

## Practice 4

1. A study was conducted to investigate the toxicity to the tobacco budworm *Heliothis virescens* of doses of the pyrethroid *trans*-cypermethrin to which the moths were beginning to show resistance. Batches of 20 moths of each sex were exposed for three days to the pyrethroid and the number in each batch that were killed was recorded. The results were

Dose ( $\mu\text{g}$ )	Dosage ( $=\log_2(\text{dose})$ )	Number killed (out of 20)	
		Males	Females
1	0	1	0
2	1	4	2
4	2	9	6
8	3	13	10
16	4	18	12
32	5	20	16

Nine (logistic regression) models (`bud.1` to `bud.9`) were fitted to these data and resulted in the residual deviances given in the table below, together with the R model specifications. For these models, `sex` is a factor with 2 levels (male; female), `dose.f` refers to dose treated as a factor with 6 levels, `dose` is the dose treated as a variable and `dosage` is  $\log_2(\text{dose})$  treated as a variable (logs to the base 2 have been used for numerical convenience). Also,  $\text{dose}^2 = \text{dose}^2$ , etc.

Model	formula specification	residual deviance	DF
<code>bud.1</code>	<code>sex + dose.f</code>	5.01	5
<code>bud.2</code>	<code>sex*dose</code>	18.16	8
<code>bud.3</code>	<code>sex + dose</code>	27.97	9
<code>bud.4</code>	<code>sex + dose + dose^2</code>	14.84	8
<code>bud.5</code>	<code>sex + dose + dose^2 + dose^3</code>	8.18	7
<code>bud.6</code>	<code>sex*dosage</code>	4.99	8
<code>bud.7</code>	<code>sex + dosage</code>	6.76	9
<code>bud.8</code>	<code>sex + dosage + dosage^2</code>	5.85	8
<code>bud.9</code>	<code>sex + dosage + dosage^2 + dosage^3</code>	5.01	7

- (a) For each of the following pairs of models explain what hypothesis is being tested if the difference between the residual deviances is compared with the relevant  $\chi^2$  distribution and give the result of the test, or explain why a test of the difference is not valid:
- model `bud.1` and model `bud.2`;
  - model `bud.1` and model `bud.3`;
  - model `bud.1` and model `bud.7`.

- (b) Which of the models listed in the table above is most appropriate for these data? Give details of any tests that you carry out and clearly state the conclusions drawn from each test.
- (c) For the model found in (b), use the parameter estimates from the relevant summaries given below to answer the following questions.
- Is the effect of sex significant in the model? Justify your answer.
  - Quantify, in terms of odds ratios, the effects of sex and dose or dosage on toxicity.
  - Find an estimate of the dose, or dosage, that would kill 50% of **male** budworm moths (the LD(50)). State, with reasons, whether the LD(50) for female moths would be greater or less than that for males.
  - Obtain an estimate of the probability that a **female** moth will die within three days if subjected to a dose of  $16\mu\text{g}$  of pyrethroid (or a dosage of 4) for three days.
- (d) A total of 240 budworms were used in this study. Describe what would have been the same and what would have been different in the output (residual deviances and their degrees of freedom, differences between residual deviances and their degrees of freedom, parameter estimates and their standard errors) had the data been treated as 240 ungrouped, 0–1 observations, rather than as 12 groups of 20 moths.

**R output for the question** (using contrasts = *contr.treatment*)

```
tox <- data.frame(dose=rep(2^(0:5), 2), dosage=rep(0:5, 2),
  sex=factor(rep(c("male", "female"), each=6)),
  killed=c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16), total=rep(20, 12))
tox$dose.f=as.factor(tox$dose)
bud.1 <- glm(killed/total~sex+dose.f, family=binomial, weight=total, data=tox)
summary(bud.1)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-4.343773	1.0487414	-4.141892	3.444531e-05
sexmale	1.089652	0.3530009	3.086826	2.023061e-03
dose.f2	1.961727	1.1113455	1.765182	7.753314e-02
dose.f4	3.250278	1.0721581	3.031529	2.433185e-03
dose.f8	4.124006	1.0731218	3.842999	1.215400e-04
dose.f16	4.972161	1.0908733	4.557964	5.165189e-06
dose.f32	6.112219	1.1580661	5.277953	1.306348e-07

```
bud.2 <- glm(killed/total~sex*dose, family=binomial, weight=total, data=tox)
summary(bud.2)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-1.7157796	0.32233098	-5.3230368	1.020491e-07
sexmale	-0.2119351	0.51523286	-0.4113384	6.808244e-01
dose	0.1156765	0.02378865	4.8626745	1.158102e-06
sexmale:dose	0.1815579	0.06691613	2.7132151	6.663383e-03

```
bud.3 <- glm(killed/total~sex+dose, family=binomial,weight=total, data=tox)
summary(bud.3)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-2.1346160	0.32029494	-6.664533	2.655090e-11
sexmale	0.9685483	0.32954266	2.939068	3.292009e-03
dose	0.1599557	0.02341362	6.831736	8.389317e-12

```
bud.4 <- glm(killed/total~sex+dose+I(dose^2), family=binomial,
             weight=total, data=tox)
summary(bud.4)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-3.003389755	0.437962665	-6.857639	7.000801e-12
sexmale	1.071220664	0.351521937	3.047379	2.308462e-03
dose	0.373538720	0.067764839	5.512279	3.542162e-08
I(dose^2)	-0.007159677	0.001993451	-3.591600	3.286544e-04

```
bud.5 <- glm(killed/total~sex+dose+I(dose^2)+I(dose^3),
             family=binomial,weight=total, data=tox)
summary(bud.5)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-4.0866830547	0.6607757993	-6.184674	6.223085e-10
sexmale	1.0973248813	0.3557180409	3.084816	2.036778e-03
dose	0.8527524241	0.2080073445	4.099627	4.138174e-05
I(dose^2)	-0.0494398191	0.0169559801	-2.915775	3.548065e-03
I(dose^3)	0.0008911737	0.0003504341	2.543057	1.098874e-02

```
bud.6 <- glm(killed/total~sex*dosage, family=binomial,
             weight=total, data=tox)
summary(bud.6)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-2.9935418	0.5526997	-5.4162175	6.087304e-08
sexmale	0.1749868	0.7783100	0.2248292	8.221122e-01
dosage	0.9060364	0.1671016	5.4220678	5.891353e-08
sexmale:dosage	0.3529130	0.2699902	1.3071324	1.911678e-01

```
bud.7 <- glm(killed/total~sex+dosage, family=binomial,
             weight=total, data=tox)
summary(bud.7)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-3.473155	0.4685202	-7.413032	1.234445e-13
sexmale	1.100743	0.3558271	3.093478	1.978249e-03
dosage	1.064214	0.1310775	8.118971	4.701542e-16

```
bud.8 <- glm(killed/total~sex+dosage+I(dosage^2), family=binomial,  
             weight=total, data=tox)  
summary(bud.8)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-3.89425764	0.68189216	-5.710958	1.123418e-08
sexmale	1.10067699	0.35563665	3.094948	1.968473e-03
dosage	1.48817861	0.48111066	3.093215	1.980008e-03
I(dosage^2)	-0.07940387	0.08441284	-0.940661	3.468786e-01

```
bud.9 <- glm(killed/total~sex+dosage+I(dosage^2)+I(dosage^3),  
             family=binomial,weight=total, data=tox)  
summary(bud.9)$coef
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-4.35929600	0.94608866	-4.607703	4.071407e-06
sexmale	1.08956896	0.35298436	3.086734	2.023683e-03
dosage	2.46176306	1.24976481	1.969781	4.886347e-02
I(dosage^2)	-0.52946973	0.51858149	-1.020996	3.072562e-01
I(dosage^3)	0.05643769	0.06335904	0.890760	3.730580e-01