

Assignment 5 — Due Nov 27, 2018

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1. Eight isolates of rose blackspot fungus

(a) Consider an additive model $Y \sim \text{Isolate} + \text{Temp}$. Complete the decomposition of the total sum of squares:

By running `r` function, we can get the table as followed:

Analysis of Variance Table

```
Response: Y
      Df Sum Sq Mean Sq F value    Pr(>F)
isolate  7  0.34814  0.04973   4.2338 0.001297 **
temp     6  2.72335  0.45389  38.6397 1.467e-15 ***
Residuals 42  0.49336  0.01175
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 1.1 Analysis of Variance Table

SOURCE	SS	DF	MS	F	P-VALUE
ISOLATE	0.35	7	0.0497	4.2338	0.001
TEMP	2.72	6	0.4539	38.6397	1.467e-15
RESIDUAL	0.49	42	0.01175		

Table 1.2 Anova table for model $Y \sim \text{Isolate} + \text{Temp}$

(b) Now consider a linear model where the covariates are polynomials of temperature.

First, fit the linear regression model:

`lm0=lm(Y~1)`

`lm1=lm(Y~1+x)`

`lm2=lm(Y~1+x+x2)`

`lm3=lm(Y~x+x2+x3)`

`lm4=lm(Y~x+x2+x3+x4)`

`lm6=lm(Y~x+x2+x3+x4+x5+x6)`

Then by using `anova` on either two linear regression models, we can get the table.

`(P1|1)=anova(lm0,lm1)`

`(P2|P1)=anova(lm1,lm2)`

`(P3|P2)=anova(lm2,lm3)`

`(P4|P3)=anova(lm3,lm4)`

`(TEMP|P4)=anova(lm4,lm6)`

`(TEMP|P3)=anova(lm3,lm6)`

SOURCE	SS	DF	MS	F	P-VALUE
P1 1	0.0117	1	0.0117	0.1781	0.6747
P2 P1	2.56781	1	2.56781	138.12	< 2.2e-16
P3 P2	0.09992	1	0.09992	5.8683	0.01894
P4 P3	0.01345	1	0.01345	0.7864	0.3793
TEMP(P6) P4	0.03045	2	0.01523	0.8867	0.4185
TEMP P3	0.0439	3	0.01463	0.8521	0.4722

Table 1.3 Anova table for linear model

(c) What does the preceding table tell you about the effect of temperature on growth? Estimate the temperature at which the growth rate is a maximum.

Based the preceding table, we can find that the model: $Y \sim x + x^2 + x^3$ is the best regression model since its p-value is small.

By optimize() function, we can calculate that temperature = 71.74756, the growth rate is a maximum reached 1.05296

2. Flushot

(a) Fit a multiple logistic regression model with the three explanatory variables by maximum likelihood estimation. Report the summary table from the R output. Obtain and interpret the maximum likelihood estimates of β_0 , β_1 , β_2 , and β_3 . State the fitted logistic response function.

Multiple Logistic Regression Model

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3$$

X1: age

X2: health awareness index, for which higher values indicate greater awareness

X3: gender, where males were coded X3 = 1 and females were coded X3 = 0

R summary table

```
Call:
glm(formula = y ~ x1 + x2 + x3, family = binomial("logit"), data = b)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.4037  -0.5637  -0.3352  -0.1542   2.9394

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.17716    2.98242  -0.395  0.69307
x1           0.07279    0.03038   2.396  0.01658 *
x2          -0.09899    0.03348  -2.957  0.00311 **
x3           0.43397    0.52179   0.832  0.40558
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 134.94  on 158  degrees of freedom
Residual deviance: 105.09  on 155  degrees of freedom
AIC: 113.09

Number of Fisher Scoring iterations: 6
```

Table 2.1 R summary table

Interpretation

$\beta_0 = -1.17716$, which means the average odds of a person having a flu shot is -1.17716..

$\beta_1 = 0.07279$, representing the odds of a person having a flu shot increase by about 7.3% with each unit increase in age.

$\beta_2 = -0.09899$, representing the odds of a person having a flu shot decrease by about 9.9% with each unit increase in awareness index.

$\beta_3 = 0.43397$, representing the difference between the log odds for male and the log odds for female is 0.43397.

Fitted Logistic Response Function

$$\log\left(\frac{p_i}{1-p_i}\right) = -1.177 + 0.07279 X_1 - 0.09899 X_2 + 0.43397 X_3$$

(b) Obtain $\exp(\beta_1)$, $\exp(\beta_2)$, and $\exp(\beta_3)$ and the respective 95% CI. Interpret the results.

		2.5 %	97.5 %
(Intercept)	0.308	0.001	106.515
x1	1.076	1.013	1.141
x2	0.906	0.848	0.967
x3	1.543	0.555	4.292

Table 2.2 Result of Confidence Interval

Interpretation

$\exp(\beta_1)=1.076$, representing estimated odds ratio for X1

95% CI for $\exp(\beta_1)$ is (1.013,1.141)

$\exp(\beta_2)=0.906$, representing estimated odds ratio for X2

95% CI for $\exp(\beta_2)$ is (0.848,0.967)

$\exp(\beta_3)=1.543$, representing estimated odds ratio for X3

95% CI for $\exp(\beta_3)$ is (0.555,4.292)

(c) What is the estimated probability that male clients aged 55 with a health awareness index of 60 will receive a flu shot? Provide a 95% CI. Interpret the results.

Estimated Probability

$$X'_h \hat{\beta} = -2.679033$$

$$s\{X'_h \hat{\beta}\} = 0.5085794$$

$$\hat{\pi}_h = \frac{\exp(X'_h \hat{\beta})}{1 + \exp(X'_h \hat{\beta})} = 0.06422197$$

The result shows that male clients aged 55 with a health awareness index of 60 receive a flu shot at the probability 6.4%.

95% CI

$$L = X'_h \hat{\beta} - z_{1-\alpha/2} s\{X'_h \hat{\beta}\} = -3.67583$$

$$U = X'_h \hat{\beta} + z_{1-\alpha/2} s\{X'_h \hat{\beta}\} = -1.682236$$

$$L^* = \{1 + \exp(-L)\}^{-1} = 0.0247027$$

$$U^* = \{1 + \exp(-U)\}^{-1} = 0.1567997$$

$$\Rightarrow CI \text{ for } \pi_h \text{ is } (0.0247, 0.1568)$$

The result shows that male clients aged 55 with a health awareness index of 60 have 95% probability to receive a flu shot at the probability between 0.0247 and 0.1568.

(d) Perform a **Wald test** to determine whether X3, client gender, can be dropped from the regression model.

Multiple Logistic Regression Model:

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3$$

Hypothesis:

$$H_0 : \beta_3 = 0 \text{ v.s. } H_1 : \beta_3 \neq 0$$

Wald test Statistic:

$$z^* = \frac{\hat{\beta}_3 - \beta_3}{s\{\hat{\beta}_3\}} \sim N(0,1)$$

$$z^* = 0.832 < z_{1-\alpha/2} = 1.96$$

Conclusion:

We accept null hypothesis, that is $\beta_3=0$ and thus X3 can be dropped from the regression model.

(e) Perform a **likelihood ratio test** to determine whether X3, client gender, can be dropped from the regression model.

Multiple Logistic Regression Model:

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3$$

Hypothesis:

$$H_0 : \beta_3 = 0 \text{ v.s. } H_1 : \beta_3 \neq 0$$

Likelihood ratio test Statistic:

$$G^2 = -2 \log \left\{ \frac{L(R)}{L(F)} \right\} = -2 \{ \log(L(R)) - \log(L(F)) \} \sim \chi^2_{df_R - df_F}$$

Analysis of Deviance Table

Model 1: y ~ x1 + x2

Model 2: y ~ x1 + x2 + x3

	Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
1	156	105.80			
2	155	105.09	1	0.70221	0.402

Table 2.3 Likelihood Radio Test

$$G^2 = 0.70221 < \chi^2_{p-q, 1-\alpha} = 3.84146$$

Thus, based on the rejection rule, we should reject null hypothesis and $\beta_3=0$ could be dropped from the model.

(f) Perform stepwise model selection based on AIC. Report the summary table for your final model.

(1) Forward stepwise+ AIC

Step 1

Start: AIC=136.94

$y \sim 1$

	Df	Deviance	AIC
+ x2	1	113.20	117.20
+ x1	1	116.27	120.27
+ x3	1	132.88	136.88
<none>		134.94	136.94

Model start with $y \sim 1$. Based on the step one, AIC=136.94. These three variables AIC are all greater than 136.94, but we should first add x2 into the model since its AIC is the smallest and thus it has most effect on the model. Then the model becomes $y \sim x2$.

Step 2

Step: AIC=117.2

$y \sim x2$

	Df	Deviance	AIC
+ x1	1	105.80	111.80
+ x3	1	111.19	117.19
<none>		113.20	117.20

After add x2 as a variable into the model, based on the step two, AIC=117.2. We should then add x1 into the model since its AIC is smaller than 117.2 and it is the smallest and thus it has most effect on the model. Then the model becomes $y \sim x2 + x1$.

Step 3

Step: AIC=111.8

$y \sim x2 + x1$

	Df	Deviance	AIC
<none>		105.80	111.80
+ x3	1	105.09	113.09

Call: glm(formula = $y \sim x2 + x1$, family = binomial("logit"), data = b)

Coefficients:

(Intercept)	x2	x1
-1.45778	-0.09547	0.07787

Degrees of Freedom: 158 Total (i.e. Null); 156 Residual

Null Deviance: 134.9

Residual Deviance: 105.8 AIC: 111.8

Now, the model becomes $y \sim x2 + x1$, and then after step three, AIC=111.8 and we find that x3's AIC is greater than 111.8, so it does not have much effect on the model. We will not add it into the model.

Finally, we get the model

$$y = -1.458 - 0.0955 * x_2 + 0.078 * x_1$$

(2) Backward stepwise+ AIC

Step 1

Start: AIC=113.09

 $y \sim x_1 + x_2 + x_3$

	Df	Deviance	AIC
- x3	1	105.80	111.80
<none>		105.09	113.09
- x1	1	111.19	117.19
- x2	1	115.80	121.80

Model start with $y \sim x_1 + x_2 + x_3$. Based on the step one, AIC=113.09. x_3 's AIC is 111.8 which is smaller than 113.09, so we should first remove x_3 from the model since its AIC is the smallest and thus it has least effect on the model. Then the model becomes $y \sim x_1 + x_2$.

Step 2

Step: AIC=111.8

 $y \sim x_1 + x_2$

	Df	Deviance	AIC
<none>		105.80	111.80
- x1	1	113.20	117.20
- x2	1	116.27	120.27

Call: glm(formula = $y \sim x_1 + x_2$, family = binomial(link = "logit"), data = b)

Coefficients:

	x1	x2
(Intercept)	-1.45778	0.07787
		-0.09547

Degrees of Freedom: 158 Total (i.e. Null); 156 Residual

Null Deviance: 134.9

Residual Deviance: 105.8 AIC: 111.8

Now, the model is $y \sim x_1 + x_2$, and AIC=111.8. x_1 and x_2 's AIC are both greater than 111.8, as they both don't need to be removed from the model. And the model is still $y \sim x_1 + x_2$.

Finally, we get the model

$$y = -1.458 - 0.0955 * x_2 + 0.078 * x_1$$

(3) Both direction selection+ AIC

Step 1

Start: AIC=136.94

 $y \sim 1$

	Df	Deviance	AIC
+ x2	1	113.20	117.20
+ x1	1	116.27	120.27
+ x3	1	132.88	136.88
<none>		134.94	136.94

Based on the step one, AIC=136.94. These three variables AIC are all greater than 136.94, but we should first add x_2 into the model since its AIC is the smallest and thus it has most effect on the model. Then the model becomes $y \sim x_2$.

Step 2

Step: AIC=117.2
 $y \sim x_2$

	Df	Deviance	AIC
+ x1	1	105.80	111.80
+ x3	1	111.19	117.19
<none>		113.20	117.20
- x2	1	134.94	136.94

After add x_2 as a variable into the model, based on the step two, AIC=117.2. We should then add x_1 into the model since its AIC is smaller than 117.2 and it is the smallest and thus it has most effect on the model. Then the model becomes $y \sim x_2 + x_1$.

Step 3

Step: AIC=111.8
 $y \sim x_2 + x_1$

	Df	Deviance	AIC
<none>		105.80	111.80
+ x3	1	105.09	113.09
- x1	1	113.20	117.20
- x2	1	116.27	120.27

Call: glm(formula = $y \sim x_2 + x_1$, family = binomial("logit"), data = b)

Coefficients:
 (Intercept) x_2 x_1
 -1.45778 -0.09547 0.07787

Degrees of Freedom: 158 Total (i.e. Null); 156 Residual
 Null Deviance: 134.9
 Residual Deviance: 105.8 AIC: 111.8

Now, the model becomes $y \sim x_2 + x_1$, and then after step three, AIC=111.8 and we find that x_3 's AIC is greater than 111.8, so it does not have much effect on the model. We will not add it into the model.

Finally, we get the model

Call: glm(formula = $y \sim x_1 + x_2$, family = binomial(link = "logit"), data = b)

Coefficients:
 (Intercept) x_1 x_2
 -1.45778 0.07787 -0.09547

Degrees of Freedom: 158 Total (i.e. Null); 156 Residual
 Null Deviance: 134.9
 Residual Deviance: 105.8 AIC: 111.8

Table 2.4 R summary table for final model

$$y = -1.458 - 0.0955 * x_2 + 0.078 * x_1$$

(g) Create an ROC plot for the final model. Interpret the results.

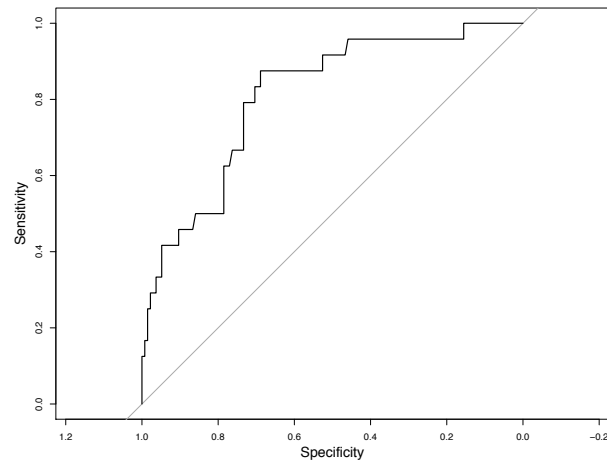


Figure 2.5 ROC Plot

Area under the curve: 0.8094

The result shows excellent discrimination, which means that the probability that predictions and the outcomes are concordant is 80.94%.

3. In a clinical trial, m subjects are assigned to each of the treatment group and the control group. In the treatment group, y_1 of the m subjects have positive response, while in the control group, y_2 subjects have positive response. We are interested in estimating the treatment effect and providing its confidence interval.

(a) Present the above problem as a logistic regression problem and give the interpretation of the regression coefficients β .

Y	control group($X_i=0$)	treatment group($X_i=1$)
# of positive response	y_2	y_1
# of negative response	$m-y_2$	$m-y_1$
total	m	m

Y_i : reaction of i th subject

$$Y_i = \begin{cases} 1, & \text{ith subject has positive response} \\ 0, & \text{ith subject has negative response} \end{cases}$$

$$Y_i \sim \text{Bernoulli}(p_i)$$

y_1, \dots, y_m belongs to control group, y_{m+1}, \dots, y_{2m} belongs to treatment group

$$\sum_{i=1}^{2m} y_i = y_1 + y_2$$

$$\sum_{i=m+1}^{2m} y_i = y_1$$

$$\sum_{i=1}^m y_i = y_2$$

$$X_i = \begin{cases} 1, & \text{ith subject belong to treatment group} \\ 0, & \text{ith subject belong to control group} \end{cases}$$

Logistic Regression Model

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_{1i}$$

Interpretation of the regression coefficients β

$$\beta = (\beta_0, \beta_1)'$$

β_0 : representing the average odds of response variable corresponding to the random samples from control group.

β_1 : representing the difference between the log odds for subjects from treatment group and the log odds for subjects from control group.

(b) Express the likelihood function as a function of β , and derive the MLE $\hat{\beta}$.

Likelihood Function

$$\Pr(Y_i = y_i; p_i) = p_i^{y_i} (1 - p_i)^{1-y_i} = \left(\frac{p_i}{1 - p_i} \right)^{y_i} (1 - p_i)$$

$$\frac{p_i}{1 - p_i} = e^{\beta_0 + \beta_1 X_{1i}}$$

$$1 - p_i = \frac{1}{1 + e^{\beta_0 + \beta_1 X_{1i}}}$$

$$\Pr(Y_i = y_i; \beta_0, \beta_1) = (e^{\beta_0 + \beta_1 X_{1i}})^{y_i} \frac{1}{1 + e^{\beta_0 + \beta_1 X_{1i}}}$$

$$L(Y; \beta_0, \beta_1) = \prod_{i=1}^{2m} \Pr(Y_i = y_i; \beta_0, \beta_1) = \prod_{i=1}^{2m} (e^{\beta_0 + \beta_1 X_{1i}})^{y_i} \frac{1}{1 + e^{\beta_0 + \beta_1 X_{1i}}}$$

MLE $\hat{\beta}$

$$X_i = 0, p_i = \frac{e^{\beta_0}}{1 + e^{\beta_0}} \triangleq p_c$$

$$X_i = 1, p_i = \frac{e^{\beta_0 + \beta_1}}{1 + e^{\beta_0 + \beta_1}} \triangleq p_t$$

$$l(Y; \beta_0, \beta_1) = \log L(Y; \beta_0, \beta_1) = \sum_{i=1}^{2m} (\beta_0 + \beta_1 X_{1i}) y_i - \log \prod_{i=1}^{2m} (1 + e^{\beta_0 + \beta_1 X_{1i}})$$

$$\frac{\partial l(Y; \beta_0, \beta_1)}{\partial \beta_0} = \sum_{i=1}^{2m} y_i - \sum_{i=1}^{2m} \frac{e^{\beta_0 + \beta_1 X_{1i}}}{1 + e^{\beta_0 + \beta_1 X_{1i}}} = 0$$

$$\frac{\partial l(Y; \beta_0, \beta_1)}{\partial \beta_1} = \sum_{i=1}^{2m} X_{1i} y_i - \sum_{i=1}^{2m} \frac{e^{\beta_0 + \beta_1 X_{1i}}}{1 + e^{\beta_0 + \beta_1 X_{1i}}} X_{1i} = 0$$

$$\Rightarrow \begin{cases} \hat{p}_t = \frac{y_1}{m} \\ \hat{p}_c = \frac{y_2}{m} \end{cases} \Rightarrow \begin{cases} \hat{\beta}_0 = \log\left(\frac{y_2}{m - y_2}\right) \\ \hat{\beta}_1 = \log\left(\frac{y_1(m - y_2)}{y_2(m - y_1)}\right) \end{cases}$$

(c) Find the asymptotic variance-covariance matrix of $\hat{\beta}$.

$$H_{2m}(\beta_0, \beta_1) = \begin{bmatrix} \frac{\partial^2 l}{\partial \beta_0^2} & \frac{\partial^2 l}{\partial \beta_0 \partial \beta_1} \\ \frac{\partial^2 l}{\partial \beta_1 \partial \beta_0} & \frac{\partial^2 l}{\partial \beta_1^2} \end{bmatrix} = \begin{bmatrix} -m \left(\frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} + \frac{e^{\beta_0}}{(1 + e^{\beta_0})^2} \right) & -m \frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} \\ -m \frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} & -m \frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} \end{bmatrix}$$

$$\sqrt{n} \left[\begin{pmatrix} \hat{\beta}_0 \\ \hat{\beta}_1 \end{pmatrix} - \begin{pmatrix} \beta_0 \\ \beta_1 \end{pmatrix} \right] \xrightarrow{d} N(0, I_1(\beta_0, \beta_1)^{-1}), \text{ where } I_1 = \frac{1}{n} I_n \text{ and } n = 2m$$

$$I_n(\beta_0, \beta_1) = -E(H_n(\beta_0, \beta_1))$$

Asymptotic variance – covariance matrix of $\hat{\beta}$ is $-H_{2m}^{-1}(\hat{\beta})$

$$-H_{2m}^{-1}(\beta_0, \beta_1) = \frac{(1 + e^{\beta_0 + \beta_1})^2 (1 + e^{\beta_0})^2}{m^2 e^{2\beta_0 + \beta_1}} \begin{bmatrix} m \frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} & -m \frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} \\ -m \frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} & m \left(\frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} + \frac{e^{\beta_0}}{(1 + e^{\beta_0})^2} \right) \end{bmatrix}$$

(d) Suppose that $m = 20$, $y_1 = 12$, and $y_2 = 9$. Give the point estimate and the corresponding 95% confidence interval for the odds ratio of having positive response between the treatment group and the control group. Can you conclude that the treatment is effective?

$$\log\left(\frac{p_i}{1 - p_i}\right) = \beta_0 + \beta_1 X_{1i}$$

$$\hat{\beta}_0 = \log\left(\frac{y_2}{m - y_2}\right) = \log\frac{9}{11} = -0.2007 \quad \hat{\beta}_1 = \log\left(\frac{y_1(m - y_2)}{y_2(m - y_1)}\right) = \log\frac{11}{6} = 0.6061$$

$\hat{OR} = \exp(\hat{\beta}_1) = \frac{11}{6}$ is the point estimate for the odds ratio of having positive response between the treatment group and the control group

$$Var(\ln(\hat{OR})) = Var(\hat{\beta}_1) = \frac{(1 + e^{\beta_0 + \beta_1})^2 (1 + e^{\beta_0})^2}{m^2 e^{2\beta_0 + \beta_1}} m \left(\frac{e^{\beta_0 + \beta_1}}{(1 + e^{\beta_0 + \beta_1})^2} + \frac{e^{\beta_0}}{(1 + e^{\beta_0})^2} \right) = 0.4104$$

$$\hat{se}(\ln(\hat{OR})) = \hat{se}(\hat{\beta}_1) = \sqrt{Var(\hat{\beta}_1)} = 0.6406$$

$$95\% \text{ CI for } \hat{\beta}_1 \text{ is } \hat{\beta}_1 \pm z_{1-\alpha/2} \hat{se}(\hat{\beta}_1) = (-0.6495, 1.8617)$$

$$95\% \text{ CI for } \hat{OR} \text{ is } e^{\hat{\beta}_1 \pm z_{1-\alpha/2} \hat{se}(\hat{\beta}_1)} = (0.5223, 6.4347)$$

From the result we can conclude that the treatment is not effective.

4. Flour beetles *Tribolium castaneum* were sprayed with one of three insecticides in solution at different doses. The number of insects killed after a six-day period is recorded below

(a) Investigate graphically the relationship between the dose, either in original units or in log units, and the kill rate.

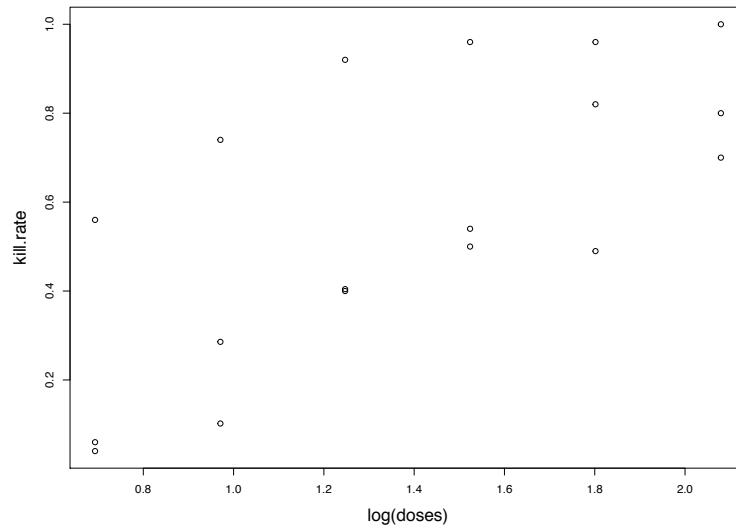


Figure 4.1 Relationship between the doses (log units) and the kill rate

Based on the graph above, the dose and kill rate are positively related.

(b) On the graph for part (a), plot the linear logistic fitted curve for each of the insecticides plus the combination.

I fit the logistic regression and I will have the model:

$$\log\left(\frac{\Pr(Y_i = 1 | X)}{1 - \Pr(Y_i = 1 | X)}\right) \triangleq \text{logit}(p_i) = X^T \beta \Leftrightarrow p_i = \frac{e^{X^T \beta}}{1 + e^{X^T \beta}}$$

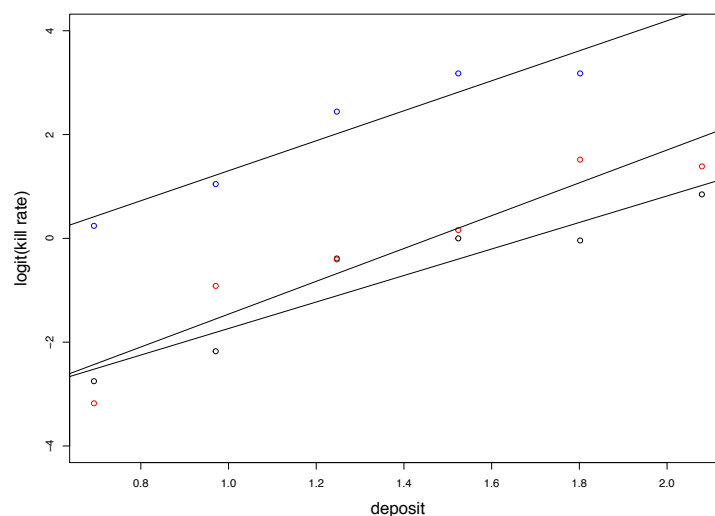


Figure 4.2 Linear Logistic Fitted Curve

(c) Consider the two models, one in which the relationship is described by three parallel straight lines in the log dose and one in which the three lines are straight but not parallel. Assess the evidence against the hypothesis of parallelism.

Model one:

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i}$$

$$X_{1i} = \begin{cases} 1, & \text{if DDT insecticide} \\ 0, & \text{otherwise} \end{cases}$$

$$X_{2i} = \begin{cases} 1, & \text{if } \gamma\text{-BHC insecticide} \\ 0, & \text{otherwise} \end{cases}$$

$$X_{3i} : \log \text{ dose}$$

Model two:

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \beta_4 X_{1i} X_{3i} + \beta_5 X_{2i} X_{3i}$$

Assess the evidence against the hypothesis of parallelism:

$$H_0 : \beta_4 = 0 \text{ v.s. } H_1 : \beta_4 \neq 0 \quad \text{and} \quad H_0 : \beta_5 = 0 \text{ v.s. } H_1 : \beta_5 \neq 0$$

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
deposit[1:17]	1	21.348	21.348	74.867	3.08e-06	***
x1[1:17]	1	11.172	11.172	39.181	6.18e-05	***
x2[1:17]	1	18.923	18.923	66.361	5.50e-06	***
deposit[1:17]:x1[1:17]	1	0.213	0.213	0.748	0.406	
deposit[1:17]:x2[1:17]	1	0.037	0.037	0.128	0.727	
Residuals	11	3.137	0.285			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1						

Figure 4.3 Anova summary table for parallelism

Based on the result, we find that p-value is 0.406 and 0.727 respectively, they are both >0.025 . So we can conclude that we should accept the null hypothesis that $\beta_4=0$ and $\beta_5=0$ which means three straight lines are parallel.

(d) Let chem denote a 3-level categorical factor, and let ldose be the log dose. Explain the relationship between the regression coefficients in the model formulae chem + ldose and chem + ldose - 1. Explain the relationship between the two covariance matrices.

Model 1: `lm.reg1=lm(killrate~chem+ldose)`

```
Call: glm(formula = y ~ log(XX$deposit) + XX$type, family = binomial(link = "logit"))

Coefficients:
(Intercept) log(XX$deposit)    XX$typeDDT    XX$typeMIXED
   -3.8397       2.6938      -0.6144       2.4170

Degrees of Freedom: 881 Total (i.e. Null);  878 Residual
Null Deviance:      1203
Residual Deviance: 819  AIC: 827
```

Figure 4.4 model 1 regression

Based on the table, we can find that

regression coefficient for intercept is -3.8397

regression coefficient for chemDDT is -0.6144

regression coefficient for chemMIXED is 2.4170

regression coefficient for deposit is 2.6938

Model 2: `lm.reg2=lm(killrate~chem+ldose-1)`

```
Call: glm(formula = y ~ log(XX$deposit) + XX$type - 1, family = binomial(link = "logit"))

Coefficients:
log(XX$deposit)    XX$typeBHC    XX$typeDDT    XX$typeMIXED
      2.694      -3.840      -4.454      -1.423

Degrees of Freedom: 882 Total (i.e. Null);  878 Residual
Null Deviance:      1223
Residual Deviance: 819  AIC: 827
```

Figure 4.5 model 2 regression

Based on the table, we can find that

regression coefficient for chemDDT is -4.454

regression coefficient for chemBHC is -3.840

regression coefficient for chemMIXED is -1.423

regression coefficient for deposit is 2.694

Comparison

Regression coefficient for deposit is the same for two models, and the coefficients for others are different.

ChemDDT in model 2 equal to coefficient for intercept added regression coefficient for chemDDT in model 1.

chemMIXED in model 2 equal to coefficient for intercept added regression coefficient for chemMIXED in model 1.

So, in this sense -1 remove the intercept:

`killrate~chem+ldose` doesn't have chemBHC but have intercept

`killrate~chem+ldose-1` doesn't have intercept but have chemBHC

Covariance Matrix

	(Intercept)	log(XX\$deposit)	XX\$typeDDT	XX\$typeMIXED
(Intercept)	0.10974859	-0.064832766	-0.010956108	-0.04278991
log(XX\$deposit)	-0.06483277	0.046061045	-0.005355279	0.01726135
XX\$typeDDT	-0.01095611	-0.005355279	0.039941979	0.01648699
XX\$typeMIXED	-0.04278991	0.017261346	0.016486990	0.05660964

Figure 4.6 Covariance Matrix for model 1

	log(XX\$deposit)	XX\$typeBHC	XX\$typeDDT	XX\$typeMIXED
log(XX\$deposit)	0.04606105	-0.06483277	-0.07018804	-0.04757142
XX\$typeBHC	-0.06483277	0.10974859	0.09879248	0.06695868
XX\$typeDDT	-0.07018804	0.09879248	0.12777835	0.07248956
XX\$typeMIXED	-0.04757142	0.06695868	0.07248956	0.08077841

Figure 4.7 Covariance Matrix for model 2

Relationship

Actually, the relationship between the two covariance matrices is a kind of linear transformation.

$$\text{Model1: } y \sim \beta_0 + \beta_1 \log(X) + \beta_1 \text{DDT} + \beta_3 \text{MIXED}$$

$$\text{Model2: } y \sim \alpha_0 \log(X) + \alpha_1 \text{BHC} + \alpha_2 \text{DDT} + \alpha_3 \text{MIXED}$$

$$\beta = (\beta_0, \beta_1, \beta_2, \beta_3)' = A * (\alpha_0, \alpha_1, \alpha_2, \alpha_3)', \text{ where } A \text{ is a transformation matrix}$$

$$\text{cov}(\beta) = A * \text{cov}(\alpha), \text{ where } A \text{ is a transformation matrix}$$

(e) On the assumption that three parallel straight lines suffice, estimate the potency of the combination relative to each of the components. Obtain a 90% confidence interval for each of these relative potencies.

Model

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i}$$

$$X_{1i} = \begin{cases} 1, & \text{if DDT insecticide} \\ 0, & \text{otherwise} \end{cases}$$

$$X_{2i} = \begin{cases} 1, & \text{if } \gamma\text{-BHC insecticide} \\ 0, & \text{otherwise} \end{cases}$$

$$X_{3i} : \log \text{dose}$$

Combination

$$\log\left(\frac{\Pr(Y_i = 1 | X_{1i} = 0, X_{2i} = 0)}{1 - \Pr(Y_i = 1 | X_{1i} = 0, X_{2i} = 0)}\right) = \beta_0 + \beta_3 X_{3i}$$

Components(ddd&bhc)

$$\log\left(\frac{\Pr(Y_i = 1 | X_{1i} = 1, X_{2i} = 0)}{1 - \Pr(Y_i = 1 | X_{1i} = 1, X_{2i} = 0)}\right) = \beta_0 + \beta_1 + \beta_3 X_{3i}$$

$$\log\left(\frac{\Pr(Y_i = 1 | X_{1i} = 0, X_{2i} = 1)}{1 - \Pr(Y_i = 1 | X_{1i} = 0, X_{2i} = 1)}\right) = \beta_0 + \beta_2 + \beta_3 X_{3i}$$

Potency

$$\log\left(\frac{P_{00} / (1 - P_{00})}{P_{10} / (1 - P_{10})}\right) = \log(OR1) = -\beta_1$$

$$\log\left(\frac{P_{00} / (1 - P_{00})}{P_{01} / (1 - P_{01})}\right) = \log(OR2) = -\beta_2$$

So, we need to estimate the coefficient beta1 and beta2.

```
Call: glm(formula = y ~ log(XX$deposit) + XX$type - 1, family = binomial(link = "logit"))

Coefficients:
log(XX$deposit)    XX$typeBHC    XX$typeDDT    XX$typeMIXED
      2.694         -3.840         -4.454         -1.423

Degrees of Freedom: 882 Total (i.e. Null);  878 Residual
Null Deviance:      1223
Residual Deviance: 819  AIC: 827
```

Figure 4.8 R summary table for general linear logistic regression

By r function, beta1=-4.454, beta2=-3.840.

Potency of the combination relative to DDT is $\exp(4.454) = 85.97$.

Potency of the combination relative to BHC is $\exp(3.840) = 46.5255$.

90% CI

90% CI for beta1 (-5.0582, -3.8812)

90% CI for beta2 (-4.3977, -3.3070)

90% CI for potency of the combination relative to DDT is (48.4825, 157.3024)

90% CI for potency of the combination relative to BHC is (27.302, 81.264)

(f) Check to see if one of the alternative link functions probit, c-log log or log log, gives an appreciably better fit. Give the answer to part (e) for the c-log log model.

1) link=probit

```
> glm(y~log(XX$deposit)+XX$type,family=binomial(link="probit"))

Call: glm(formula = y ~ log(XX$deposit) + XX$type, family = binomial(link = "probit"))

Coefficients:
(Intercept) log(XX$deposit)    XX$typeDDT    XX$typeMIXED
   -2.2734         1.5902         -0.3535         1.4304

Degrees of Freedom: 881 Total (i.e. Null);  878 Residual
Null Deviance:      1203
Residual Deviance: 817  AIC: 825
> glm(y~log(XX$deposit)+XX$type-1,family=binomial(link="probit"))

Call: glm(formula = y ~ log(XX$deposit) + XX$type - 1, family = binomial(link = "probit"))

Coefficients:
log(XX$deposit)    XX$typeBHC    XX$typeDDT    XX$typeMIXED
      1.5902         -2.2734         -2.6269         -0.8431

Degrees of Freedom: 882 Total (i.e. Null);  878 Residual
Null Deviance:      1223
Residual Deviance: 817  AIC: 825
```

Figure 4.9 R summary table for link=probit

When link =probit, AIC=825 which is smaller than link=logit AIC=827.

So link function probit, gives an appreciably better fit.

2) link= c-log log

```
> glm(y~log(XX$deposit)+XX$type,family=binomial(link="cloglog"))

Call: glm(formula = y ~ log(XX$deposit) + XX$type, family = binomial(link = "cloglog"))

Coefficients:
(Intercept) log(XX$deposit)    XX$typeDDT    XX$typeMIXED
      -2.8115         1.6655        -0.4242         1.4376

Degrees of Freedom: 881 Total (i.e. Null);  878 Residual
Null Deviance:      1203
Residual Deviance: 826.2    AIC: 834.2
> glm(y~log(XX$deposit)+XX$type-1,family=binomial(link="cloglog"))

Call: glm(formula = y ~ log(XX$deposit) + XX$type - 1, family = binomial(link = "cloglog"))

Coefficients:
log(XX$deposit)    XX$typeBHC    XX$typeDDT    XX$typeMIXED
      1.665         -2.811        -3.236         -1.374

Degrees of Freedom: 882 Total (i.e. Null);  878 Residual
Null Deviance:      1216
Residual Deviance: 826.2    AIC: 834.2
```

Figure 4.10 R summary table for link=cloglog

When link =cloglog, AIC=834.2 which is larger than link=logit AIC=827.

So link function cloglog, gives an appreciably better fit.

Answer to part (e) for the c-log log model

By r function, beta1=-3.236, beta2=-2.811.

Potency of the combination relative to DDT is $\exp(3.236) = 25.4318$.

Potency of the combination relative to BHC is $\exp(2.811) = 16.6265$.

90% CI

90% CI for beta1 (-3.630462, -2.856884)

90% CI for beta2 (-3.185522, -2.452735)

90% CI for potency of the combination relative to DDT is (17.4072, 37.73024)

90% CI for potency of the combination relative to BHC is (11.62008, 24.1799)

(g) Under the linear logistic model, estimate the combination dose required to give a 99% kill rate, and obtain a 90% confidence interval for this dose.

```
Call: glm(formula = y ~ log(XX$deposit) + XX$type, family = binomial(link = "logit"))

Coefficients:
(Intercept) log(XX$deposit)    XX$typeDDT    XX$typeMIXED
      -3.8397         2.6938        -0.6144         2.4170

Degrees of Freedom: 881 Total (i.e. Null);  878 Residual
Null Deviance:      1203
Residual Deviance: 819    AIC: 827
```

Figure 4.11 Linear Logistic Model

$$\log it(p_i) = -8397 + 2.6938 * \text{ldose} - 0.6144 * \text{DDT} + 2.4170 * \text{MIXED}$$

When give a 99% kill rate, the combination ldose=2.2339, dose=9.3367

90% confidence interval for this dose is (5.2834, 19.3627)

(h) Give a brief summary of your conclusions regarding the effectiveness of these three insecticides.

```
Call: glm(formula = y ~ log(XX$deposit) + XX$type - 1, family = binomial(link = "logit"))
```

Coefficients:

log(XX\$deposit)	XX\$typeBHC	XX\$typeDDT	XX\$typeMIXED
2.694	-3.840	-4.454	-1.423

Degrees of Freedom: 882 Total (i.e. Null); 878 Residual

Null Deviance: 1223

Residual Deviance: 819 AIC: 827

Figure 4.11 R summary table for effectiveness of insecticide

Based on the r summary table, we can find that the mixed insecticide can have a better effect on the kill rate. BHC ranks second and DDT has the worst effect on kill rate.

Appendix

```
#1(a)
a=read.table("fungus.txt",header = TRUE)
Y=c(a$X1,a$X2,a$X3,a$X4,a$X5,a$X6,a$X7,a$X8)
temp=c("55", "60", "65", "70", "75", "80", "85","55", "60", "65", "70", "75", "80", "85",
        "55", "60", "65", "70", "75", "80", "85","55", "60", "65", "70", "75", "80", "85",
        "55", "60", "65", "70", "75", "80", "85","55", "60", "65", "70", "75", "80", "85",
        "55", "60", "65", "70", "75", "80", "85","55", "60", "65", "70", "75", "80", "85")
isolate=c("X1","X1","X1","X1","X1","X1","X1","X2","X2","X2","X2","X2","X2","X2","X3","X3","X
3","X3","X3","X3","X3",

"X4","X4","X4","X4","X4","X4","X4","X5","X5","X5","X5","X5","X5","X5","X6","X6","X6","X6","X
6","X6","X6",
        "X7","X7","X7","X7","X7","X7","X7","X8","X8","X8","X8","X8","X8","X8")
lm.reg=lm(Y~isolate+temp)
summary(lm.reg)
anova(lm.reg)

#1(b)
fug = read.table("fungus.txt",header = T)
fug = unlist(fug)[-1:7]]
fung = data.frame("fungus" = fug,"temp" = factor(rep(seq(55,85,by=5),8)),"iso" =
factor(rep(1:8,each = 7)))
fung
temp

a=read.table("fungus.txt",header = TRUE)
a
Y=c(a$X1,a$X2,a$X3,a$X4,a$X5,a$X6,a$X7,a$X8)
x=rep(seq(55,85,by=5),8)
x2=x^2;x3=x^3;x4=x^4;x5=x^5;x6=x^6
lm6=lm(Y~x+x2+x3+x4+x5+x6)
anova(lm6)
lm0=lm(Y~1)
lm1=lm(Y~1+x)
lm2=lm(Y~1+x+x2)
lm3=lm(Y~x+x2+x3)
lm4=lm(Y~x+x2+x3+x4)
lm5=lm(Y~x+x2+x3+x4+x5)
anova(lm0,lm1)
anova(lm1,lm2)
anova(lm2,lm3)
anova(lm3,lm4)
```

```
anova(lm4,lm6)
```

```
anova(lm3,lm6)
```

```
#1(c)
```

```
lm3=lm(Y~x+x2+x3)
```

```
fun=function(x){
```

```
  return(-sum(c(1,x,x^2,x^3)*lm3$coefficients))
```

```
}
```

```
optimize(fun,c(55,85))
```

```
#2(a)
```

```
b=read.table("flushot.txt",header = TRUE)
```

```
b
```

```
glm.reg=glm(data=b,y~x1+x2+x3,family=binomial(link="logit"))
```

```
summary(glm.reg)
```

```
ci95=confint.default(glm.reg)
```

```
#2(b)
```

```
round(cbind(exp(glm.reg$coefficients),exp(confint.default(glm.reg))),3)
```

```
#2(c)
```

```
pnew = predict.glm(glm.reg, newdata=data.frame(x1=55,x2=60,x3=1), se.fit=T, type="link")
```

```
hat = pnew$fit
```

```
se.hat = pnew$se.fit
```

```
phat = exp(hat)/(1+exp(hat))
```

```
data.frame("lowerbound"=hat-qnorm(0.975)*se.hat,"upperbound"=hat+qnorm(0.975)*se.hat)
```

```
uphat = exp(hat-qnorm(0.975)*se.hat)/(1+exp(hat-qnorm(0.975)*se.hat))
```

```
lohat = exp(hat+qnorm(0.975)*se.hat)/(1+exp(hat+qnorm(0.975)*se.hat))
```

```
data.frame("lower bound"=uphat ,"upper bound"=lohat) # c.i for estimated prob
```

```
#2(e)
```

```
anova(glm(data=b,y~x1+x2,family = binomial("logit")),glm.reg,test = "Chisq")
```

```
#2(f)
```

```
b=read.table("flushot.txt",header = TRUE)
```

```
glm.reg=glm(data=b,y~x1+x2+x3,family=binomial(link="logit"))
```

```
glm0=glm(data=b,y~1,family = binomial("logit"))
```

```
#aic
```

```
step(glm0,scope=list(upper=glm.reg),direction = "both")
```

```
step(glm0,scope=list(upper=glm.reg),direction = "forward")
```

```
step(glm.reg)
```

```
#bic
```

```
step(glm0,scope=list(upper=glm.reg),direction = "both",k=log(length(y)))
```

```
step(glm0,scope=list(upper=glm.reg),direction = "forward",k=log(length(y)))
```

```
step(glm.reg,k=log(length(y)))
```

```

#final model
glm.reg=glm(data=b,y~x1+x2,family=binomial(link="logit"))
glm.reg

#2(g)
b=read.table("flushot.txt",header = TRUE)
glm.reg.final=glm(y~x1+x2,family=binomial(link="logit"))
install.packages("pROC")
library(pROC)
y=b$y
flushot.roc=roc(y~fitted(glm.reg.final))
plot(flushot.roc,cex.lab=1.5)
auc(flushot.roc)

```

```

#4(a)
par(mfrow=c(1,1))
kill.rate=c(3/50,5/49,19/47,19/38,24/49,35/50,2/50,14/49,20/50,27/50,41/50,40/50,28/50,37/50,46/50,48/50,48/50,50/50)
doses=c(2.00,2.64,3.48,4.59,6.06,8.00,2.00,2.64,3.48,4.59,6.06,8.00,2.00,2.64,3.48,4.59,6.06,8.00)
log(doses)
doses.killrate=lm(kill.rate~doses)
plot(log(doses),kill.rate,cex.lab=1.5)

#4(b)
data=data.frame("deposit"=c(2.00,2.64,3.48,4.59,6.06,8.00),
                "ddt"=c(3/50,5/49,19/47,19/38,24/49,35/50),
                "bhc"=c(2/50,14/49,20/50,27/50,41/50,40/50),
                "both"=c(28/50,37/50,46/50,48/50,48/50,50/50))

logit = function(x){
  log(x/(1-x))
}

data$deposit = log(data$deposit)
plot(data$deposit,logit(data$ddt),ylim=c(-4,4),xlab="deposit",ylab="logit(kill rate)",cex.lab=1.5)
points(data$deposit,logit(data$bhc),col="red")
points(data$deposit,logit(data$both),col="blue")

d = lm(logit(ddt)~deposit,data=data)
abline(reg=d)
b = lm(logit(bhc)~deposit,data=data)
abline(reg=b)
combine = lm(logit(data$both[1:5])~deposit[1:5],data=data)
abline(reg=combine)

```

```

#4(c)
insect=c(rep(0,6),rep(1,6),rep(2,6))
x1=c(rep(1,6),rep(0,6),rep(0,6))
x2=c(rep(0,6),rep(1,6),rep(0,6))

insec_type = factor(insect, levels = c(0, 1, 2),
                    labels = c("DDT", "BHC", "MIXED"))
dose=rep(c(2.00, 2.64, 3.48, 4.59, 6.06, 8.00),3)
logdose=log(dose)
killrate=c(3/50,5/49,19/47,19/38,24/49,35/50,2/50,14/49,20/50,27/50,41/50,40/50,28/50,37/
50,46/50,48/50,48/50,50/50)
data=data.frame("killrate"=killrate,"deposit"=logdose,"x1"=x1,"x2"=x2)
logit = function(x){
  log(x/(1-x))
}
data.lm=lm((logit(killrate)[1:17]~data$deposit[1:17]+data$x1[1:17]+data$x2[1:17]))
data.aov1 =
aov(logit(killrate)[1:17]~deposit[1:17]+x1[1:17]+x2[1:17]+x1[1:17]*deposit[1:17],data=data)
summary(data.aov1)
data.aov2 =
aov(logit(killrate)[1:17]~deposit[1:17]+x1[1:17]+x2[1:17]+x1[1:17]*deposit[1:17],data=data)
summary(data.aov2)

#4(d)
insect=c(rep(0,6),rep(1,6),rep(2,6))

insec_type = factor(insect, levels = c(0, 1, 2),
                    labels = c("DDT", "BHC", "MIXED"))

dose=rep(c(2.00, 2.64, 3.48, 4.59, 6.06, 8.00),3)
killed=c(3,5,19,19,24,35,2,14,20,27,41,40,28,37,46,48,48,50)
unkilled=c(50,49,47,38,49,50,50,49,rep(50,10))-killed
data=data.frame("killed"=killed,"unkilled"=unkilled,"deposit"=dose,"type"=insec_type)

# making binary var
y=c()
for(i in 1:length(killed)){
  yi=c(rep(1,killed[i]),rep(0,unkilled[i]))
  y=c(y,yi)
}

total=killed+unkilled
cumsum(total)
total=c(0,total)

```

```
XX = matrix(0,ncol = 2,nrow =sum(total))
X=as.matrix(data[,c(3,4)])
cum=cumsum(total)
for(i in 1:(length(cum)-1)){
  k=((cum[i]+1):(cum[i+1]))
  v=X[i,]
  for(j in 1:length(k)){
    XX[k[j],]=v
  }
}
XX=data.frame(XX)
XX$X1=as.numeric(as.character(XX$X1))
colnames(XX)=c("deposit","type")
head(XX)

#regression
glm1=glm(y~log(XX$deposit)+XX$type,family=binomial(link="logit"))
glm2=glm(y~log(XX$deposit)+XX$type-1,family=binomial(link="logit"))
#var-cor
summary(glm1)$cov.unscaled
summary(glm2)$cov.unscaled

#4(e)
confint(glm2,level = 0.9)

#4(f)
glm(y~log(XX$deposit)+XX$type,family=binomial(link="probit"))
glm(y~log(XX$deposit)+XX$type-1,family=binomial(link="probit"))

glm(y~log(XX$deposit)+XX$type,family=binomial(link="cloglog"))
glmcc=glm(y~log(XX$deposit)+XX$type-1,family=binomial(link="cloglog"))
confint(glmcc,level = 0.9)

#4(g)
dose=c(2.00, 2.64, 3.48, 4.59, 6.06, 8.00)
ldose=log(dose)
kill.rate.both=c(28/50,37/50,46/50,48/50,48/50,50/50)
lm.both=lm(kill.rate.both~ldose)
confint(lm.both,level = 0.9)
```
