MATHEMATICAL TRIPOS Part III

Tuesday 5 June 2007 1.30 to 4.30

PAPER 43

APPLIED STATISTICS

Attempt **FOUR** questions. There are **FIVE** questions in total. The questions carry equal weight.

STATIONERY REQUIREMENTS

Cover sheet Treasury Tag Script paper **SPECIAL REQUIREMENTS** None

You may not start to read the questions printed on the subsequent pages until instructed to do so by the Invigilator. 1 The data in the table below refer to an investigation into the effectiveness of two new teaching methods (B and C) compared to the existing teaching method (A). Twenty-one children are given an initial aptitude test and then each child is taught using one of the three teaching methods. Their scores in an achievement test at the end of the investigation are also recorded.

Teaching Method

			0				
I	A]	В	(С		
final achievement score	initial aptitude score	final achievement score	initial aptitude score	final achievement score	initial aptitude score		
6	3	8	4	6	3		
4	1	9	5	7	2		
5	3	7	5	7	2		
3	1	9	4	7	3		
4	2	8	3	8	4		
3	1	5	1	5	1		
6	4	7	2	7	4		

The aim of the analysis in the S-Plus output below is to investigate any differences in effectiveness of the teaching methods, taking into account differences in initial aptitudes between the three groups of children. Interpret the commands and output in detail. Which is your preferred model, and what do you conclude about the different teaching methods? Illustrate with suitable sketch graph(s).

```
> teachingdata <- read.table("teachingdata", header=T)</pre>
> attach(teachingdata)
> score
  1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
 6
    4 5 3 4 3
                     8 9 7 9 8 5 7 6 7 7 7 8 5 7
                  6
> aptitude
  1 2 3 4 5
                     8 9 10 11 12 13 14 15 16 17 18 19 20 21
                67
  3
             2
                   4
                      4 5 5 4 3 1 2 3 2 2 3 4 1 4
    1
       3 1
                1
> group <- rep(1:3, each=7)
> Group <- factor(group)</pre>
> options(contrasts=c("contr.treatment","contr.poly"))
> teach1.lm <-</pre>
  lm (score {\catcode'\~ = 11 ~} aptitude * Group)
> anova(teach1.lm)
Analysis of Variance Table
Response: score
Terms added sequentially (first to last)
                                        F Value
                                                     Pr(F)
               Df Sum of Sq
                               Mean Sq
                    36.57548 36.57548 56.94218 0.0000018
     aptitude
                1
        Group
                2
                    16.93200
                               8.46600 13.18021
                                                 0.0004969
                2
                     0.66714
                               0.33357
                                        0.51932 0.6052426
aptitude:Group
    Residuals 15
                     9.63490
                               0.64233
> teach2.lm <-
 lm (score {\catcode'\~ = 11 ~} aptitude + Group)
> anova(teach2.lm)
Analysis of Variance Table
Response: score
Terms added sequentially (first to last)
          Df Sum of Sq
                          Mean Sq
                                   F Value
                                                   Pr(F)
 aptitude
           1
               36.57548
                         36.57548 60.35534 0.0000005428
          2
                          8.46600 13.97024 0.0002578664
   Group
               16.93200
Residuals 17
               10.30204
                          0.60600
```

4

> summary(teach2.lm, cor=F) Call: lm (formula = score {\catcode'\~ = 11 ~} aptitude + Group) Residuals: Min 1Q Median Max ЗQ -1.739 -0.5796 0.07347 0.4898 1.004Coefficients: Value Std.Error t value Pr(>|t|) (Intercept) 2.8367 0.4235 6.6988 0.0000 aptitude 0.7429 0.1421 5.2267 0.0001 0.0002 Group2 2.1878 0.4545 4.8139 Group3 1.8612 0.4240 4.3901 0.0004 Residual standard error: 0.7785 on 17 degrees of freedom Multiple R-Squared: 0.8386 F-statistic: 29.43 on 3 and 17 degrees of freedom, \$\phantom {-} \qquad \qquad \qquad\$ the p-value is 5.889e-07

2 Let Y_1, \ldots, Y_n be independent random variables with the density of Y_i given by

$$f_{Y_i}(y_i) = \exp\left\{\frac{y_i\theta_i - b(\theta_i)}{\phi} + c(y_i, \phi)\right\},\qquad(*)$$

and suppose that $g(\mu_i) = \boldsymbol{\beta}^T \boldsymbol{x}_i$ where $\mu_i = \mathbb{E}(Y_i), \boldsymbol{\beta} = (\beta_1, \dots, \beta_p)^T$ and \boldsymbol{x}_i is a known $p \times 1$ vector of covariates, $i = 1, \dots, n$. Write down expressions for $\mathbb{E}(Y_i)$ and $\operatorname{var}(Y_i)$ in terms of derivatives of $b(\theta_i)$ and ϕ .

Explain the terms canonical link function, variance function, scaled deviance and deviance.

Now suppose that Y_i has a normal distribution with mean μ_i and variance σ^2 , i = 1, ..., n. Show that the density of Y_i can be written as in (*), and identify θ_i , $b(\theta_i)$ and ϕ . Suppose $g(\mu_i) = \beta^T \boldsymbol{x}_i$ where $g(\cdot)$ is the canonical link function. Derive the relationship between the deviance and the residual sum of squares.

The S-Plus commands below refer to serum cholesterol levels (millimoles per litre) in chol, age (years) in age, and body mass index (weight (kg) divided by the square of height (m)) in bmi for thirty women. Four models are fitted to the data as shown. Models 1, 2, 3 and 4 have deviances 27.10, 31.64, 35.82 and 49.70 respectively. Explain carefully how to test whether serum cholesterol levels are associated with body mass index, taking account of the possible effect of age, and give your conclusions.

>	chol1.lm	<-	lm	(chol	${\catcode'\"=}$	11	~}	age + bmi)	#	Model	1
>	chol2.lm	<-	lm	(chol	$\catcode'^=$	11	~}	age)	#	Model	2
>	chol3.lm	<-	lm	(chol	$\catcode'^=$	11	~}	bmi)	#	Model	3
>	chol4.lm	<-	lm	(chol	${\catcode'}^=$	11	~}	1)	#	Model	4

[Hint: If $F_{n_1,n_2}(0.05)$ and $\chi^2_{\nu}(0.05)$ denote the upper five percentage points of an F_{n_1,n_2} and χ^2_{ν} distribution respectively then

 $F_{1,28}(0.05) = 4.196$, $F_{1,27}(0.05) = 4.210$, $\chi_1^2(0.05) = 3.841$

3 Let Y_{ij} , i = 1, ..., n and j = 1, ..., k, be independent random variables where Y_{ij} has a $Bin(m, p_{ij})$ distribution.

Suppose that

$$\log\left(\frac{p_{ij}}{1-p_{ij}}\right) = \mu + \alpha_i \qquad i = 1, \dots, n, \quad j = 1, \dots, k,$$

where $\alpha_1 = 0$. Derive equations satisfied by the maximum likelihood estimators $\hat{\mu}, \hat{\alpha}_2, \ldots, \hat{\alpha}_n$. When n = 2, find the asymptotic distribution of $\hat{\mu}$.

As part of an investigation into the effect of radiation on cancer cells, 27 dishes, each containing 400 cells, were irradiated. This experiment was spread over nine days, with three dishes being irradiated each day. In the (edited) S-Plus output below, the number of cells surviving in each dish is in survived, and day contains the day on which the corresponding dish was irradiated.

- (i) Explain the S-Plus commands and output carefully. Write down in detail the models fitted in model1.glm and model2.glm, defining any notation you use.
- (ii) Determine the values of the four numbers that have been replaced by asterisks in the output. Investigate whether there is a day effect, and comment on the fit of your preferred model.

```
> day
           4
               5
                         8
                            9 10 11 12 13 14 15
  1
     2
        3
                  6
                     7
  1
     1
        1
           2
               2
                  2
                     3
                         3
                            3
                               4
                                  4
                                      4
                                         5
                                           55
 16 17 18 19 20 21 22 23 24 25 26 27
  6
    6
       6
           7
              7
                  7
                     8
                        8
                            8
                               9
                                  9
                                     9
> survived
      2
           3
               4
                            7
                                8
                                    9
                                        10
                                                12
                   5
                        6
                                            11
                                                     13
                                                         14
                                                             15
  1
178 193 217 109 112 115
                           66
                               75
                                   80 118 125 137 123 146 170
 16 17
        18
             19
                  20
                      21
                           22
                               23
                                   24
                                        25
                                            26
                                                27
115 130 133 200 189 173
                           88
                               76
                                   90 121 124 136
> Day <- factor (day)
> ncells <- rep (400,27)
> prop <- survived / ncells</pre>
> options(contrasts = c ("contr.treatment",
                           "contr.poly"))
> model1 <- glm (prop ~ 1, family = binomial, weights = ncells)</pre>
> model2 <- glm (prop ~ Day, family = binomial, weights = ncells)</pre>
```

4 The S-Plus output below refers to an experiment to investigate whether crossfertilised plants for a particular species of corn plant tend to be taller than self-fertilised plants. In the experiment, there were fifteen pots, each containing one cross-fertilised plant and one self-fertilised plant. In the output, the vectors **cross** and **self** contain the heights of the fifteen cross-fertilised and self-fertilised plants in the order of the pots.

A statistician has used three different directives, each giving a different p-value, as shown in the output, and has asked you for advice about how to proceed. In each of the three cases, explain which test has been carried out, stating the null and alternative hypotheses carefully. Without doing any calculations, explain how the test statistics V and Z have been obtained in tests 1 and 3 respectively, and indicate briefly how the p-values have been obtained in all three tests. Write a paragraph for the statistician explaining which test(s) is (are) most relevant for these data, and giving your conclusions about heights of cross-fertilised and self-fertilised plants.

Test 1 > wilcox.test (cross,self, paired = T, alternative = "greater") Exact Wilcoxon signed-rank test data: cross and self signed-rank statistic V = 96, n = 15, p-value = 0.0206 alternative hypothesis: mu is greater than 0 # Test 2 > wilcox.test (cross, self, paired = T, alt = "greater", exact = F) Wilcoxon signed-rank test data: cross and self signed-rank normal statistic with correction Z = 2.0163, p-value = 0.0219alternative hypothesis: mu is greater than 0 # Test 3 > wilcox.test (cross, self, alt = "greater", exact = F) Wilcoxon rank-sum test data: cross and self rank-sum normal statistic with correction Z = 3.0105, p-value = 0.0013alternative hypothesis: mu is greater than 0

5 (a) Explain what is meant by a generalised additive model for independent normally distributed random variables.

Suppose that $n \ge 3$ and consider a set of points $\{(x_i, y_i) : i = 1, ..., n\}$ where $x_1 < ... < x_n$.

- (b) What is meant by a natural cubic spline interpolating these points?
- (c) Now consider

$$y_i = g(x_i) + \epsilon_i$$
, $i = 1, \ldots, n$,

where $\epsilon_1, \ldots, \epsilon_n$ are independent $N(0, \sigma^2)$ random variables. Define the penalised sum of squares with smoothing parameter $\lambda > 0$, and the cubic smoothing spline $\hat{g}_{\lambda}(\cdot)$.

- (d) Define the generalised cross-validation score in terms of the influence matrix A, and explain how it can be used to choose λ .
- (e) Below is the R output (with figure) from an analysis of simulated data $\{(x_i, y_i) : i = 1, ..., 401\}$. Describe carefully the output produced. You are required to write out the form of the model fitted. What is the range of x? From the figure, suggest an alternative simpler model to fit.

```
> library (mgcv)
> model.gam <- gam (y ~ s (x, bs = "cr"))</pre>
> summary (model.gam) # Slightly abbreviated output
Family: gaussian
Link function: identity
Formula: y ~ s (x, bs = "cr")
Parametric coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.13241
                          0.05426
                                     -2.44
                                              0.0151 *
Signif.codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1''1
Approximate significance of smooth terms:
        edf Est.rank p-value
s(x) 8.237
                9.000
                        <2e-16
                               ***
Signif.codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1''1
R-sq.(adj) = 0.983 Deviance explained = 98.4 %
GCV score = 0.99018 Scale est. = 0.96737 n = 401
```



END OF PAPER