

short with old Q on board

Variables in model	-2 log L
none	215.940
bun	207.453
bun, protein	203.641
bun, protein, Hb	200.503

collett p84

1) The data studies the time until death for multiple myeloma patients. The variable  $Hb$  = serum haemoglobin, the variable  $protein$  was an indicator for the Bence-Jones protein (0 = absent, 1 = present), and the variable  $bun$  = blood urea nitrogen. Let the full model contain  $bun$ ,  $protein$ , and  $Hb$ . Use the table above.

a) If the reduced model uses  $bun$  and  $protein$ , test whether the reduced model is good.

i)  $H_0$  reduced model is good  $H_A$  use the full model

$$ii) \chi^2(RIF) = 203.641 - 200.503 = 3.128$$

$$= -2 \log L(\text{red}) - [-2 \log L(\text{full})]$$

iii)  $p\text{-val} = P(\chi^2_1 > 3.128) \text{ so } .05 < p\text{-val} < .1$

$\chi^2$	.1	.05
1	2.71	3.84

iv) fail to reject  $H_0$ , the reduced model is good

b) If the reduced model uses  $bun$ , test whether the reduced model is good.

i)  $H_0$  the reduced model is good  $H_A$  use the full model

$$ii) \chi^2(RIF) = 207.453 - 200.503 = 6.95$$

iii)  $p\text{-val} = P(\chi^2_2 > 6.95)$

$$.025 < p\text{-val} < .05$$

$\chi^2$	.05	.025
2	5.99	7.38

iv) reject  $H_0$  use the full model

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full model	coef	exp(coef)	se(coef)	z	p
trt	0.295	1.343	0.20755	1.4194	0.16
celltypesmallcell	0.862	2.367	0.27528	3.1297	0.017
celltypeadeno	1.20	3.307	0.30092	3.9747	0.000
celltypelarge	0.401	1.494	0.28269	1.4196	0.16
karno	-0.0328	0.968	0.00551	-5.9580	0.000
diagtime	0.000081	1.000	0.00914	0.0089	0.99
age	-0.00871	0.991	0.00930	-0.9361	0.35
prior	0.00716	1.007	0.02323	0.3082	0.76

Likelihood ratio test=62.1 on 8 df, p=1.8e-10 n= 137

reduced model	coef	exp(coef)	se(coef)	z	p
trt	0.2617	1.30	0.20092	1.30	0.19
celltypesmallcell	0.8250	2.28	0.26891	3.07	0.022
celltypeadeno	1.1540	3.17	0.29504	3.91	0.0009
celltypelarge	0.3946	1.48	0.28224	1.40	0.16
karno	-0.0313	0.97	0.00517	-6.05	0.000

Likelihood ratio test=61.1 on 5 df, p=7.3e-12 n= 137

2) The data is for lung cancer.  $Y$  = survival time. The predictors are *trt* (1=standard, 2=test), the factor *celltype* (1=squamous, 2=smallcell, 3=adeno, 4=large), *karno* = Karnofsky performance score (100=good), *diagtime* = months from diagnosis to randomization, *age* in years, and *prior* = prior therapy (0=no, 1=yes). Test whether the reduced model is good.

i)  $H_0$  the reduced model is good  $H_A$  use the full model

ii)  $\chi^2(RIF) = 62.1 - 61.1 = 1.0$

iii)  $pval = P(\chi^2_3 \geq 1)$

$\chi^2$	1	0.25
3		4.11

$\uparrow$   
8-5 = # predictors in full but not reduced

$pval > 0.25$

iv) fail to reject  $H_0$ , the reduced model is good