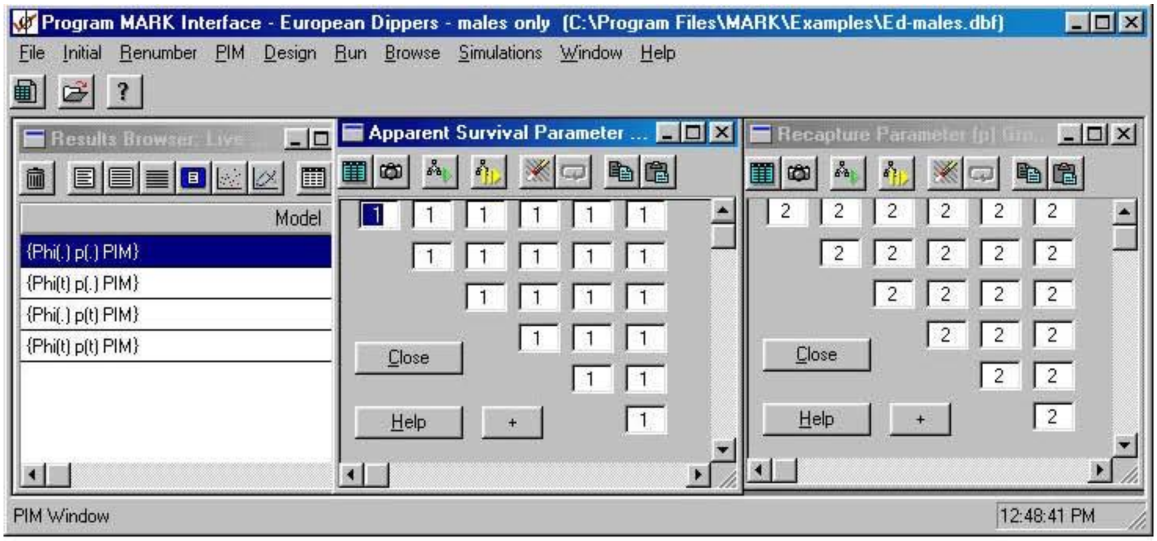
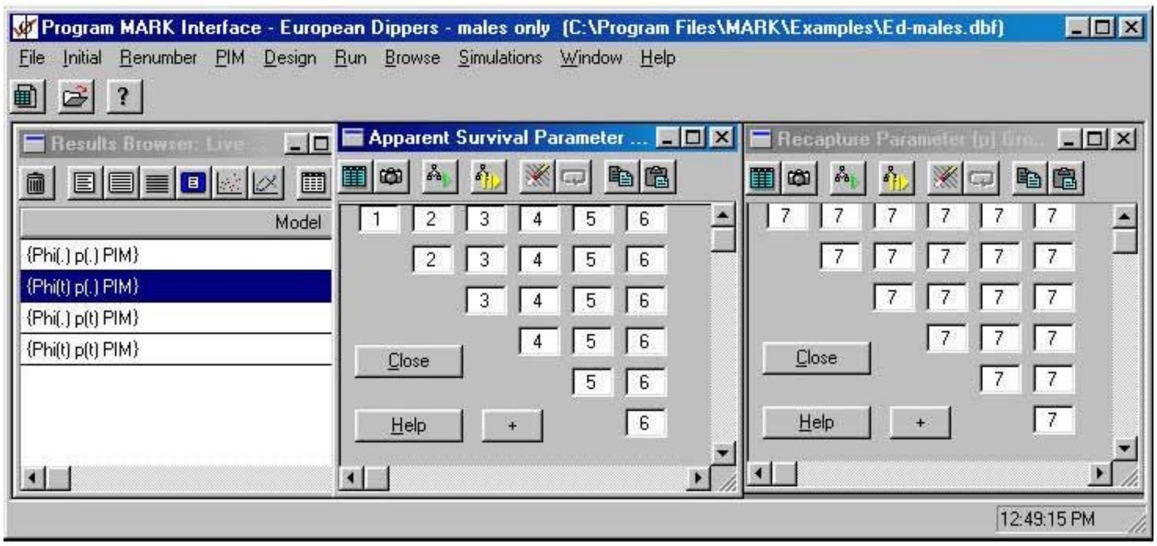
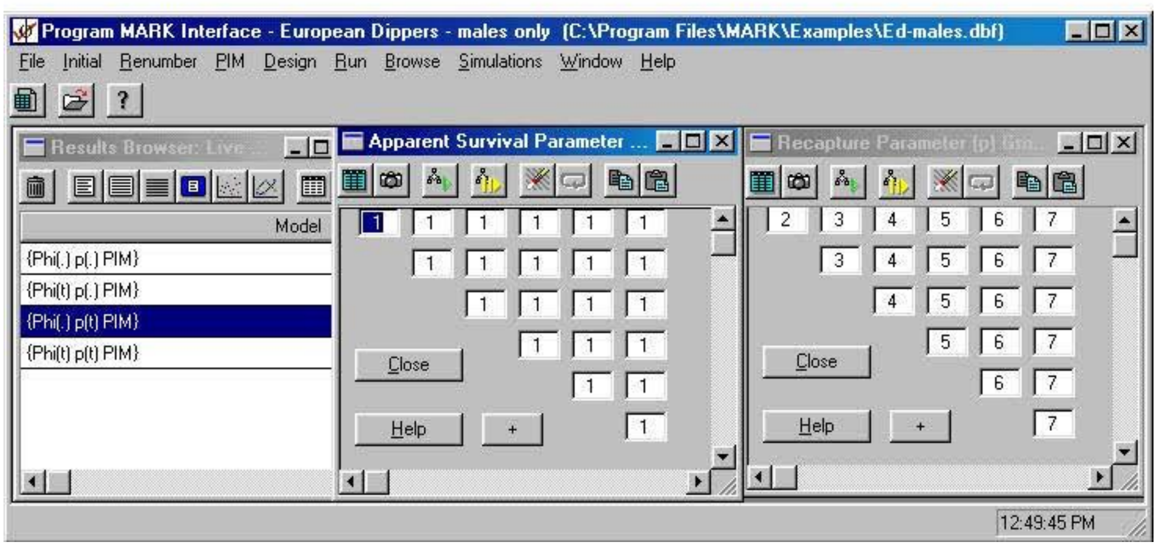
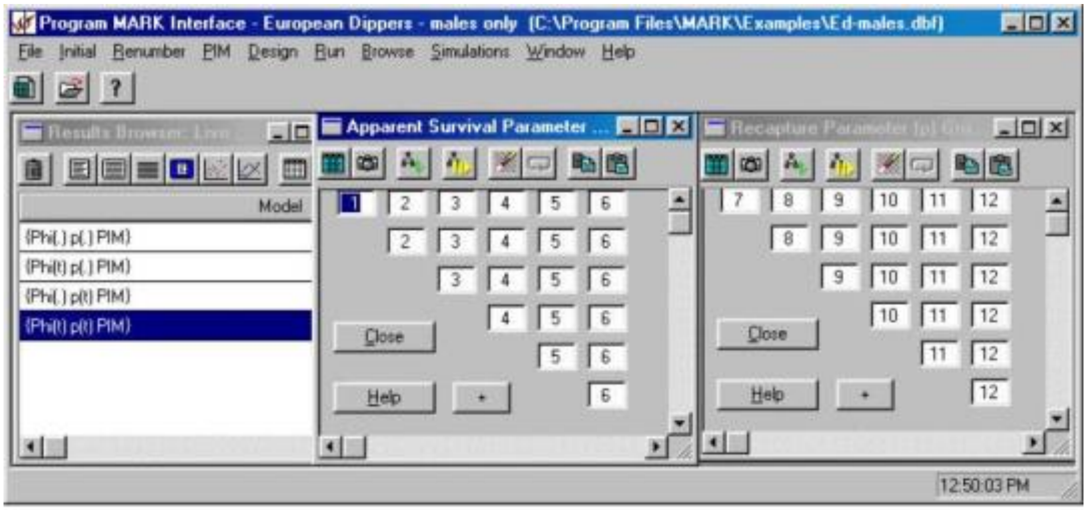
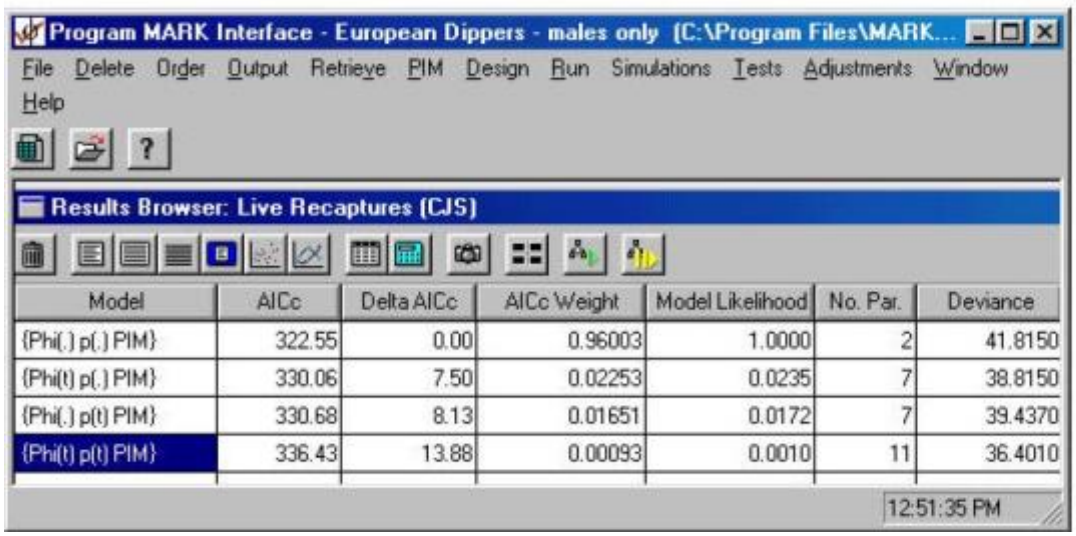

Program MARK Interface - European Dippers - males only (C:\Program Files\MARK\Examples\Ed-males.dbf)
File Initial Renumber PIM Design Run Browse Simulations Window Help
Results Browser: Live
Model
{Phi(.) p(.) PIM}
{Phi(t) p(.) PIM}
{Phi(.) p(t) PIM}
{Phi(t) p(t) PIM}
Apparent Survival Parameter ...
1 1 1 1 1 1
1 1 1 1 1
1 1 1 1
1 1 1
1 1
1
Close
Help
+
Recapture Parameter (p) Gro...
2 2 2 2 2 2
2 2 2 2 2
2 2 2 2
2 2 2
2 2
2
Close
Help
+
PIM Window
12:48:41 PM


Program MARK Interface - European Dippers - males only (C:\Program Files\MARK\Examples\Ed-males.dbf)
File Initial Renumber PIM Design Run Browse Simulations Window Help
Results Browser: Live
Model
{Phi(.) p(.) PIM}
{Phi(t) p(.) PIM}
{Phi(.) p(t) PIM}
{Phi(t) p(t) PIM}
Apparent Survival Parameter ...
1 2 3 4 5 6
2 3 4 5 6
3 4 5 6
4 5 6
5 6
6
Close
Help
+
Recapture Parameter (p) Gro...
7 7 7 7 7 7
7 7 7 7 7
7 7 7 7
7 7 7
7 7
7
Close
Help
+
12:49:15 PM


Program MARK Interface - European Dippers - males only (C:\Program Files\MARK\Examples\Ed-males.dbf)
File Initial Renumber PIM Design Run Browse Simulations Window Help
Results Browser: Live
Model
{Phi(.) p(.) PIM}
{Phi(t) p(.) PIM}
{Phi(.) p(t) PIM}
{Phi(t) p(t) PIM}
Apparent Survival Parameter ...
1 1 1 1 1 1
1 1 1 1 1
1 1 1 1
1 1 1
1 1
1
Close
Help
+
Recapture Parameter (p) Gro...
2 3 4 5 6 7
3 4 5 6 7
4 5 6 7
5 6 7
6 7
7
Close
Help
+
12:49:45 PM





Deviance plays the role of residual sum of squares in linear regression. To assess the significance of a factor(s), we compare the Deviance for models with and without the factor in question. You'll see how to calculate the deviance for this model type on the next page.

Likelihood Ratio Tests: Deviance_Reduced Model – Deviance_General Model ~chi-squared

European Dippers - males only

Reduced Model	General Model	Chi-sq.	df	Prob.
{Phi(.) p(.) PIM}	{Phi(t) p(.) PIM}	3.000	5	0.7000
{Phi(.) p(.) PIM}	{Phi(.) p(t) PIM}	2.378	5	0.7947
{Phi(.) p(.) PIM}	{Phi(t) p(t) PIM}	5.414	9	0.7968
{Phi(t) p(.) PIM}	{Phi(.) p(t) PIM}	-0.622	0	*******
{Phi(t) p(.) PIM}	{Phi(t) p(t) PIM}	2.414	4	0.6601
{Phi(.) p(t) PIM}	{Phi(t) p(t) PIM}	3.036	4	0.5518

NOTE: the LRT works only for nested models, i.e., comparison #4 is not conceptually valid even if the test were possible mathematically.

Another role of Deviance is in testing for GOF – this will be the next major topic that we tackle. Here's a table that we'll use to gain understanding of how the saturated model's deviance and deviance *df* are calculated. A saturated model fits perfectly and is sometimes a model in the model set (e.g., S(week) in lab 1) and sometimes not (like in Lab 3 where we can't run such a model but can calculate the deviance as below).

EH	n_i		R_i		Contribution to DEV (n_i*ln(n_i/R_i))		Releases & Re-releases prior to occ. 7	Pieces of Information (rows-1)
1111110	1		12	12	-2.4849066		6	4
1111000	1			12	-2.4849066		4	
1100000	4			12	-4.3944492		8	
1010000	1			12	-2.4849066		2	
1000000	5			12	-4.3773437		5	
0111100	1		20	20	-2.9957323		4	3
0111000	1			20	-2.9957323		3	
0110000	7			20	-7.3487549		14	
0100000	11			20	-6.576207		11	
0011110	1		25	25	-3.2188758		4	4
0011100	4			25	-7.3303259		12	
0011000	8			25	-9.1154743		16	
0010110	1			25	-3.2188758		3	
0010000	11			25	-9.0307861		11	
0001111	6		22	22	-7.7956979		18	4
0001110	3			22	-5.9772905		9	
0001100	6			22	-7.7956979		12	
0001001	1			22	-3.0910425		1	
0001000	6			22	-7.7956979		6	
0000111	10		22	22	-7.8845736		20	2
0000110	3			22	-5.9772905		6	
0000100	9			22	-8.0443609		9	
0000011	12		23	23	-7.8070508		12	1
0000010	11			23	-8.1135884		11	
0000001	17		17	17	0			
/* SUM	**141**		**141**	**lnL**	**-138.33957**		**207**	**18**
				-2lnL	**276.679136**			

The -2lnL value of 276.679, effective sample size of 207, and d.f. of 18 can now be used in comparisons and tests for fitted models. E.g., model Phi(.), p(.), has 2 parameters and -2lnL = 318.494, the deviance is 318.494 – 276.679 = 41.815, and deviance d.f. = 16 (18 – 2).

Discussion of Questions that some students have struggled with in past years.

1. $5\ \hat{\phi}'s, 5\ \hat{p}'s, \&\ 1\ \text{combo.} = \hat{\phi}_1, \hat{\phi}_2, ..., \hat{\phi}_5, \hat{p}_2, \hat{p}_3, ..., \hat{p}_6,$ and $\hat{\phi}_6 \cdot \hat{p}_7$
2. Sine link gets it right: *k*=11. Logit link gets it wrong: *k*=10.
3. Students typically do pretty well with this one but … some forget to check the # of parameters in all of the models. For part *b*, you could do model averaging as

long as you were paying attention to the problem with *phi*$_6$ in the *phi(t),p(t)* model. For example, if you just do model averaging, for this parameter, you'll see the following:

Apparent Survval Parameter (Phi) Group 1 Parameter 6

Model	Weight	Estmate	Standard Error
{Phi(.) p(.) PIM}	0.96003	0.5658226	0.0355404
{Phi(t) p(.) PIM}	0.02253	0.6319703	0.0796463
{Phi(.) p(t) PIM}	0.01650	0.5560768	0.0342813
{Phi(t) p(t) PIM}	0.00093	0.7637583	514.1293800
Weighted Average		0.5673361	0.5140185
Unconditional SE			15.6690091

95% CI for Wgt. Ave. Est. (logit trans.) is 0.0000000 to 1.0000000
Percent of Variation Attributable to Model Variation is 99.89%

You don't have much model-selection uncertainty here and so you could just use the best model to make inferences if you wanted to.

Parameter	Estimate	Standard Error	Lower	Upper
1:Phi	0.5658226	0.0355404	0.4953193	0.6337593
2:p	0.9231757	0.0363182	0.8149669	0.9704014

4. Here's how to calculate the probability of getting a 1000000 encounter history (see text on this topic on page 420 of Williams et al.). Be sure you understand.

$$\chi_7 = 1$$
$$\chi_6 = (1-\phi_6) + \phi_6 \cdot (1-p_7) \cdot \chi_7$$
$$\chi_5 = (1-\phi_5) + \phi_5 \cdot (1-p_6) \cdot \chi_6$$
$$\chi_4 = (1-\phi_4) + \phi_4 \cdot (1-p_5) \cdot \chi_5$$
$$\chi_3 = (1-\phi_3) + \phi_3 \cdot (1-p_4) \cdot \chi_4$$
$$\chi_2 = (1-\phi_2) + \phi_2 \cdot (1-p_3) \cdot \chi_3$$
$$\chi_1 = (1-\phi_1) + \phi_1 \cdot (1-p_2) \cdot \chi_2$$

So, for model phi(.), p(.) with MLE's of phi=0.5658226 & p=0.9231757, the probability of an individual having a 1000000 for its encounter history is 0.4539083.

In **R**, you'd simply type:

```
phi=.5658226
p=.9231757
x7=1
x6=(1-phi)+phi*(1-p)*x7
x5=(1-phi)+phi*(1-p)*x6
x4=(1-phi)+phi*(1-p)*x5
x3=(1-phi)+phi*(1-p)*x4
x2=(1-phi)+phi*(1-p)*x3
x1=(1-phi)+phi*(1-p)*x2
x1  # = 0.4539083
```