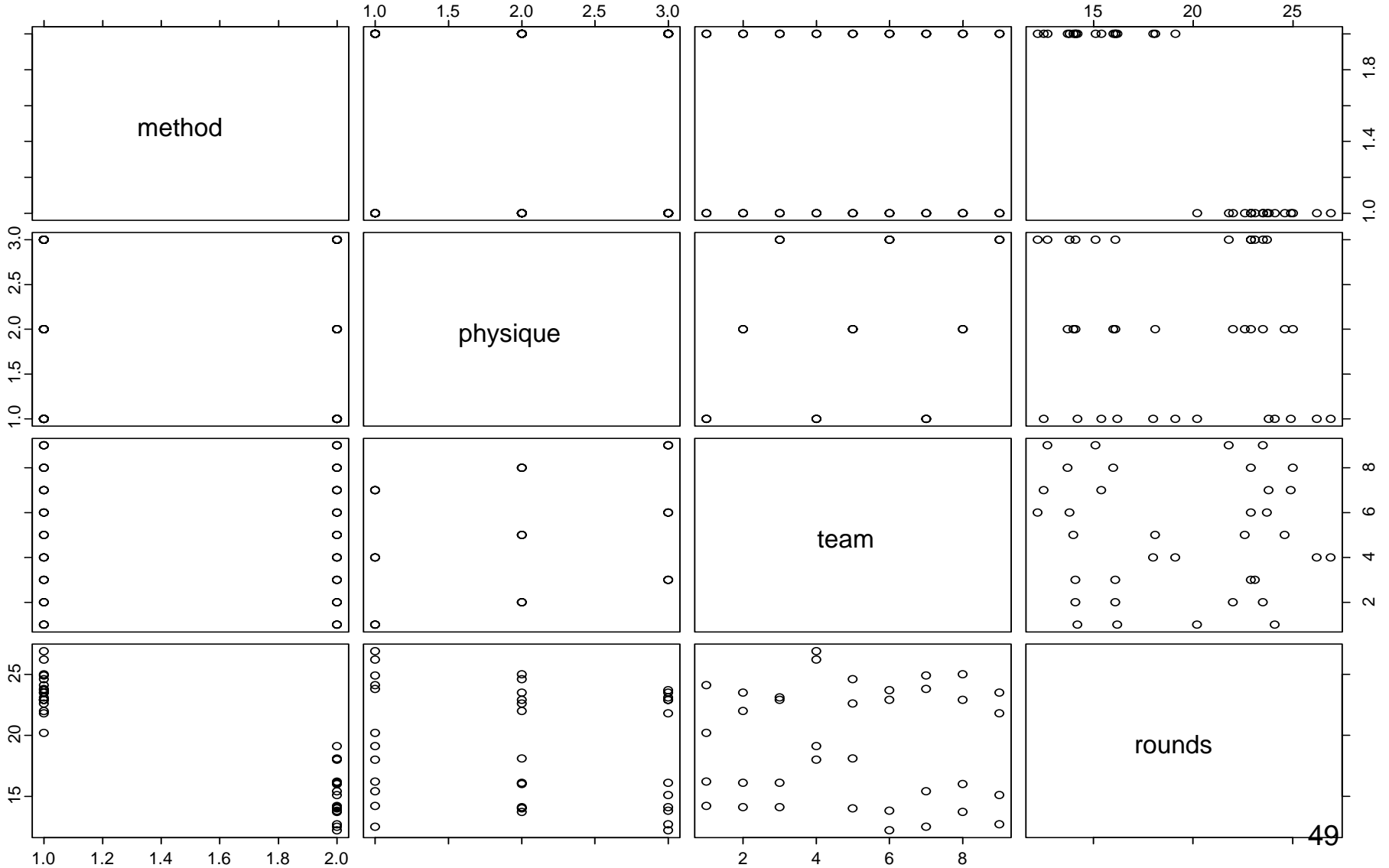
gun

	Method	Physique	Team	Rounds
1	M1	S	T1	20.2
2	M2	S	T1	14.2
3	M1	A	T2	22.0
4	M2	A	T2	14.1
5	M1	H	T3	23.1
6	M2	H	T3	14.1
7	M1	S	T4	26.2
8	M2	S	T4	18.0
9	M1	A	T5	22.6
10	M2	A	T5	14.0
11	M1	H	T6	22.9
12	M2	H	T6	12.2
13	M1	S	T7	23.8
14	M2	S	T7	12.5
15	M1	A	T8	22.9
16	M2	A	T8	13.7
17	M1	H	T9	21.8
18	M2	H	T9	12.7
19	M1	S	T1	24.1
20	M2	S	T1	16.2

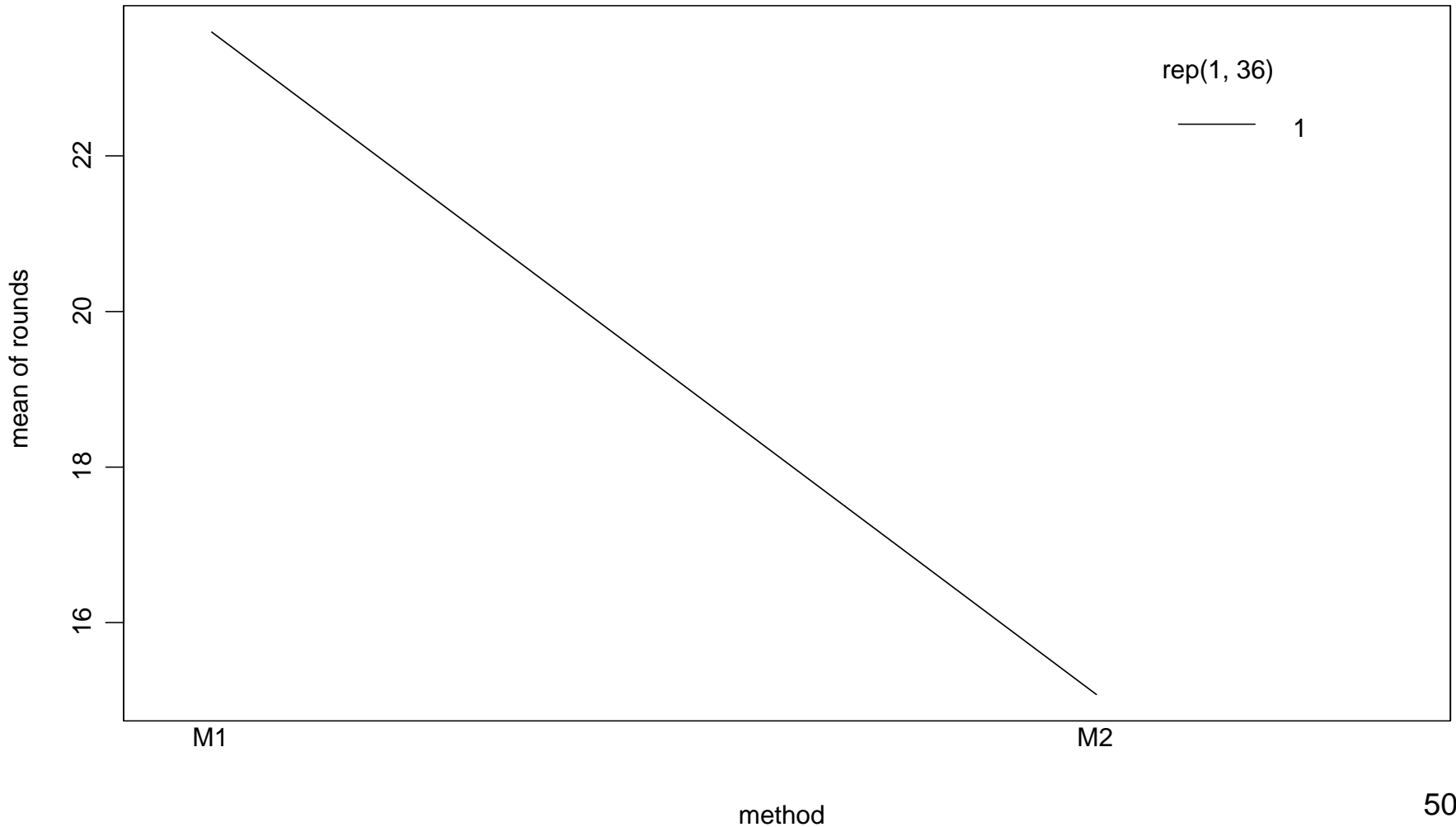
Speed of firing of naval guns

	Slight	Average	Heavy
Method 1	T1: 20.2, 24.1 T4: 26.2, 26.9 T7: 23.8, 24.9	T2: 22.0, 23.5 T5: 22.6, 24.6 T8: 22.9, 25.0	T3: 23.1, 22.9 T6: 22.9, 23.7 T9: 21.8, 23.5
Method 2	T1: 14.2, 16.2 T4: 18.0, 19.1 T7: 12.5, 15.4	T2: 14.1, 16.1 T5: 14.0, 18.1 T8: 13.7, 16.0	T3: 14.1, 16.1 T6: 12.2, 13.8 T9: 12.7, 15.1

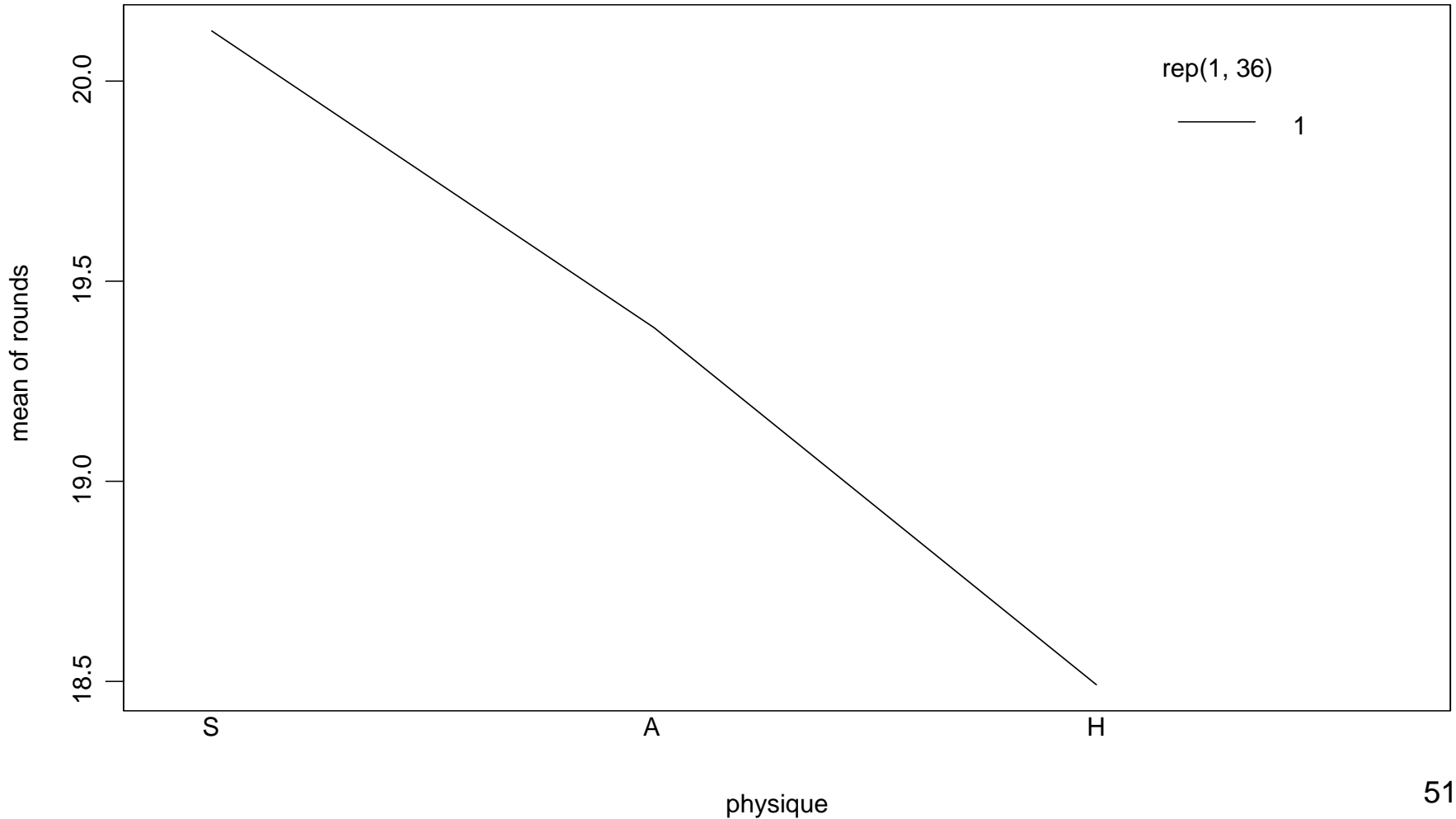
pairs(gun2)



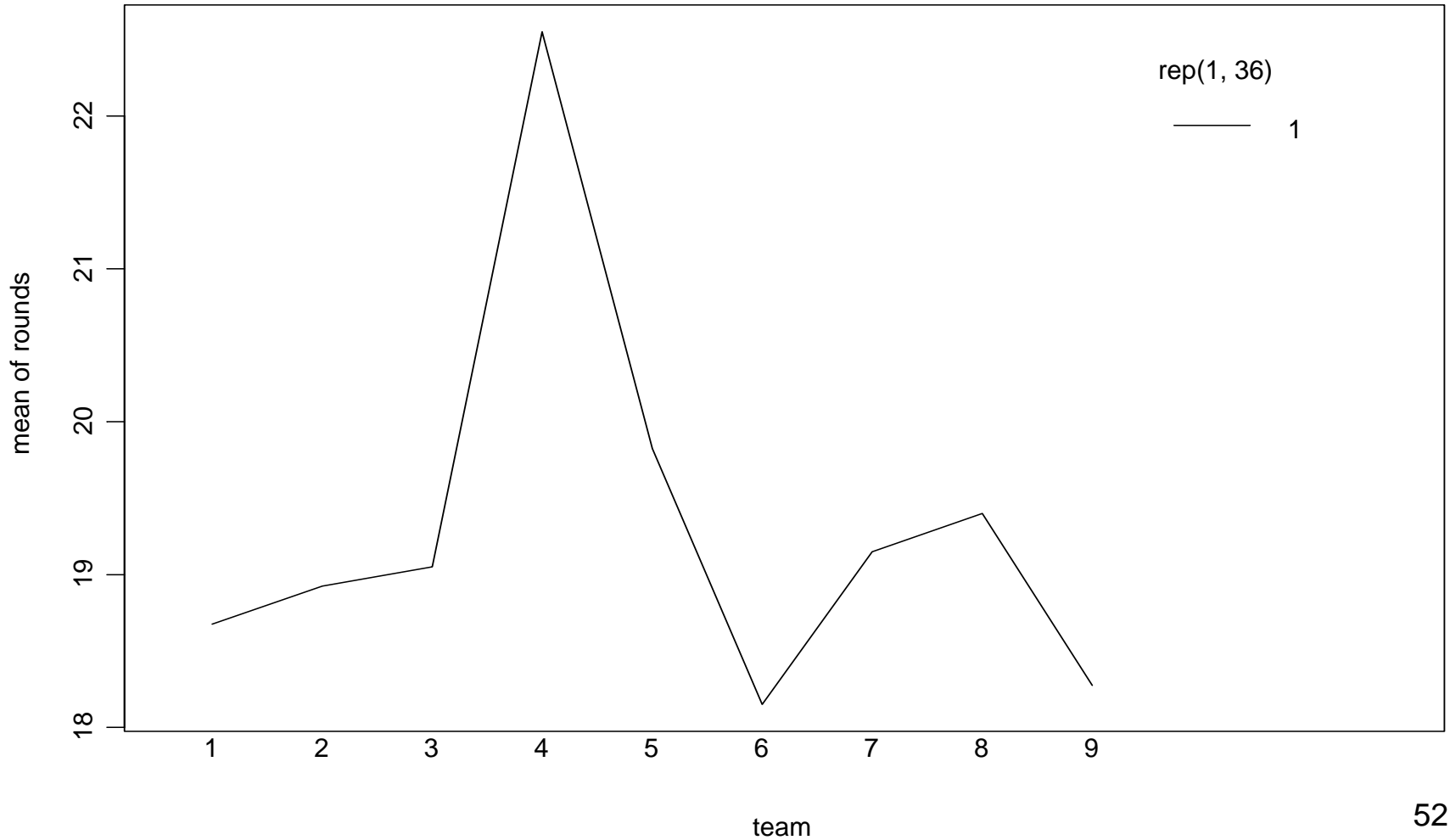
Method Effect



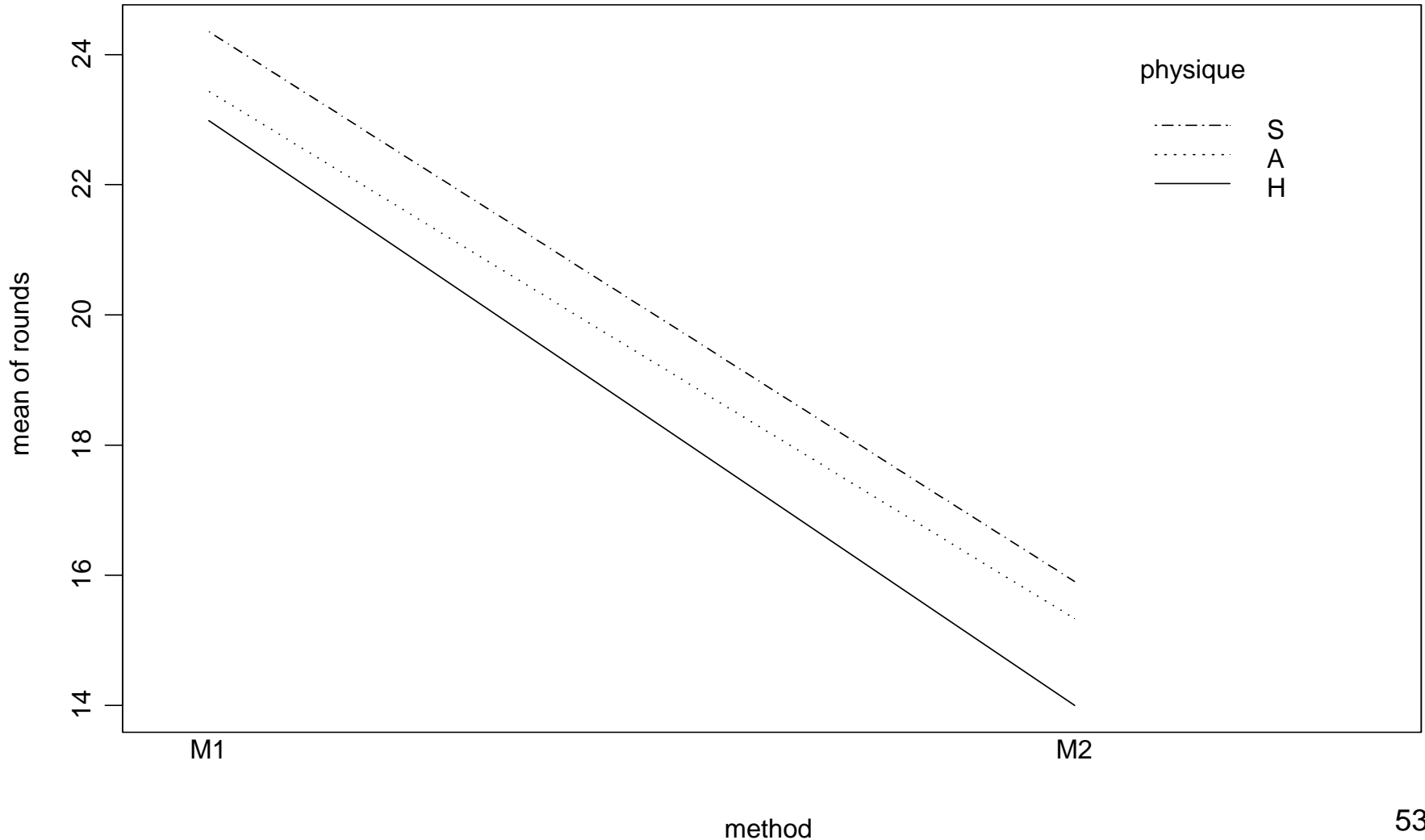
Physique Effect



Team Effect



Method-Physique Interaction



ANOVA tables for firing of naval guns example (with teams numbered 1-9)

```
> summary(aov(rounds~phys*meth*team))
```

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
phys	2	16.0517	8.0258	3.4736	0.0529995
meth	1	651.9511	651.9511	282.1621	0.0000000
team	6	39.2583	6.5431	2.8318	0.0403140
phys:meth	2	1.1872	0.5936	0.2569	0.7762240
meth:team	6	10.7217	1.7869	0.7734	0.6009376
Residuals	18	41.5900	2.3106		

```
> summary(aov(rounds~phys*meth*team%in%phys))
```

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
phys	2	16.0517	8.0258	3.4736	0.0529995
meth	1	651.9511	651.9511	282.1621	0.0000000
phys:meth	2	1.1872	0.5936	0.2569	0.7762240
team %in% phys	6	39.2583	6.5431	2.8318	0.0403140
meth:(team %in% phys)	6	10.7217	1.7869	0.7734	0.6009376
Residuals	18	41.5900	2.3106		

```
> model.tables(gunaov, type="mean")
```

```
Tables of means
```

```
Grand mean
```

```
19.333
```

```
Method
```

```
    M1    M2
```

```
23.589 15.078
```

```
Physique
```

```
    S    A    H
```

```
20.125 19.383 18.492
```

```
Team %in% Physique
```

```
Dim 1 : Physique
```

```
Dim 2 : Team
```

```
    T1    T2    T3
```

```
S 18.675 22.550 19.150
```

```
A 18.925 19.825 19.400
```

```
H 19.050 18.150 18.275
```

Tables of means

Grand mean

19.333

method

	M1	M2
	23.589	15.078
rep	18.000	18.000

physique

	S	A	H
	20.125	19.383	18.492
rep	12.000	12.000	12.000

team %in% physique

Dim 1 : physique

Dim 2 : team

	1	2	3	4	5	6	7	8	9
S	18.675			22.550			19.150		
rep	4.000	0.000	0.000	4.000	0.000	0.000	4.000	0.000	0.000
A		18.925			19.825			19.400	
rep	0.000	4.000	0.000	0.000	4.000	0.000	0.000	4.000	0.000
H			19.050			18.150			18.275
rep	0.000	0.000	4.000	0.000	0.000	4.000	0.000	0.000	4.000

Summaries of firing of naval guns example (without interaction)

```
Call: aov(formula = Rounds ~ Method + Physique/Team, data = gun)
```

```
Residuals:
```

```
      Min      1Q      Median      3Q      Max
-2.731 -0.7368 2.498e-016 0.9972 2.531
```

```
Residual standard error: 1.434 on 26 degrees of freedom
```

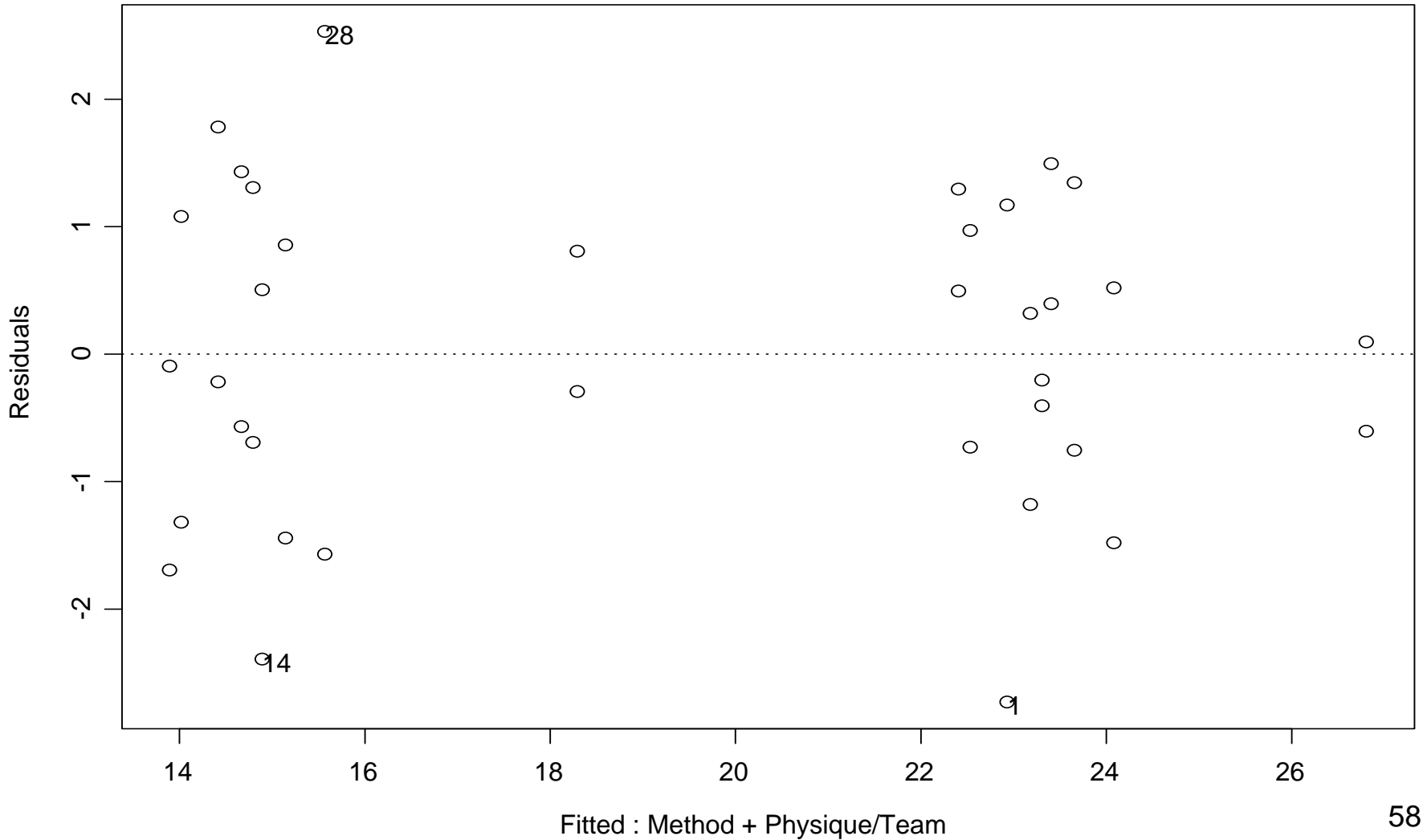
```
Multiple R-Squared: 0.9297
```

```
F-statistic: 38.19 on 9 and 26 degrees of freedom, the p-value is
9.602e-013
```

```
> summary(gunaov)
```

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
Method	1	651.9511	651.9511	316.8426	0.00000000
Physique	2	16.0517	8.0258	3.9005	0.03300457
Team %in% Physique	6	39.2583	6.5431	3.1799	0.01782181
Residuals	26	53.4989	2.0576		

Plot of residual vs fit for gun.aov



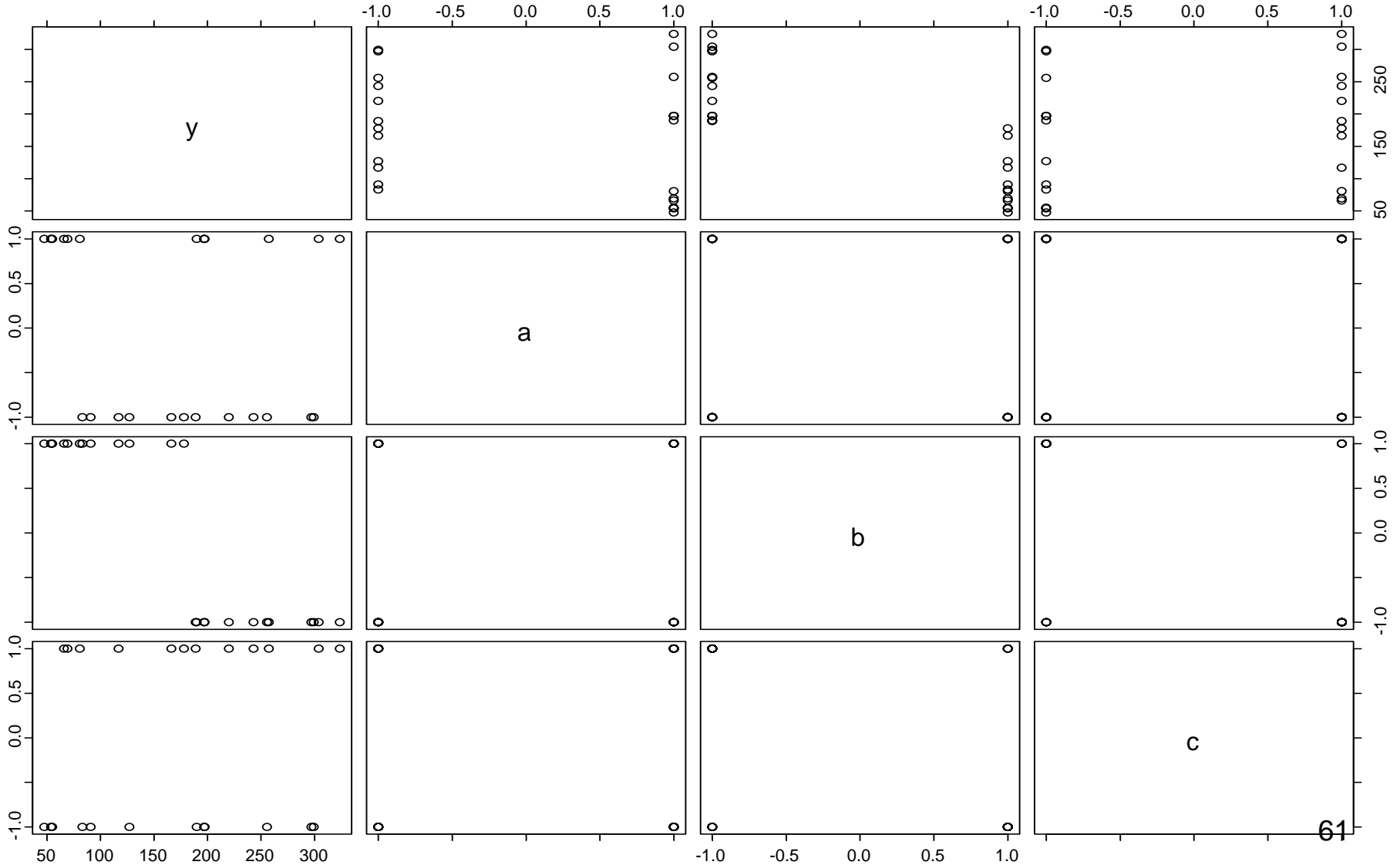
2^k Factorial Designs

- Exploratory experimental studies.
- Multifactor experiment in which each factor studied at two levels.
- Used to screen large number of factors to identify the most important.
- Sometimes 2 levels naturally occur e.g. present or absent, smoker or non-smoker
- k factors $\Rightarrow 2^k$ treatment combinations

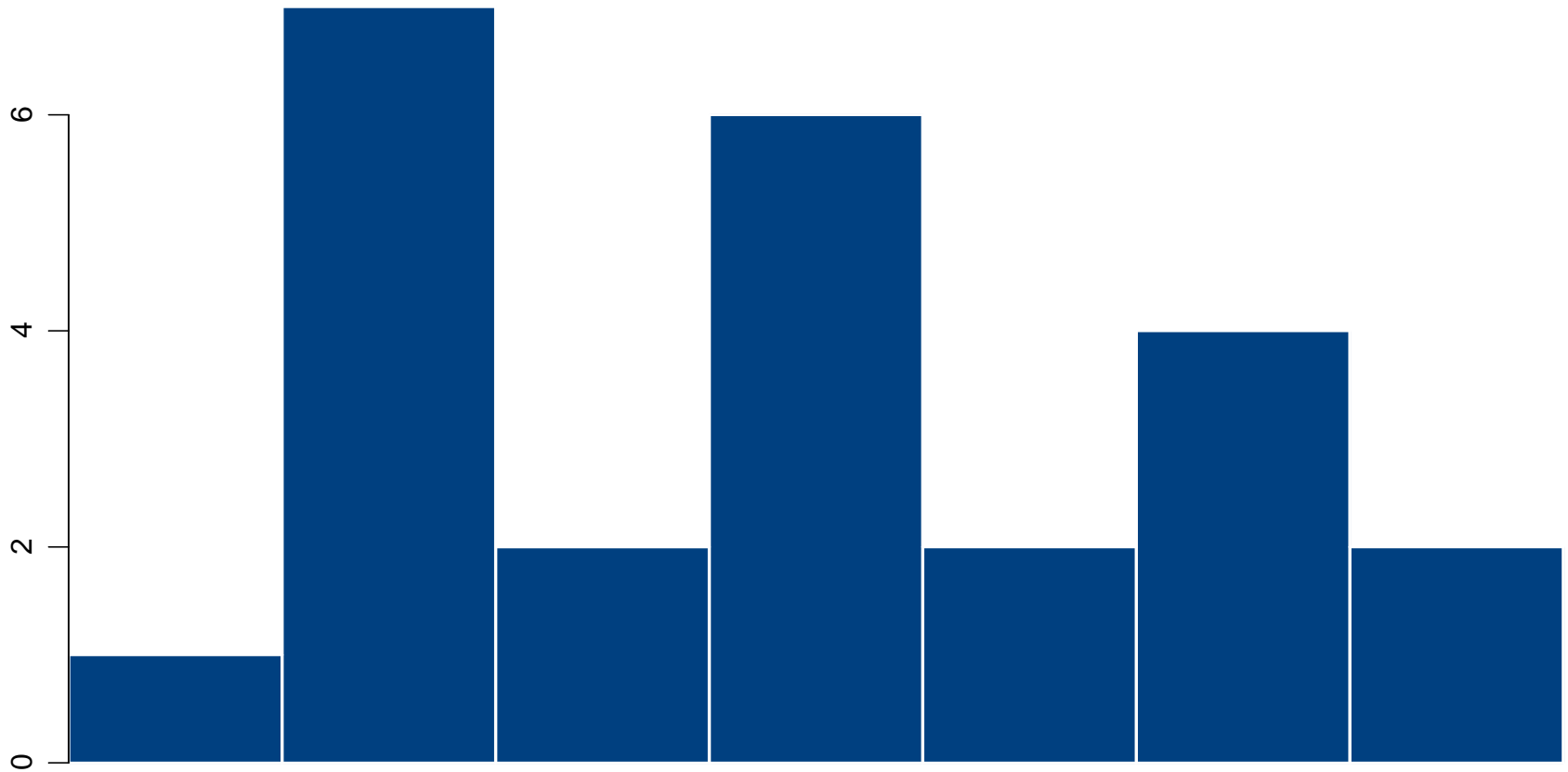
2^k Factorial Design Example

Example: 13.19, page 553 of the course textbook.

pairs(nw.df)

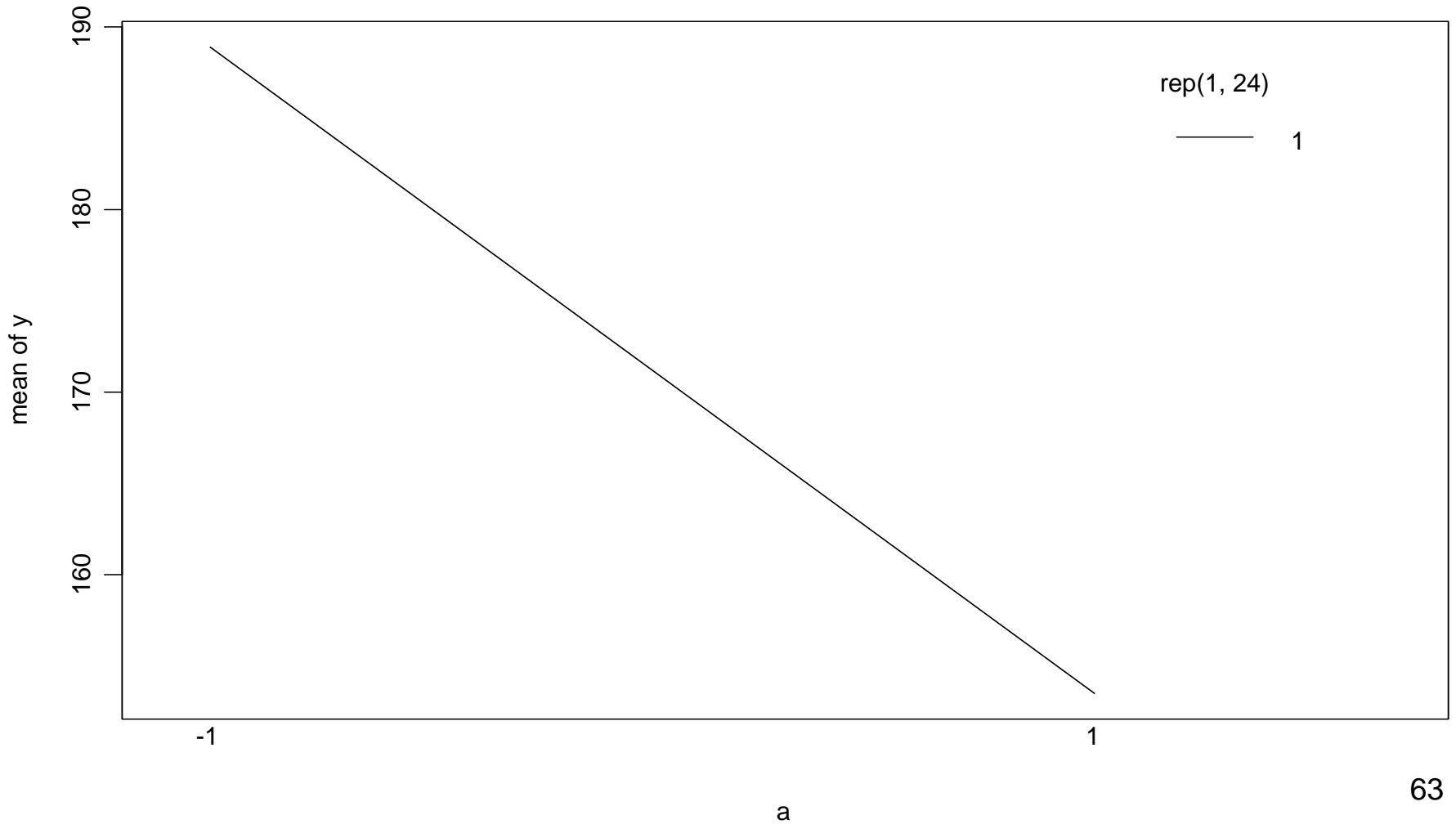


hist(y)

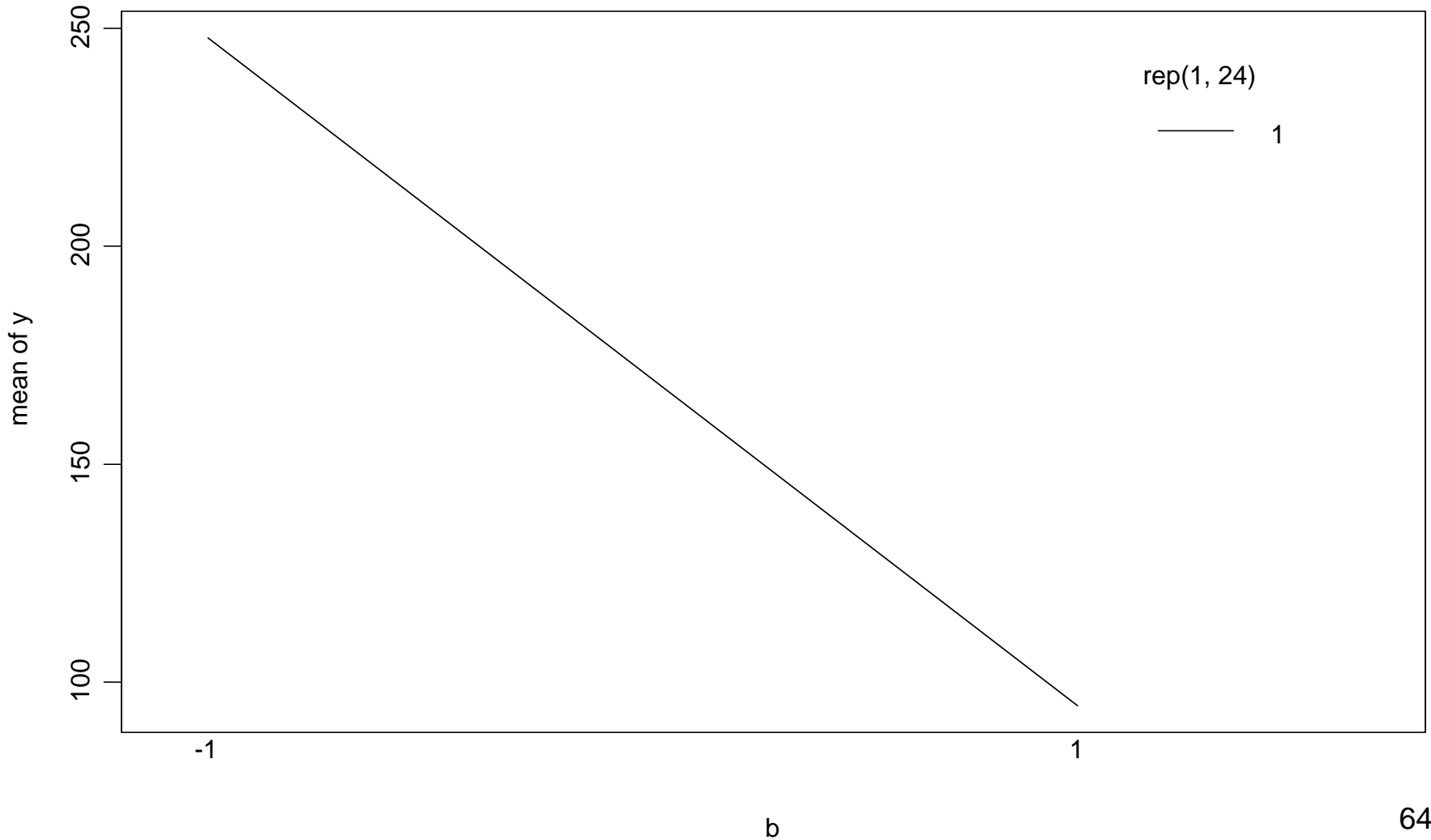


y

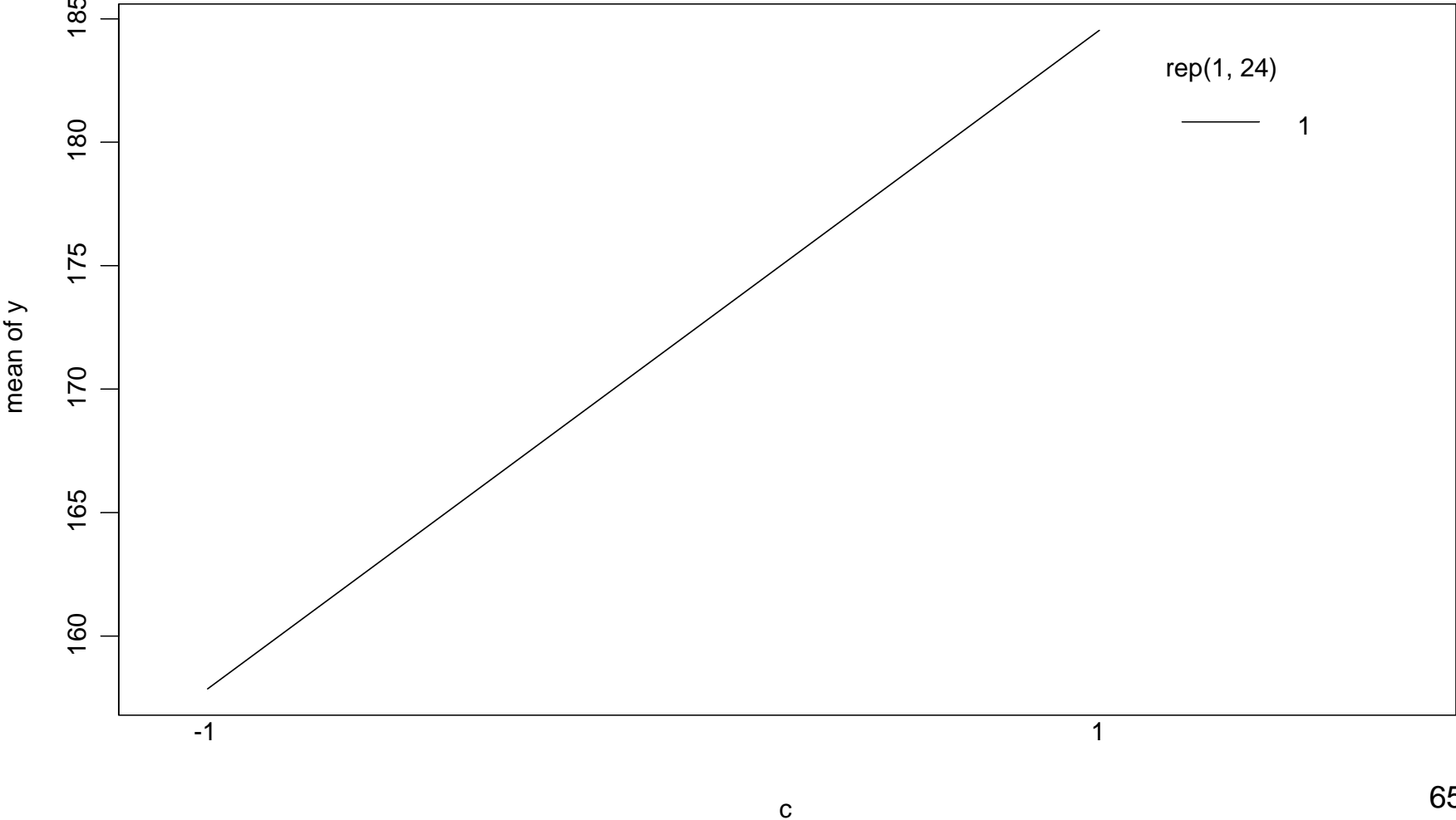
Effect of a



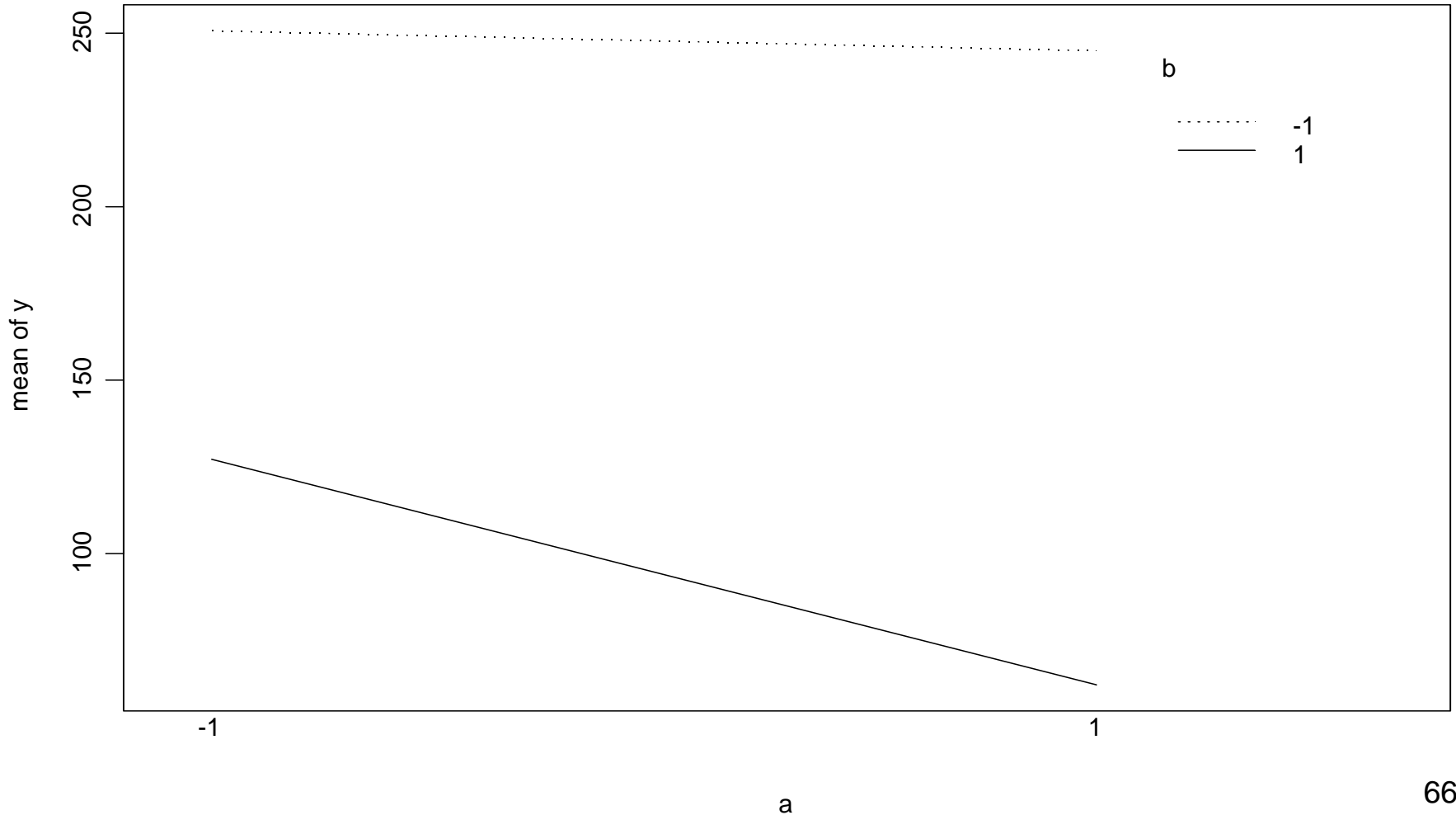
Effect of b



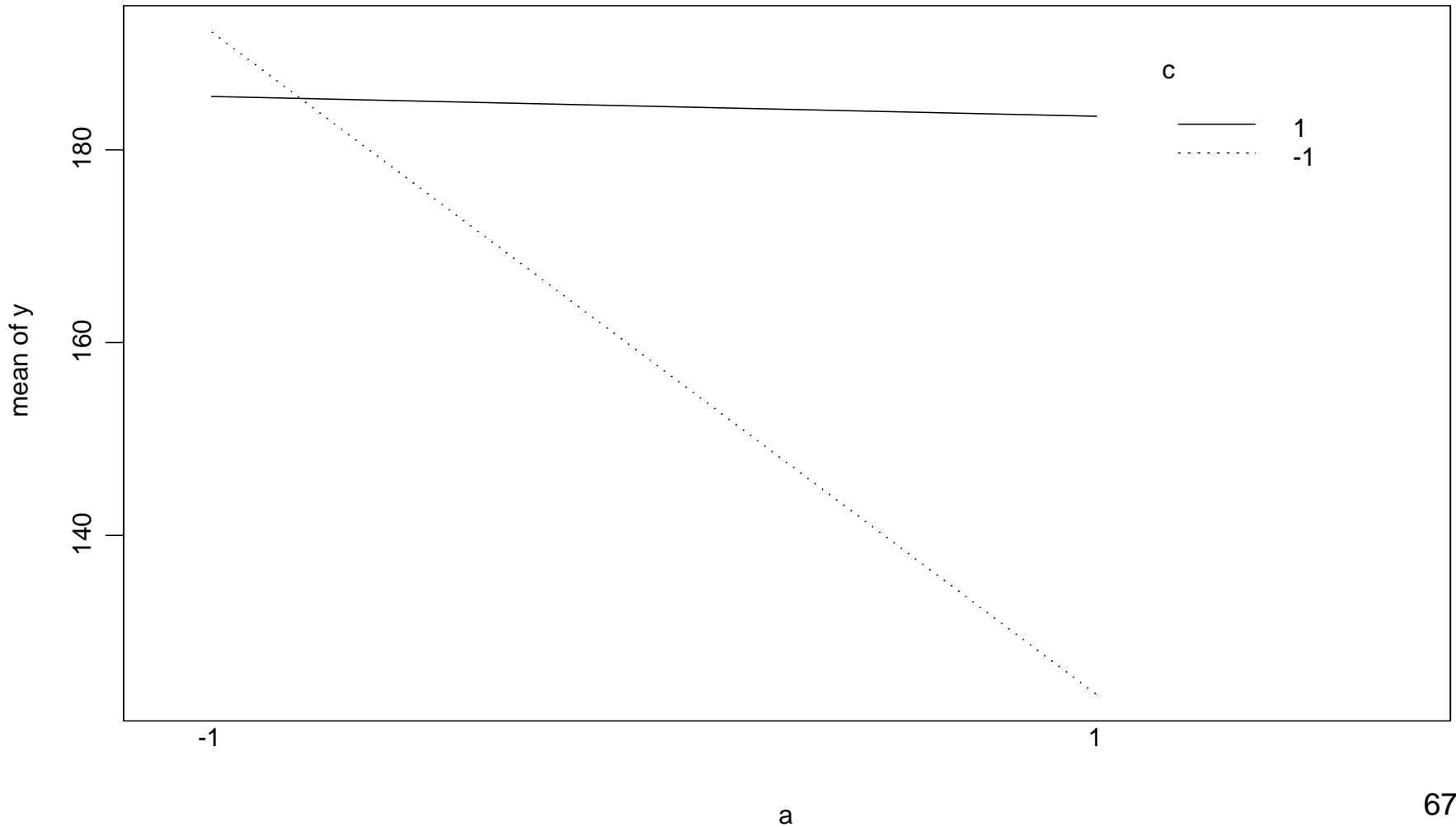
Effect of c



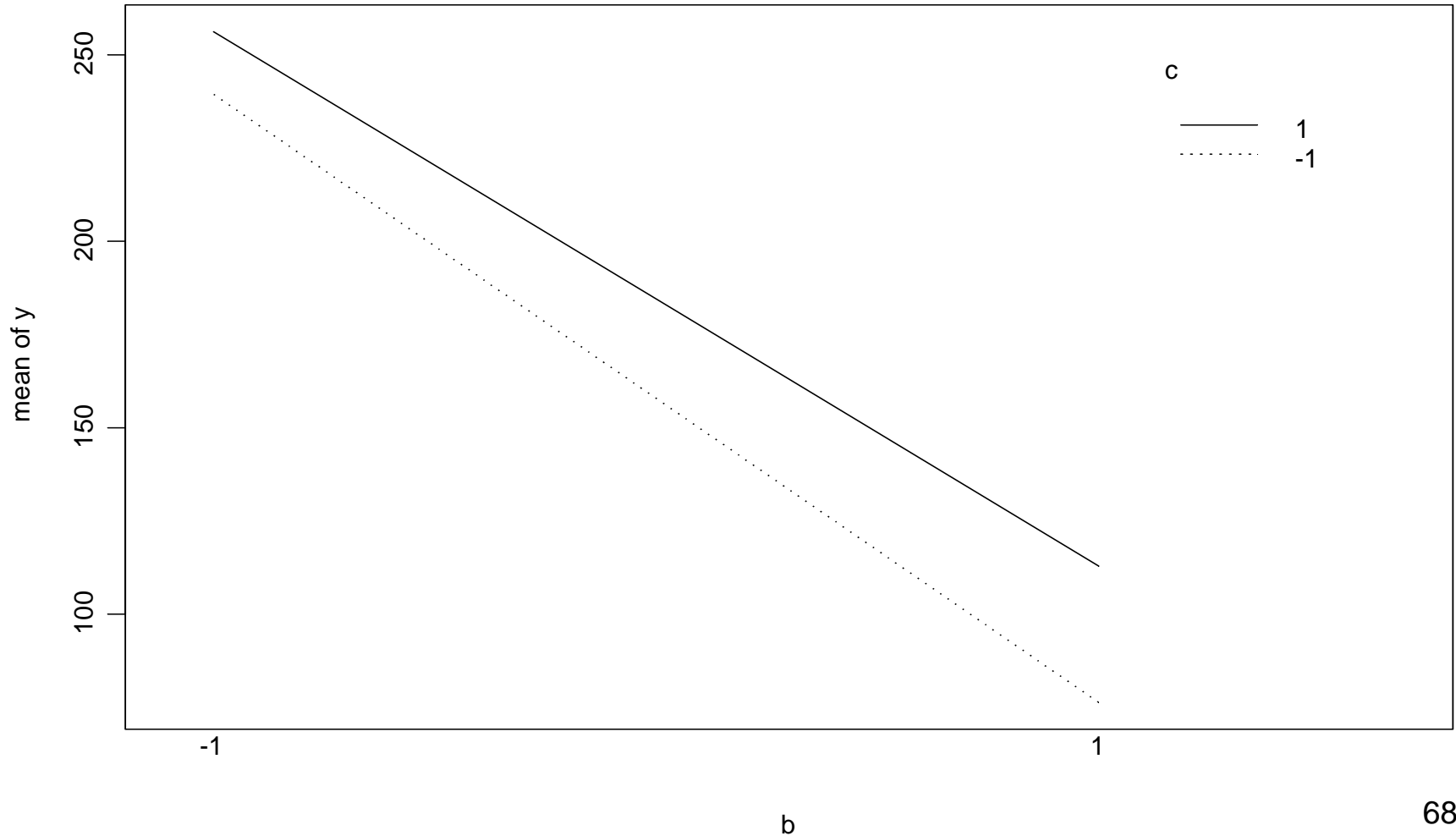
interaction.plot(a,b,y)



interaction.plot(a,c,y)



interaction.plot(b,c,y)



summary.lm(nw.aov)

Call: aov(formula = y ~ a * b * c, data = nw.df)

Residuals:

Min	1Q	Median	3Q	Max
-37.67	-6.861	2.388	12.67	28.67

Coefficients:

	Value	Std. Error	t value	Pr(> t)
(Intercept)	171.1942	4.6675	36.6780	0.0000
a	-17.6942	4.6675	-3.7909	0.0016
b	-76.5833	4.6675	-16.4078	0.0000
c	13.3333	4.6675	2.8566	0.0114
a:b	-14.8050	4.6675	-3.1719	0.0059
a:c	16.6667	4.6675	3.5708	0.0026
b:c	4.9442	4.6675	1.0593	0.3052
a:b:c	-25.0558	4.6675	-5.3682	0.0001

Residual standard error: 22.87 on 16 degrees of freedom

Multiple R-Squared: 0.9556

F-statistic: 49.21 on 7 and 16 degrees of freedom, the p-value is
1.209e-009

Effect (of going from low to high level) is 2*regression coefficient

```

model.matrix(nw.aov)
  (Intercept)  a  b  c a:b a:c b:c a:b:c
1             1 -1 -1 -1  1  1  1  -1
2             1  1 -1 -1 -1 -1  1  1
3             1 -1  1 -1 -1  1 -1  1
4             1 -1 -1  1  1 -1 -1  1
5             1  1  1 -1  1 -1 -1 -1
6             1  1 -1  1 -1  1 -1 -1
7             1 -1  1  1 -1 -1  1 -1
8             1  1  1  1  1  1  1  1
9             1 -1 -1 -1  1  1  1 -1
10            1  1 -1 -1 -1 -1  1  1
11            1 -1  1 -1 -1  1 -1  1
12            1 -1 -1  1  1 -1 -1  1
13            1  1  1 -1  1 -1 -1 -1
14            1  1 -1  1 -1  1 -1 -1
15            1 -1  1  1 -1 -1  1 -1
16            1  1  1  1  1  1  1  1
17            1 -1 -1 -1  1  1  1 -1
18            1  1 -1 -1 -1 -1  1  1
19            1 -1  1 -1 -1  1 -1  1
20            1 -1 -1  1  1 -1 -1  1
21            1  1  1 -1  1 -1 -1 -1
22            1  1 -1  1 -1  1 -1 -1
23            1 -1  1  1 -1 -1  1 -1
24            1  1  1  1  1  1  1  1

```

X'X Matrix

```
t(X)%*%X
```

	(Intercept)	a	b	c	a:b	a:c	b:c	a:b:c
(Intercept)	24	0	0	0	0	0	0	0
a	0	24	0	0	0	0	0	0
b	0	0	24	0	0	0	0	0
c	0	0	0	24	0	0	0	0
a:b	0	0	0	0	24	0	0	0
a:c	0	0	0	0	0	24	0	0
b:c	0	0	0	0	0	0	24	0
a:b:c	0	0	0	0	0	0	0	24

$$n^*(X'X)^{-1} X'$$

```
> solve(t(X)%*%X)%*%t(X)*24
      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
(Intercept)  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
      a -1  1 -1 -1  1  1 -1  1 -1  1 -1 -1  1  1 -1  1 -1  1 -1 -1  1  1 -1  1
      b -1 -1  1 -1  1 -1  1  1 -1 -1  1 -1  1 -1  1  1 -1 -1  1 -1  1 -1  1  1
      c -1 -1 -1  1 -1  1  1  1 -1 -1 -1  1 -1  1  1  1 -1 -1 -1  1 -1  1  1  1
      a:b  1 -1 -1  1  1 -1 -1  1  1 -1 -1  1  1 -1 -1  1  1 -1 -1  1  1 -1 -1  1
      a:c  1 -1  1 -1 -1  1 -1  1  1 -1  1 -1 -1  1 -1  1  1 -1  1 -1 -1  1 -1  1
      b:c  1  1 -1 -1 -1 -1  1  1  1  1 -1 -1 -1 -1  1  1  1  1 -1 -1 -1 -1  1  1
      a:b:c -1  1  1  1 -1 -1 -1  1 -1  1  1  1 -1 -1 -1  1 -1  1  1  1 -1 -1 -1  1
```


summary(nw.aov)

```
> summary(nw.aov)
```

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
a	1	7514.0	7514.0	14.3712	0.0016031
b	1	140760.2	140760.2	269.2166	0.0000000
c	1	4266.7	4266.7	8.1604	0.0114229
a:b	1	5260.5	5260.5	10.0612	0.0059164
a:c	1	6666.7	6666.7	12.7506	0.0025519
b:c	1	586.7	586.7	1.1221	0.3052037
a:b:c	1	15067.1	15067.1	28.8171	0.0000628
Residuals	16	8365.6	522.9		

Plot of residual vs. fit for nw.aov

