

Chapter 8: Experiments with two factors

Introductory Statistics for Engineering Experimentation

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Outline

8.1 Interaction

8.2 More than one observation per cell

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Chapter 8: Experiments with two factors

- Recall from chapter 3 that when we have a response on a continuous scale and two categorical covariates, we can consider the observations as being in the *cells* of a *two-way layout* determined by the levels of the two factors.
- There will always be one experimental factor whose levels are of interest in themselves. The second factor may be a *blocking factor*: a known source of variability for which we are controlling.
- If the factors are **A** and **B** we write the number of levels of the factors as I and J , respectively, and the number of observations in the (i, j) th cell as $n_{ij}, i = 1, \dots, I; j = 1, \dots, J$.
- In a *balanced* experiment all the n_{ij} are equal so we simply write the number of observations per cell as n . The text provides methods for balanced designs only. The methods we will describe can be applied to unbalanced designs too.

Replicated vs. non-replicated designs

- If none of the n_{ij} are zero then we have a *complete layout*, which is a type of *full factorial design*.
- When there is at least one of the $n_{ij} > 1$ the design is said to be *replicated*.
- Observations in the same cell are called *replicates*.
- In chapter 3 we discussed fitting models of the form

$$\mathcal{Y}_{ijk} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \epsilon_{ijk}, \quad i = 1, \dots, I; \quad j = 1, \dots, J; \quad k = 1, \dots, n_{ij}$$

when we have replicates. This model allows for interactions (the $\alpha\beta_{ij}$ terms).

- Our first test is on the null hypothesis that all the interactions are zero. If we do not reject this hypothesis then we simplify the model to the *additive model*

$$\mathcal{Y}_{ijk} = \mu + \alpha_i + \beta_j + \epsilon_{ijk}, \quad i = 1, \dots, I; \quad j = 1, \dots, J; \quad k = 1, \dots, n_{ij}$$

- We can fit a model with interactions to unreplicated data but cannot do further analysis. Thus we only fit the additive model

Overview of techniques

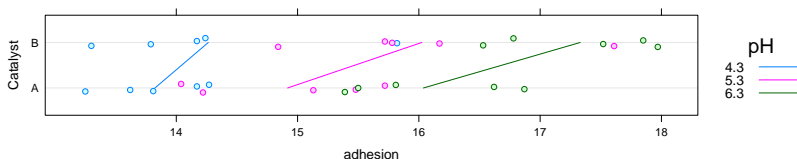
- We use interaction plots to assess the changes due to the levels of the factors and due to possible interaction.
- If there are replicates we fit the model with interactions and test first for a significant interaction term. If the interactions are not significant then we fit the additive model.
- For an additive model we can perform multiple comparisons on the levels of the factors separately (but only for experimental factors, not for blocking factors) For a model with significant interactions we cannot separate the effects of the factors.
- For an unreplicated design we can fit a model with interactions but cannot do any further analysis. We must fit the additive model even though we do not know if it is appropriate.

R functions used in this chapter

- Interaction plots are obtained with `dotplot`.
- We use `aov` to fit the models, `summary` or `anova` to obtain the analysis of variance table, and `model.tables` to obtain estimates of the cell means or the effects.
- We use `TukeyHSD` to perform multiple comparisons when appropriate.
- We assess residual plots obtained with `plot(fm, which = 1)` and `plot(fm, which = 2)`

Section 8.1, Interaction

- Recall that in an interaction plot a lack of interaction is indicated by more-or-less parallel lines joining the averages.



```
> summary(fm1 <- aov(adhesion ~ cat * factor(pH), adhesion2))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
cat	1	6.712	6.712	11.4424	0.00246
factor(pH)	2	34.924	17.462	29.7694	3.161e-07
cat:factor(pH)	2	1.003	0.502	0.8553	0.43772
Residuals	24	14.078	0.587		

Section 8.2 More than one observation per cell

- When we fit the model with interactions we always test first for significant interactions. The null hypothesis is

$$H_0 : \alpha\beta_{ij} = 0, \text{ for all } i, j$$

- If we do not reject this hypothesis then we fit the additive model.
- For the `adhesion2` anova (previous slide) the p-value for the interaction, labeled `cat:factor(pH)`, is 0.4377 so we do not reject H_0 .
- The additive model fit is

```
> summary(fm2 <- aov(adhesion ~ cat + factor(pH), adhesion2))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
cat	1	6.712	6.712	11.571	0.002176
factor(pH)	2	34.924	17.462	30.105	1.708e-07
Residuals	26	15.081	0.580		

Multiple comparisons for an additive model

- With an additive model it makes sense to perform multiple comparisons on the levels of factors separately.
- In the previous example one of the factors (`cat`) is a two-level factor. We do not need to perform multiple comparisons for such a factor (when you have only two levels there is only one possible comparison of levels).
- We can use the optional argument `which` to `TukeyHSD` to restrict to only the nontrivial multiple comparisons.

```
> TukeyHSD(fm2, which = "factor(pH)")
```

Tukey multiple comparisons of means

95% family-wise confidence level

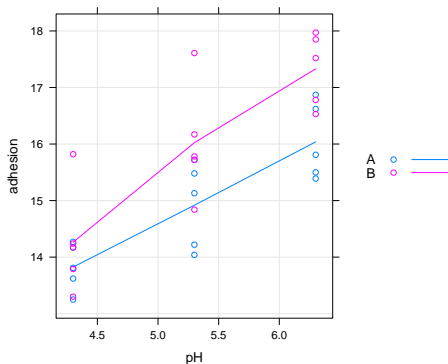
```
Fit: aov(formula = adhesion ~ cat + factor(pH), data = adhesion2)
```

```
$'factor(pH)'
```

	diff	lwr	upr	p adj
5.3-4.3	1.427	0.5806392	2.273361	0.0008057
6.3-4.3	2.640	1.7936392	3.486361	0.0000001
6.3-5.3	1.213	0.3666392	2.059361	0.0040071

Alternative analysis of adhesion2

- This is jumping ahead a bit but for data like the `adhesion2` data we are losing power by treating the numeric `pH` variable as a factor. Over the observed range the adhesion is close to linear in `pH` for both catalysts.



Alternative analysis of adhesion2 (cont'd)

- We could fit a model that is linear in pH allowing for different slopes and intercepts for the two catalysts.

```
> summary(fm3 <- lm(adhesion ~ pH * cat, adhesion2))
Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	9.0596	1.2554	7.216	1.16e-07
pH	1.1070	0.2341	4.728	6.88e-05
catB	-1.3118	1.7755	-0.739	0.467
pH:catB	0.4260	0.3311	1.287	0.210

Residual standard error: 0.7403 on 26 degrees of freedom
 Multiple R-squared: 0.7488, Adjusted R-squared: 0.7198
 F-statistic: 25.83 on 3 and 26 DF, p-value: 5.825e-08

```
> anova(fm3)
```

Analysis of Variance Table

Response: adhesion

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
pH	1	34.848	34.848	63.5812	1.881e-08
cat	1	6.712	6.712	12.2460	0.001699
pH:cat	1	0.907	0.907	1.6555	0.209545
Residuals	26	14.250	0.548		

Alternative analysis of adhesion2 (cont'd)

- Notice that each the interaction term in this model (labeled `pH:catB` now) has only 1 degree of freedom so the `anova` results provide exactly the same information as the t-test in the summary.
- Because the interaction term is not significant we reduce to an additive model (corresponding to parallel lines w.r.t. `pH` for each of the two catalysts).

```
> summary(fm4 <- lm(adhesion ~ pH + cat, adhesion2))
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.9307	0.9088	8.727	2.42e-09
pH	1.3200	0.1675	7.879	1.80e-08
catB	0.9460	0.2736	3.458	0.00182

Residual standard error: 0.7493 on 27 degrees of freedom

Multiple R-squared: 0.7328, Adjusted R-squared: 0.713

F-statistic: 37.01 on 2 and 27 DF, p-value: 1.834e-08

Yet another analysis of adhesion2

- When we have a two-level factor (like the `cat` factor) or when we have a numeric factor observed only at a few, equally-spaced levels, it can be useful to convert such factors to `ordered` factors.
- For more than two levels the ordered factor produces coefficients for linear, quadratic, cubic, etc. terms. We can check if the higher order terms are not significant and reduce the model accordingly (always proceeding from the highest order down).
- For a two-level `ordered` factor the default parameterization of the model has certain advantages in the analysis of two-level factorial designs.
- The analysis of variance table is the same whether we use `factor` or `ordered`

Yet another analysis of adhesion2 (cont'd)

```
> ad2 <- within(adhesion2, {opH <- ordered(pH); ocat <- ordered(
> anova(fm5 <- lm(adhesion ~ ocat * opH, ad2))
```

Analysis of Variance Table

Response: adhesion

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ocat	1	6.712	6.712	11.4424	0.00246
opH	2	34.924	17.462	29.7694	3.161e-07
ocat:opH	2	1.003	0.502	0.8553	0.43772
Residuals	24	14.078	0.587		

```
> summary(fm6 <- lm(adhesion ~ ocat + opH, ad2))
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	15.39967	0.13905	110.749	< 2e-16
ocat.L	0.66892	0.19665	3.402	0.00218
opH.L	1.86676	0.24084	7.751	3.18e-08
opH.Q	-0.08737	0.24084	-0.363	0.71973

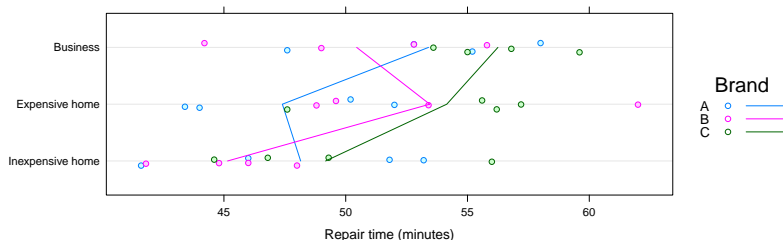
Residual standard error: 0.7616 on 26 degrees of freedom

Multiple R-squared: 0.7341, Adjusted R-squared: 0.7034

F-statistic: 23.93 on 3 and 26 DF, p-value: 1.206e-07

The quadratic term (`opH.Q`) is not significant so we reduce to model `fm4`.

Example 8.2.9



```
> ## compare to anova table on p. 316
> summary(fm7 <- aov(time ~ brand * type, computer))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
brand	2	99.41	49.71	2.4045	0.10939
type	2	219.34	109.67	5.3053	0.01139
brand:type	4	113.08	28.27	1.3676	0.27131
Residuals	27	558.15	20.67		

Example 8.2.9 (cont'd)

```
> ## remove insignificant interaction term
> summary(fm8 <- aov(time ~ brand + type, computer))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
brand	2	99.41	49.71	2.2956	0.11757
type	2	219.34	109.67	5.0651	0.01249
Residuals	31	671.23	21.65		

```
> ## remove insignificant brand term
> summary(fm9 <- aov(time ~ type, computer))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
type	2	219.35	109.67	4.6963	0.01604
Residuals	33	770.64	23.35		

Example 8.2.9 (cont'd)

```
> TukeyHSD(fm9)
```

```
  Tukey multiple comparisons of means
```

```
    95% family-wise confidence level
```

```
Fit: aov(formula = time ~ type, data = computer)
```

```
$type
```

	diff	lwr	upr	p adj
Expensive home-Inexpensive home	4.175 -0.6659665	9.015966	0.1019591	
Business-Inexpensive home	5.875 1.0340335	10.715966	0.0145559	
Business-Expensive home	1.700 -3.1409665	6.540966	0.6678201	