Appendix

Appendix

1. Data Collection

The data were collected from the treatment cards and x-ray cards. These forms are shown below.

Treatment card (TB patients registration of TB division : Annex 4)

CATEGORIES OF REGISTRATION

Registration		Discharge	
Date	Categories	Date	Categories

SENSITIVITY TEST

No.	Date of sending sputum for exam.	S	H	R	E	K	C

Registration : 1. New detection 2. Transferred in 3. Relapsed 4. Coming back after 6 months lost
Discharge : 1. Complete treatment 2. Transfer out 3. Dead 4. Over 6 months loss 5. Changing of diagnosis/others

Laboratory Results

Date	Methods of examination/results

Male	Code no.	Address	Number
Female	First name		Date
Age	Family name	District	
	Occupation	Province	
Marital status		Religion	

Symptoms
( ) Cough day/month
( ) Sputum/colour
( ) Haempotysis day/month
( ) Chest pain day/month
( ) Exhaustion day/month
( ) Fever day/month
( ) Others day/month

History of BCG/BCG scar
1. Vaccinate ( ) one scar
( ) two scar
( ) no scar
2. Non vaccinated

History of TB treatment

History of other diseases

History of drug hypersensitivity

History of contact ..... persons
Under 5 yr. ..... persons

( ) Extra pulm. TB found

Individual card or x-ray card (Annex 3)

Code					Address	Medical certificate
X-ray number		Date				
Name		Age ..... Year Sex Male Female			Subdistrict	X-ray result
					District	..... (Signature of examinee)
[] Normal [] Pulmonary TB [] Suggestive active [] Noncavitary [] Cavitary [] Suggestive inactive [] Non-TB pulmonary [] Pleural [] Cardiac [] Other [] Un-identified [] Tech-inadequate [] Extra pulmonary	MF	FS	Sputum result [] neg Micro [] Pos [] neg Culture [] Pos [] Treat here [] Transferred out	Date	Province + [] BCG scar - [] Symptoms [] Cough [] Haemoptysis [] Expectoated cough [] Previous treatment [] Duration [] Contact [] Others	Normal X-ray ..... (Signature of medical officer) TB division CDC department

2. Data Structure

The raw data were constructed in database system by using Microsoft Access. The data were exported to Microsoft Excel and then separated into two files. The next step, replaced missing value by using Programmer's file editor program and saved the two files namely, "tb1.num" and "tb2.num", respectively

The file "tb1" consists of 12 columns namely, ID, gender, age, marital status, occupation, religion, receiving BCG, smoking, drinking, other diseases, family history and HIV.

0001	1	44	2	7	1	nan	1	1	0	0	0
0002	1	57	2	2	1	0	0	0	0	0	0
0003	1	44	2	2	1	nan	1	0	0	0	0
0004	1	57	2	3	1	0	1	0	0	0	0
0005	1	41	2	2	1	0	1	1	0	2	0
.....											
1078	1	39	nan	nan	nan	nan	nan	nan	0	0	0
1079	1	58	nan	nan	nan	nan	nan	nan	0	0	1
1080	1	42	nan	nan	nan	nan	nan	nan	0	0	0

The file "tb2" consists of 12 columns namely, ID, cough, haemoptysis, chest pain, dyspnea, fever, weakness, weight loss, other symptoms, chest x-ray finding, degree of sputum and HIV. The raw data as shown below.

0001	30	0	0	30	3	0	0	0	1	1	0
0002	15	0	15	10	nan	0	0	1	1	2	0
0003	30	1	0	0	0	0	0	0	2	0	0
0004	1095	0	0	60	30	0	0	0	2	0	0
0005	14	5	4	4	0	0	0	0	0	2	0
.....											
1078	150	0	150	90	nan	0	1	0	1	1	0
1079	180	0	60	0	nan	0	1	0	0	1	1
1080	60	0	150	150	nan	0	1	1	1	3	0

3. Data Analysis

The data graphed by using ASP with student Matlab version 5 (McNeil, 1998). The summaries of all variables of interest in Section 1 of Chapter 3, were estimated by using the following commands. (Statements after the % symbol are explanations.)

```
% program tb1.m create Figures 3.1 & 3.2 (top panels)
getfile tb1
y=getnum;
y0=y(:,12)==0;
new0=y(y0,[1:11]);
putnum(new0);
dn=getdn;
dn={'TB patients without HIV infection (comparison group)'};
putdn(dn);
describe hist=1 type=0 font=9                % The top Figure 3.1
y1=y(:,12)==1;
new1=y(y1,[1:11]);
putnum(new1);
dn=getdn;
dn={'TB patients with HIV infection (study group)'};
putdn(dn);
describe hist=1 type=0 font=9                % The top Figure 3.2
```

```
% program tb2.m to create Figure 3.1 & 3.2 (bottom)
getfile tb2
y=getnum;
y0=y(:,12)==0;
new0=y(y0,:);
putnum(new0)
dn=getdn;
dn={'TB patients without HIV infection (comparison group)'};
putdn(dn)
describe hist=1 col=2:11 font=9                % The bottom Figure 3.1
y1=y(:,12)==1;
new1=y(y1,:);
putnum(new1)
dn=getdn;
dn={'TB patients with HIV infection (study group)'};
putdn(dn)
describe hist=1 col=2:11 font=9                % The bottom Figure 3.2
```

The raw data are considered to recode for analysis. The programs for coding data into categorical before investigated the association between the outcome and the determinants are as follows.

```
% program tb1a.m to create file newtb1.num with recoded age, marital status,
% occupation, and family history with TB
getfile tb1
y=getnum;
ag = y(:,3);                                   % select age
ok1 = ag<30;
ok2 = ag>=30 & ag<40;
ok3 = ag>=40 & ag<50;
ok4 = ag>=50 & ag<60;
ok5 = ag>=60;
ag(ok1) = 1+0*ag(ok1);
ag(ok2) = 2+0*ag(ok2);
```

```
ag(ok3) = 3+0*ag(ok3);
ag(ok4) = 4+0*ag(ok4);
ag(ok5) = 5+0*ag(ok5);
y(:,3) = ag;
ms = y(:,4);                          % select marital status
ok1 = ms==1;
ok2 = ms==2;
ok3 = ms==3 | ms==4 | ms==5;
ms(ok1) = 1+0*ms(ok1);
ms(ok2) = 2+0*ms(ok2);
ms(ok3) = 3+0*ms(ok3);
y(:,4) = ms;
oc = y(:,5);                          % select occupation
ok1 = oc==2;
ok2 = oc==3;
ok3 = oc==4;
ok4 = oc==1 | oc==5 | oc==6 | oc==7 | oc==8;
oc(ok1) = 1+0*oc(ok1);
oc(ok2) = 2+0*oc(ok2);
oc(ok3) = 3+0*oc(ok3);
oc(ok4) = 4+0*oc(ok4);
y(:,5) = oc;
od = y(:,10);                         % other diseases
ok0 = od==0;
ok1 = od==1 | od==2 | od==3 | od==4 | od==5 | od==6 | od==7;
od(ok0) = 0+0*od(ok0);
od(ok1) = 1+0*od(ok1);
y(:,10) = od;
hc = y(:,11);                         % family history with TB
ok1 = hc==0;
ok2 = hc==1 | hc==2 | hc==3 | hc==4;
hc(ok1) = 1+0*hc(ok1);
hc(ok2) = 2+0*hc(ok2);
```

```
y(:,11) = hc;
putnum(y)
dn=getdn;
dn={'TB patients with and without HIV infection'};
putdn(dn)
putfile('newtb1','scale=0');          % After recoding, put the newfile "newtb1"
```

% program tb2a.m to create the file newtb2.num (combination of newtb1 and tb2)
% and grouped data of cough, haemoptysis, chest pain, dyspnea and fever.

```
getfile newtb1
x=getnum;
x1=x(:,1:3);
putnum(x1);
getfile tb2
y = getnum;
co = y(:,2);                          % group cough days
ok1 = co<=60;
ok2 = co>60 & co<=90;
ok3= co>90;
co(ok1) = 1+0*co(ok1);
co(ok2) = 2+0*co(ok2);
co(ok3) = 3+0*co(ok3);
y(:,2)=co;
hae = y(:,3);                         % group haemoptysis
ok0 = hae==0;
ok1 = hae>=1;
hae(ok0) = 0+0*hae(ok0);
hae(ok1) = 1+0*hae(ok1);
y(:,3)= hae;
ch = y(:,4);                          % group chest pain
ok1 = ch<=30;
ok2 = ch>30 & ch<=90;
ok3 = ch>90;
ch(ok1) = 1+0*ch(ok1);
```

```
ch(ok2) = 2+0*ch(ok2);
ch(ok3) = 3+0*ch(ok3);
y(:,4) = ch;
dy = y(:,5);                          % group dyspnea
ok1 = dy<=30;
ok2 = dy>30 & dy<=90;
ok3 = dy>90;
dy(ok1) = 1+0*dy(ok1);
dy(ok2) = 2+0*dy(ok2);
dy(ok3) = 3+0*dy(ok3);
y(:,5) = dy;
fe = y(:,6);                          % group fever
ok1 = fe<=60;
ok2 = fe>60 & fe<=90;
ok3 = fe>90;
fe(ok1) = 1+0*fe(ok1);
fe(ok2) = 2+0*fe(ok2);
fe(ok3) = 3+0*fe(ok3);
y(:,6) = fe;
putnum(y)
y1=y(:,2:12);
putnum(y1)
new=[x1 y1];
putnum(new)
putfile('newtb2','scale=0')           % After recoding, put the newfile "newtb2"
```

After grouping data into categorical and saving in the new files, crude odds ratio and 95% confidence intervals were computed as shown in Section 2 of Chapter 3. These commands are as follows.

```
% Program newtb1.m compute 95% CI of crude odds ratio and adjusted odds ratio in
% each variable of demographic factors and intervening variables.
getfile newtb1
y=getnum;
```

```
setvar y=12 x='2 12'                    % gender
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='3 12'                    % age
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=4 x='12 4'                     % marital status
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='5 12'                    % occupation
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='6 12'                    % religion
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='7 12'                    % BCG
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='8 12'                    % smoking
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='9 12'                    % drinking
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='10 12'                   % other diseases
```

```
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=12 x='11 12'                    % family history with TB
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
```

% Program newtb2.m compute 95% CI of crude odds ratio in each variable of % disease characteristics .

```
getfile newtb2
y=getnum;
setvar y=14 x='4 14'                     % cough
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='5 14'                     % haemoptysis
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='6 14'                     % chest pain
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='7 14'                     % dyspnea
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='8 14'                     % fever
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='9 14'                     % weakness
stratify
```

```
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='10 14'                    % weight loss
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='11 14';                   % other symptoms
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9 trim=0;
setvar y=14 x='12 14';                   % chest x-ray finding
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
setvar y=14 x='13 14';                   % degree of sputum
stratify
setvar y=2 x=1 z=4 res=1
orplot res=1 log=1 font=9;
```


The confounding in Section 3 of Chapter 3 are investigated by using adjusted odds ratio and 95% confidence intervals of Mantel-Haenszel test. The following commands are shown below.

```
% Adjusted of 95% CI of Mantel-Haenszel odds ratio between outcomes and
% determinants.
getfile newtb1
y=getnum;
setvar y=3 x='12 2 3'                    % age adjusted for gender
stratify
setvar y=3 x=1:2 z=5 res=1
orplot res=1 log=1 font=9;
setvar y=4 x='12 3 4'                    % marital status adjusted for age
stratify
setvar y=3 x=1:2 z=5 res=1
```

```
orplot res=1 log=1 font=9;
setvar y=5 x='12 3 5'                    % occupation adjusted for age
stratify
setvar y=3 x=1:2 z=5 res=1
orplot res=1 log=1 font=9;
```

% Compute adjusted odds ratio in each variable of characteristics of disease.

```
getfile newtb2
y=getnum;
setvar y=5 x='14 3 5'                    % haemoptysis adjusted for age
stratify
setvar y=3 x=1:2 z=5 res=1
orplot strat=1 res=1 log=1 font=9;
setvar y=8 x='14 3 8'                    % fever adjusted for age
stratify
setvar y=3 x=1:2 z=5 res=1
orplot res=1 log=1 font=9;
setvar y=9 x='14 3 9'                    % weakness adjusted for age
stratify
setvar y=3 x=1:2 z=5 res=1
orplot strat=1 res=1 log=1 font=9;
setvar y=10 x='14 3 10'                  % weight loss adjusted for age
stratify
setvar y=3 x=1:2 z=5 res=1
orplot strat=1 res=1 log=1 font=9;
setvar y=12 x='14 3 12'                  % chest x-ray finding adjusted for age
stratify
setvar y=3 x=1:2 z=5 res=1
orplot res=1 log=1 font=9;
```

All significant variables in crude odds ratios were adjusted for gender or age, and put in one graph for simplified comparison in each variable. The following commands are as follows.

```
% Program plotor.m, plot adjusted odds ratio and 95% CI of all variables
% (figure 3.3).
axis([-3 4 0 48])
box on
hold on
for y=0:.5:48
 plot(0,y,':')
end
%chest x-rays
plot(log(1.39)./log(2), 1,'.');
for x=log(0.29)./log(2):.01:log(6.66)./log(2)
 plot(x,1,'-')
end
plot(log(0.56)./log(2), 2,'.')
for x=log(0.38)./log(2):.01:log(0.83)./log(2)
 plot(x,2,'-')
end
plot(log(1.76)./log(2), 3,'.')
for x=log(1.19)./log(2):.01:log(2.6)./log(2)
 plot(x,3,'-')
end
for x=-3:.01:4
 plot(x,6,'-')
end
text(0.5,4,'Homogeneity test : chi-q(8) =20.581, p = 0.00835','fontsize',7)
text(0.5,5,'Independent test : chi-sq(2) = 8.704, p = 0.0129','fontsize',7)
%weight loss
plot(log(1.76)./log(2), 7,'.')
for x=log(1.14)./log(2):.01:log(2.73)./log(2)
 plot(x,7,'-')
end
for x=-3:.01:4
 plot(x,10,'-')
```

```
end
text(0.5,8,'Homogeneity test : chi-q(4) = 5.989, p= 0.2','fontsize',7)
text(0.5,9,'Independent test : chi-sq(1) = 6.572, p = 0.0104','fontsize',7)
%weakness
plot(log(1.77)./log(2), 11,'.')
for x=log(1.17)./log(2):.01:log(2.67)./log(2)
 plot(x,11,'-')
end
for x=-3:.01:4
 plot(x,14,'-')
end
text(0.5,12,'Homogeneity test : chi-q(4) = 2.911 , p=0.573 ','fontsize',7)
text(0.5,13,'Independent test : chi-sq(1) = 7.442, p =0.00637','fontsize',7)
% fever
plot(log(0.45)./log(2), 15,'.')
for x=log(0.19)./log(2):.01:log(1.06)./log(2)
 plot(x,15,'-')
end
plot(log(3.44)./log(2), 16,'.')
for x=log(1.11)./log(2):.01:log(10.70)./log(2)
 plot(x,16,'-')
end
plot(log(1.31)./log(2), 17,'.')
for x=log(0.36)./log(2):.01:log(4.74)./log(2)
 plot(x,17,'-')
end
for x=-3:.01:4
 plot(x,20,'-')
end
text(0.5,18,'Homogeneity test : chi-q(8) = 5.866, p= 0.662','fontsize',7)
text(0.5,19,'Independent test : chi-sq(2) = 5.169, p = 0.0754','fontsize',7)
% haemoptysis
plot(log(0.33)./log(2), 21,'.')
```

```
for x=log(0.18)./log(2):.01:log(0.61)./log(2)
 plot(x,21,'-')
end
for x=-3:.01:4
 plot(x,24,'-')
end
text(0.5,22,'Homogeneity test : chi-q(4) = 7.349 , p= 0.119 ','fontsize',7)
text(0.5,23,'Independent test : chi-sq(1) = 13.983, p = 0.00018','fontsize',7)
% occupation
plot(log(1.08)./log(2), 25,'.')
for x=log(0.64)./log(2):.01:log(1.81)./log(2)
 plot(x,25,'-')
end
plot(log(1.55)./log(2), 26,'.')
for x=log(0.74)./log(2):.01:log(3.24)./log(2)
 plot(x,26,'-')
end
plot(log(1.88)./log(2), 27,'.')
for x=log(1.17)./log(2):.01:log(3.01)./log(2)
 plot(x,27,'-')
end
plot(log(0.48)./log(2), 28,'.')
for x=log(0.31)./log(2):.01:log(0.77)./log(2)
 plot(x,28,'-')
end
for x=-3:.01:4
 plot(x,31,'-')
end
text(0.5,29,'Homogeneity test : chi-q(12) = 18.576, p= 0.0993','fontsize',7)
text(0.5,30,'Independent test : chi-sq(3) = 12.223, p = 0.00666','fontsize',7)
% Marital status
plot(log(1.46)./log(2), 32,'.')
for x=log(0.84)./log(2):.01:log(2.52)./log(2)
```

```
 plot(x,32,'-')
end
plot(log(0.63)./log(2), 33,'.')
for x=log(0.39)./log(2):.01:log(1.0)./log(2)
 plot(x,33,'-')
end
plot(log(1.73)./log(2), 34,'.')
for x=log(0.82)./log(2):.01:log(3.65)./log(2)
 plot(x,34,'-')
end
for x=-3:.01:4
 plot(x,37,'-')
end
text(0.5,35,'Homogeneity test : chi-q(8) = 24.221, p= 0.0021','fontsize',7)
text(0.5,36,'Independent test : chi-sq(2) = 4.613, p = 0.0996','fontsize',7)
% age
plot(log(0.39)./log(2), 38,'.')
for x=log(0.22)./log(2):.01:log(0.70)./log(2)
 plot(x,38,'-')
end
plot(log(0.68)./log(2), 39,'.')
for x=log(0.40)./log(2):.01:log(1.16)./log(2)
 plot(x,39,'-')
end
plot(log(0.31)./log(2), 40,'.')
for x=log(0.16)./log(2):.01:log(0.60)./log(2)
 plot(x,40,'-')
end
plot(log(3.12)./log(2), 41,'.')
for x=log(2.11)./log(2):.01:log(4.61)./log(2)
 plot(x,41,'-')
end
plot(log(1.77)./log(2), 42,'.')
```

```
for x=log(1.13)./log(2):.01:log(2.76)./log(2)
 plot(x,42,'-')
end
text(0.5,43,'Homogeneity test : chi-q(4) = 21.851, p = 0.00021','fontsize',7)
text(0.5,44,'Independent test : chi-sq(4) = 52.556, p= 0','fontsize',7)
title('TB patients with and without HIV infection')
xlabel('base-2 logarithm of odds ratio & 95% CI')
y=[1:46];
ylabs=str2mat('miliary','cavity','non-cavity',' ','chest x-ray',' ','present',' ','weight loss');
ylabs=str2mat(ylabs,' ','present',' ','weakness',' ','>90 days','61-90 days');
ylabs=str2mat(ylabs,'<=60 days',' ','fever',' ','present',' ','haemoptysis',' ');
ylabs=str2mat(ylabs,'others','merchant','wage earner','agriculture',' ','occupation');
ylabs=str2mat(ylabs,' ','others','married','single',' ','marital status');
ylabs=str2mat(ylabs,' ','>60 yrs.','50-59 yrs.','40-49 yrs.','30-39 yrs.','<30 yrs.',' ','age');
ylabs=str2mat(ylabs,' ','Factor vs HIV+');
nylabs=size(ylabs,1);
ylabwid=size(ylabs,2);
for j=1:nylabs
 lab=deblank(ylabs(j,:));
 nblanks=ylabwid-length(lab);
 ylabs(j,:)=[blanks(nblanks) lab];
end
set(gca,'fontsize',7,'YTick',y,'YTicklabel',ylabs)
```

Logistic regression was used for statistical modeling in Chapter 4. The missing data were coded as the categorical variables to reduce the bias before fitting the logistic regression model. The following commands for model building and model fitting are shown.

```
% program chap4a.m recoded missing data, create Figure 4.1 - 4.4
% (model building) and put new file for model fitting.
getfile newtb1;
x = getnum;
lab = getlab;
```

```
% recode age
ag = x(:,3);
ok1 = ag==1;
ok2 = ag==2;
ok3 = ag==3 | ag==4 | ag==5;
ag(ok1) = 1+0*ag(ok1);
ag(ok2) = 2+0*ag(ok2);
ag(ok3) = 3+0*ag(ok3);
lab{3} = {'1 < 30 years' '2 30-39 years' '3 >= 40 years'};
x(:,3) = ag;
% recode missing marital status as 'married'
z = x(:,4);
z = (z==1)+2*(z==2)+3*(z==3)+2*isnan(z);
lab{4} = {'1 single' '2 married/mis' '3 others'};
x(:,4) = z;
% recode missing occupation as 'unknown'
z = x(:,5);
z = (z==1)+2*(z>1)+3*isnan(z);
x(:,5) = z;
lab{5} = { '1 agric' '2 others' '3 unknown'};
% recode religion
z = x(:,6);
z = (z==1)+2*(z==2)+3*isnan(z);
x(:,6) = z;
lab{6} = { '1 bud' '2 islam' '3 unknown'};
% recode missing BCG, smoking & drinking
for j=7:9
  z = x(:,j);
  z = 0*(z==0)+1*(z==1)+0*isnan(z);
  x(:,j) = z;
  lab{j} = {'0 no/unknown' '1 yes'};
end
% recode other diseases
```

```
z = x(:,10);
z = 0*(z==0)+1*(z==0)+2*isnan(z);
x(:,10) = z;
lab{10} = {'0 no' '1 yes' '2 unknown'};
% recode family history with TB
z = x(:,11);
z = 0*(z==1)+1*(z==2)+2*isnan(z);
x(:,11) = z;
lab{11} = {'0 no' '1 yes' '2 unknown'};
putnum(x)
putlab(lab)
setvar y=12 x='3 4 5 6 7 9 10 11'   % newtb1 full model (figure 4.1)
lreg font=7 'ref=3 2'
setvar y=12 x='3 5 11'              % newtb1 (omitted 2,8,7,4,6,10,9 figure 4.2)
lreg font=7 'ref=3'
% recode missing data in tb2
getfile tb2;                        % raw data
y = getnum;
lab = getlab;
% recode cough, haemoptysis, chest pain, dyspnea, fever
for j=2:6
  z = y(:,j);
  z = 0*(z==0)+1*(z>=1)+1*isnan(z);
  y(:,j) = z;
  lab{j} = {'0 no' '1 yes'};
end
% recode chest x-ray finding
z = y(:,10);
z = (z==0)+2*(z==1)+1*(z==2)+1*isnan(z);
y(:,10) = z;
lab{10} = {'1 others' '2 cavity'};
% recode degree of sputum
z = y(:,11);
```

```
z = (z==0)+2*(z==1)+2*(z==2)+2*(z==3)+1*isnan(z);
y(:,11) = z;
lab{11} = {'1 negative' '2 positive'};
putnum(y)
putlab(lab)
setvar y=12 x='2:11'                    % tb 2 full model (figure 4.3)
lreg font=7
setvar y=12 x='3 4 7 8 9 10'            % tb 2 (omitted 11,5,6,2  figure 4.4)
lreg font=7
new=[x(:,[1 3 5 8 9 10 11]) y(:,[3 4 7 8 9 10 12])];
putnum(new)
putfile('chap4','scale=0')              % After recoding, put the newfile "chap4"
```

After creating newfile "chap4" , the following commands for the logistic model fitting are as follows.

```
% program chap4ab.m for logistic regression ( fitting the model).
getfile chap4
y=getnum;
setvar y=14 x='2 3 7 8 9 10 11 12 13'   % full model (figure 4.5)
lreg 'ref=3' font=7
setvar y=14 x='2 3 8 9 10 11 12 13'     % omitted family history (figure 4.6)
lreg 'ref=3' font=7
setvar y=14 x='2 3 8 10 11 12 13'       % omitted chest pain (figure 4.7 )
lreg 'ref=3' font=7                     % penultimate model
% recode occupation
z = y(:,3);
z = (z==1)+2*(z==2)+2*(z==3);
y(:,3) = z;
putnum(y)
lab = getlab;
lab{3} = {'1 agriculture' '2 others/unknown' };
putlab(lab)
setvar y=14 x='2 3 8 10 11 12 13'       % final model (figure 4.8)
```

```
lreg 'ref=3' font=7
setvar y=14 x='2 3 8 10 11 12 13 4'        % adjusted for smoking
lreg 'ref=3' font=7
setvar y=14 x='2 3 8 10 11 12 13 5'        % adjusted for drinking
lreg 'ref=3' font=7
setvar y=14 x='2 3 8 10 11 12 13 6'        % adjusted for other diseases
lreg 'ref=3' font=7

% THE END
```