

Chapter 9

Designed Experiments

1. `chicks` contains the data of Table 9.8. To fit the linear model given in Example 9.4 without first eliminating the pair parameters by differencing, display the analysis of variance table, and view the estimates:

```
chicks  # print data
summary(aov(y~Pair+Treat,data=chicks)) # analysis of variance
options(contrasts=c("contr.treatment","contr.poly"))
chicks.lm <- lm(y~Pair+Treat,data=chicks) # fit linear model
summary(chicks.lm,correlation=F) # summary w/o correlations of estimates
```

The `options` statement gives the parametrization used in the example. Note the parameter estimates for the amino acids and their standard errors, and the estimate of error variance.

To perform the intra- and inter-block analyses directly, we make two new dataframes `chick1` and `chick2`:

```
attach(chicks)
i <- 2*c(1:15)
chick1 <- data.frame(y=y[i]-y[-i],
  His=(Treat[i]=="His-")-(Treat[-i]=="His-"),
  Arg=(Treat[i]=="Arg-")-(Treat[-i]=="Arg-"),
  Thr=(Treat[i]=="Thr-")-(Treat[-i]=="Thr-"),
  Val=(Treat[i]=="Val-")-(Treat[-i]=="Val-"),
  Lys=(Treat[i]=="Lys-")-(Treat[-i]=="Lys-"))
chick2 <- data.frame(y=y[-i]+y[i],
  His=(Treat[i]=="His-")+(Treat[-i]=="His-"),
  Arg=(Treat[i]=="Arg-")+(Treat[-i]=="Arg-"),
  Thr=(Treat[i]=="Thr-")+(Treat[-i]=="Thr-"),
  Val=(Treat[i]=="Val-")+(Treat[-i]=="Val-"),
  Lys=(Treat[i]=="Lys-")+(Treat[-i]=="Lys-"))
detach("chicks")
chick1 # new data frame suitable for intra-block fit
chick1.lm <- glm(y~Arg+His+Thr+Val+Lys-1,data=chick1)
summary(chick1.lm)
chick2 # new data frame suitable for inter-block fit
chick2.lm <- glm(y~Arg+His+Thr+Val+Lys,data=chick2)
summary(chick2.lm)
```

Again note the estimates and their standard errors. Why are the estimates of error variance different for these fits and that above?

To compute the intra-block effects on the original scale, and 95% confidence intervals:

```
nu <- 10
est <- matrix(coef(chick1.lm),5,3)
chick1.sum <- summary(chick1.lm)
se <- sqrt(diag(chick1.sum$cov.unscaled*chick1.sum$dispersion))
10^( est + outer(se*qt(0.975,df=nu),c(0,-1,1)) )
```

For the pooled analysis:

```
t1 <- coef(chick1.lm)
s1 <- sqrt(diag(chick1.sum$cov.unscaled*chick1.sum$dispersion))
chick2.sum <- summary(chick2.lm)
t2 <- coef(chick2.lm)[-1]
s2 <- sqrt(diag(chick2.sum$cov.unscaled*chick2.sum$dispersion))[-1]
w <- 1/s1^2/(1/s1^2+1/s2^2)
est <- w*t1 + (1-w)*t2
s <- sqrt(1/(1/s1^2+1/s2^2))
cbind(est,s)
```

To compute the degrees of freedom using the calculation in Exercise 9.2.3 and then to compute the estimates and confidence intervals on the original scale:

```
n1 <- 10; n2 <- 9; s1 <- s1[1]; s2 <- s2[1]
nu <- (s1^2+s2^2)^2/(s1^4/n1+s2^4/n2)
nu # equivalent df for variance estimate
10^( est + outer(s*qt(0.975,df=nu),c(0,-1,1)) )
```

The balanced nature of the experiment is seen by computing the $X^T X$ matrix for the intra-block model, and its inverse:

```
X <- as.matrix(chick1[, -1])
X
crossprod(X)
solve(crossprod(X))
```

The effect of a lack of balance is seen by dropping certain pairs:

```
solve(crossprod(X[-15,]))
```

Explain the change to the matrix $(X^T X)^{-1}$ in terms of which treatment pairs have here been dropped from the model.

(Section 9.2; Cox and Snell, 1981, pp. 95–97)