

Fundamentals of Statistical Modeling (VT21)

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Lab 5

Load the dataset and the `mlci` command

```
. version 14
. use https://raw.githubusercontent.com/anddis/fsm/master/data/lab5_1.dta, clear
. run https://raw.githubusercontent.com/anddis/fsm/master/do/mlci.do
```

Exercise 1

We consider again the oral cancer dataset (see Lab 4). We measure time to death (y) due to oral cancer ($d = 1$) (continuous line in the graphs) or to other causes ($d = 2$) (dashed line in the graphs). Just to get started, we exclude the censored observations ($d = 0$) from our estimation procedure (note the `if d != 0` at the end of the `mlexp` command).

We model the joint distribution $f(y, d)$ through the conditional expansion

$$f(y, d) = f(d|y)f(y).$$

We consider a log-normal distribution for $f(y)$ and a bernoulli distribution for $f(d|y)$. Estimate the model's parameters. Remember to constrain the bounded parameters. How do we interpret $\exp(\gamma_1)$?

```
. local G = "(log(y)-{mu})/exp({theta})"
. local g = "(1/exp({theta})/y)"
. local eta = "invlogit({gamma0}+{gamma1}*y)"
. local f1 = "normalden(`G`)*`g`"
. local f2 = "`eta`^(d==1)*(1-`eta`)^(d==2)"
. mlexp (log(`f1`*`f2`)) if d != 0
initial:      log likelihood = -677.80543
alternative:  log likelihood = -849.52367
rescale:      log likelihood = -669.37878
rescale eq:   log likelihood = -583.30772
Iteration 0:  log likelihood = -583.30772
Iteration 1:  log likelihood = -576.92245
Iteration 2:  log likelihood = -576.89028
Iteration 3:  log likelihood = -576.89028
Maximum likelihood estimation
Log likelihood = -576.89028      Number of obs      =      184
```

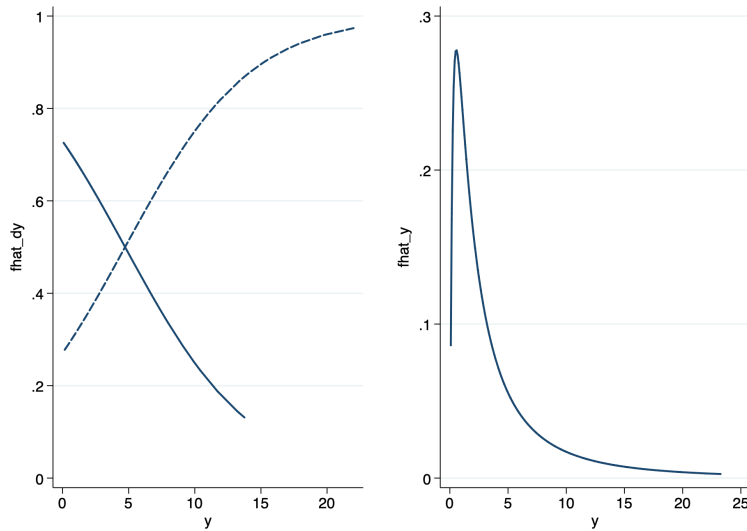
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
/mu	.9087088	.0902927	10.06	0.000	.7317384 1.085679
/theta	.2027691	.0521286	3.89	0.000	.1005989 .3049393
/gamma0	.9899309	.2317795	4.27	0.000	.5356514 1.44421
/gamma1	-.2094189	.0433561	-4.83	0.000	-.2943954 -.1244425

```
. mlci exp /theta
1.22479 95% CI: 1.105833, 1.356543
. mlci invlogit /gamma0
```

```
.7290743    95% CI: .6308002, .8091058
. mlci exp /gamma1
.8110554    95% CI: .7449819, .882989
```

Plot the estimated distributions $\hat{f}(y)$ and $\hat{f}(d|y)$. Interpret the plots.

```
. gen fhat_y = normalden((log(y) - _b[/mu]) / exp(_b[/theta]))*(1 / y / exp(_b[/theta]))
. tw (line fhat_y y, sort), name(p1, replace) legend(rows(1))
.
. gen fhat_dy = invlogit(_b[/gamma0]+_b[/gamma1]*y) if d == 1
(171 missing values generated)
. replace fhat_dy = 1-invlogit(_b[/gamma0]+_b[/gamma1]*y) if d == 2
(88 real changes made)
. tw (line fhat_dy y if d==1, sort lc(navy)) ///
> (line fhat_dy y if d==2, sort lc(navy) lp(-)), ///
> name(p2, replace) legend(off) ylabel(0(0.2)1)
. graph combine p2 p1, name(c1, replace)
. graph export c1.png, replace
(file c1.png written in PNG format)
```



Exercise 2

Some of the times (y) are actually right-censored. Estimate the model's parameters by modifying the likelihood accordingly to take this into account (last equation on slide 137). Remember to constrain the bounded parameters.

```
. tab d
```

	d	Freq.	Percent	Cum.
Censored		83	31.09	31.09
Oral ca. death		96	35.96	67.04
Other death		88	32.96	100.00
Total		267	100.00	

```
. local G = "(log(y)-{mu})/exp({theta})"
. local g = "(1/exp({theta})/y)"
. local eta = "invlogit({gamma0}+{gamma1}*y)"
. local f1 = "normalden(`G`)*`g`"
. local S = "1-normal(`G`)"
. local f2 = "`eta`^(d==1)*(1-`eta`)^(d==2)"
. mlexp ((d!=0)*log(`f1`*`f2`)+(d==0)*log(`S`))
initial:      log likelihood = -1018.5702
alternative:  log likelihood = -1000.4936
rescale:      log likelihood = -931.72631
```

```

rescale eq:    log likelihood = -705.99993
Iteration 0:    log likelihood = -705.99993
Iteration 1:    log likelihood = -689.39801
Iteration 2:    log likelihood = -688.25879
Iteration 3:    log likelihood = -688.25814
Iteration 4:    log likelihood = -688.25814

```

Maximum likelihood estimation

Log likelihood = -688.25814 Number of obs = 267

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
/mu	1.615544	.1030555	15.68	0.000	1.413559	1.817529
/theta	.4444992	.0548368	8.11	0.000	.3370211	.5519773
/gamma0	.9899305	.2317795	4.27	0.000	.535651	1.44421
/gamma1	-.2094188	.0433561	-4.83	0.000	-.2943953	-.1244424

```

. mlci exp /theta
1.559709   95% CI: 1.400769, 1.736684
. mlci invlogit /gamma0
.7290742   95% CI: .6308002, .8091057
. mlci exp /gamma1
.8110555   95% CI: .744982, .8829891

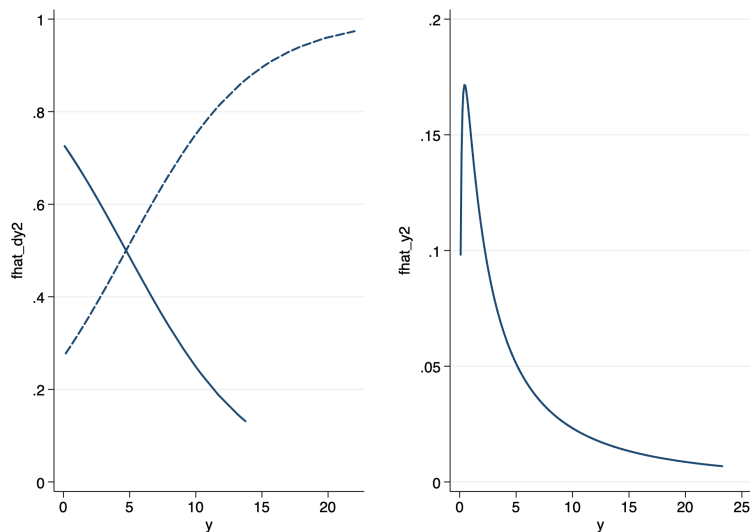
```

Plot the estimated distributions $\hat{f}(y)$ and $\hat{f}(d|y)$.

```

. gen fhat_y2 = normalden((log(y) - _b[/mu]) / exp(_b[/theta]))*(1 / y / exp(_b[/theta]))
. tw (line fhat_y2 y, sort), name(p3, replace) legend(rows(1))
.
. gen fhat_dy2 = invlogit(_b[/gamma0]+_b[/gamma1]*y) if d == 1
(171 missing values generated)
. replace fhat_dy2 = 1-invlogit(_b[/gamma0]+_b[/gamma1]*y) if d == 2
(88 real changes made)
. tw (line fhat_dy2 y if d==1, sort lc(navy)) ///
> (line fhat_dy2 y if d==2, sort lc(navy) lp(-)), ///
> name(p4, replace) legend(rows(1)) legend(off) ylabel(0(0.2)1)
. graph combine p4 p3, name(c2, replace)
. graph export c2.png, replace
(file c2.png written in PNG format)

```



Extra 1

Plot the estimated cumulative incidence functions $\hat{F}(y, d = 1)$ and $\hat{F}(y, d = 2)$ (see slide 140) and overlay them to their nonparametric counterparts obtained using Stata's `stcrreg` command.

$$\hat{F}(y, 1) = \int_0^y \hat{f}_{Y,D}(u, d = 1) du = \int_0^y \hat{f}_Y(u) \hat{f}_{D|Y}(d = 1|u) du$$

and

$$\hat{F}(y, 2) = \int_0^y \hat{f}_{Y,D}(u, d = 2) du = \int_0^y \hat{f}_Y(u) \hat{f}_{D|Y}(d = 2|u) du$$

```
. sum y, meanonly
. range y1 r(min) r(max)
. gen f1 = normalden((log(y1)-_b[/mu])/exp(_b[/theta]))/exp(_b[/theta])/y1 * invlogit(_b[/gamma0]+_b[/gamma1]*y1)
. gen f2 = normalden((log(y1)-_b[/mu])/exp(_b[/theta]))/exp(_b[/theta])/y1 * (1-invlogit(_b[/gamma0]+_b[/gamma1]*y1))
. sort y1
. gen F1 = sum(f1)*(r(max)-r(min))/(_N-1)
. gen F2 = sum(f2)*(r(max)-r(min))/(_N-1)
.
. stset y, fail(d==1)
      failure event:  d == 1
obs. time interval:  (0, y]
exit on or before:  failure
```

267	total observations	
0	exclusions	

267	observations remaining, representing	
96	failures in single-record/single-failure data	
1,620.864	total analysis time at risk and under observation	
	at risk from t =	0
	earliest observed entry t =	0
	last observed exit t =	23.258

```
. stcrreg, compete(d==2)
      failure _d:  d == 1
      analysis time _t:  y
Competing-risks regression
No. of obs      =      267
No. of subjects =      267
Failure event   : d == 1
Competing event: d == 2
No. failed      =      96
No. competing   =      88
No. censored    =      83
Wald chi2(0)    =      0.00
Prob > chi2     =      .
Log pseudolikelihood = -508.69926
```

_t	SHR	Robust Std. Err.	z	P> z	[95% Conf. Interval]
----	-----	------------------	---	------	----------------------

```
. predict cif1, basecif
. stset y, fail(d==2)
      failure event:  d == 2
obs. time interval:  (0, y]
exit on or before:  failure
```

267	total observations	
0	exclusions	

267	observations remaining, representing	
88	failures in single-record/single-failure data	
1,620.864	total analysis time at risk and under observation	
	at risk from t =	0
	earliest observed entry t =	0
	last observed exit t =	23.258

```
. stcrreg, compete(d==1)
      failure _d:  d == 2
      analysis time _t:  y
Competing-risks regression
No. of obs      =      267
No. of subjects =      267
```

```

Failure event : d == 2                      No. failed      =      88
Competing event: d == 1                    No. competing   =      96
                                           No. censored    =      83
                                           Wald chi2(0)    =      0.00
Log pseudolikelihood = -442.87519           Prob > chi2      =      .

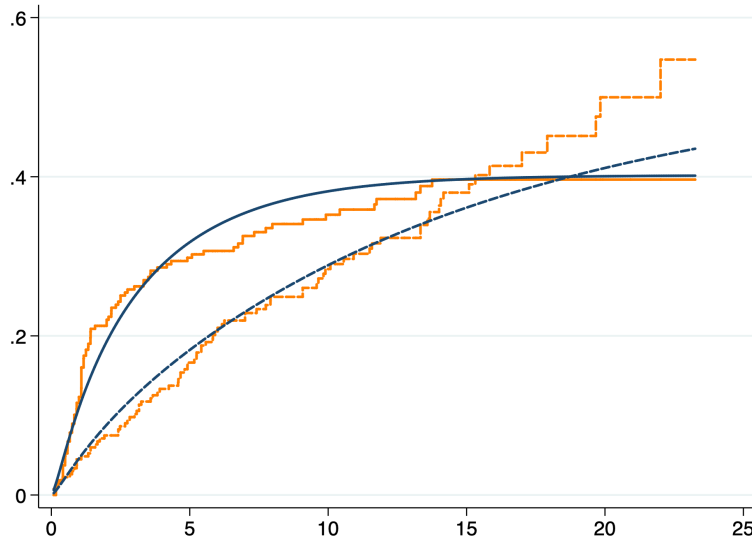
```

_t	SHR	Robust Std. Err.	z	P> z	[95% Conf. Interval]
----	-----	---------------------	---	------	----------------------

```

. predict cif2, basecif
.
. tw (line cif1 cif2 y, sort connect(J J) lc(orange orange) lp(1 -)) ///
> (line F1 F2 y1, sort lc(navy navy) lp(1 -)), legend(off) name(p5, replace)
. graph export p5.png, replace
(file p5.png written in PNG format)

```



Extra 2

We now model the joint distribution $f(y, d, x)$ through conditional expansion.

$$f(y, d, x) = f(d|y, x)f(y|x)f(x),$$

The variable x is tumor grade at diagnosis: low ($x = 0$, blue in the graphs) or high ($x = 1$, red in the graphs). We consider a log-normal distribution for $f(y|x)$ and a bernoulli distribution for both $f(d|y, x)$ and $f(x)$.

Estimate the model's parameters. Remember to constrain the bounded parameters. How do we interpret the model's parameters?

```

. local G = "(log(y)-({beta0}+{beta1}*x))/exp({theta})"
. local g = "(1/exp({theta})/y)"
. local eta = "invlogit({gamma0}+{gamma1}*y+{gamma2}*x)"
. local psi = "invlogit({delta})"
. local f1 = "normalden(`G`)*`g`"
. local S = "1-normal(`G`)"
. local f2 = "`eta`^(d==1)*(1-`eta`)^(d==2)"
. local f3 = "`psi`^(x==1)*(1-`psi`)^(x==0)"
. mlexp ((d!=0)*log(`f1`*`f2`)+(d==0)*log(`S`)+log(`f3`))
initial:      log likelihood = -1203.6405
alternative:  log likelihood = -1193.8352
rescale:      log likelihood = -1105.7963
rescale eq:   log likelihood = -876.80228

```

```

Iteration 0:  log likelihood = -876.80228
Iteration 1:  log likelihood = -864.00194
Iteration 2:  log likelihood = -863.66655
Iteration 3:  log likelihood = -863.66597
Iteration 4:  log likelihood = -863.66597

```

Maximum likelihood estimation

```

Log likelihood = -863.66597          Number of obs   =          267

```

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
/beta0	2.048152	.1475271	13.88	0.000	1.759004	2.3373
/beta1	-.8251894	.1958675	-4.21	0.000	-1.209083	-.4412961
/theta	.4088398	.0546405	7.48	0.000	.3017463	.5159332
/gamma0	.7617058	.3079601	2.47	0.013	.1581151	1.365297
/gamma1	-.2047134	.043271	-4.73	0.000	-.2895229	-.1199038
/gamma2	.3611933	.328396	1.10	0.271	-.2824511	1.004838
/delta	.0974553	.1225434	0.80	0.426	-.1427252	.3376359

```

. mlci exp /beta1
.438152 95% CI: .2984709, .6432022
. mlci exp /theta
1.505071 95% CI: 1.352218, 1.675201
.
. mlci exp /gamma1
.8148808 95% CI: .7486206, .8870057
. mlci exp /gamma2
1.435041 95% CI: .7539335, 2.731464
.
. mlci invlogit /delta
.5243446 95% CI: .4643791, .5836161

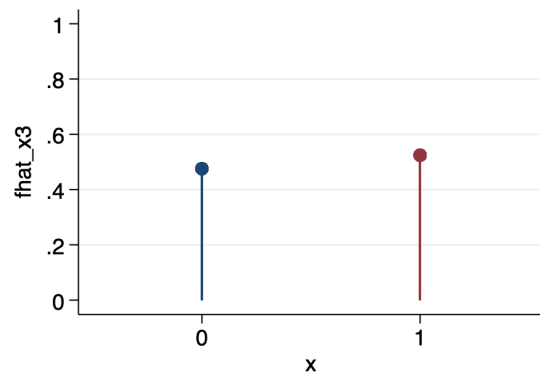
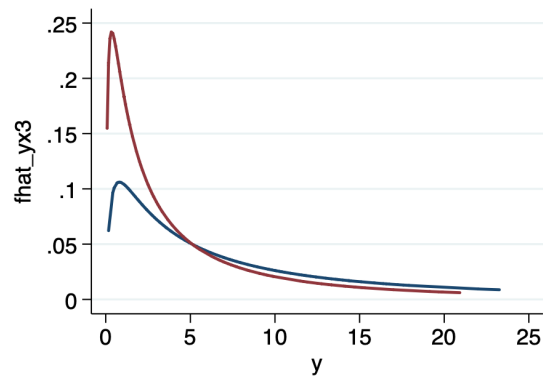
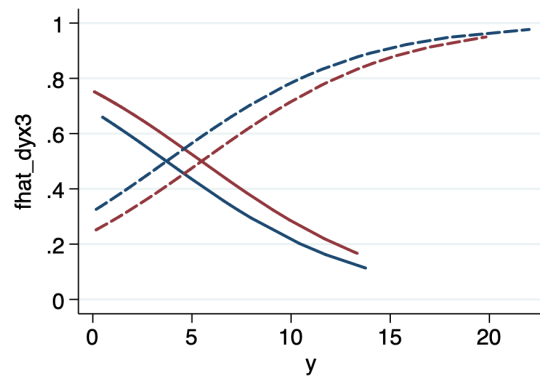
```

Plot the estimated distributions $\hat{f}(d|y, x)$, $\hat{f}(y|x)$, and $\hat{f}(x)$.

```

. gen fhat_dy3 = invlogit(_b[/gamma0]+_b[/gamma1]*y+_b[/gamma2]*x) if d == 1
(171 missing values generated)
. replace fhat_dy3 = 1-invlogit(_b[/gamma0]+_b[/gamma1]*y+_b[/gamma2]*x) if d == 2
(88 real changes made)
. tw (line fhat_dy3 y if x == 0 & d == 1, sort lc(navy)) ///
> (line fhat_dy3 y if x == 1 & d == 1, sort lc(maroon)) ///
> (line fhat_dy3 y if x == 0 & d == 2, sort lc(navy) lp(-)) ///
> (line fhat_dy3 y if x == 1 & d == 2, sort lc(maroon) lp(-)), ///
> name(p6, replace) legend(rows(1)) legend(off) ylabel(0(0.2)1)
.
. gen fhat_yx3 = normalden((log(y) - (_b[/beta0]+_b[/beta1]*x)) / exp(_b[/theta]))*(1 / y / exp(_b[/theta]))
. tw (line fhat_yx3 y if x == 0, sort lc(navy)) ///
> (line fhat_yx3 y if x == 1, sort lc(maroon)), name(p7, replace) legend(off)
.
. gen fhat_x3 = invlogit(_b[/delta]) if x==1
(127 missing values generated)
. replace fhat_x3 = 1-invlogit(_b[/delta]) if x==0
(127 real changes made)
.
. tw (dropline fhat_x3 x if x == 1, lc(maroon) lc(maroon) mc(maroon)) ///
> (dropline fhat_x3 x if x == 0, lc(navy) lc(navy) mc(navy)), ///
> name(p8, replace) legend(off) ylabel(0(0.2)1) xlabel(0 1) xscale(range(-.5 1.5))
. graph combine p6 p7 p8, name(c3, replace)
. graph export c3.png, replace
(file c3.png written in PNG format)

```



Exercise 3

We recruited 2,784 subjects in Sweden at the time of their first myocardial infarction. We took a blood sample and measured LDL cholesterol (mmol/L) on a first follow-up visit, 1 month after the MI (variable `ldl1`). We then measured LDL cholesterol again 6 months after the MI (second follow-up visit) (variable `ldl2`). Plot the sample histogram of the 2 variables. What can we say about them?

```
. use https://raw.githubusercontent.com/anddis/fsm/master/data/lab5_2.dta, clear
.
. su ldl1 ldl2, detail
```

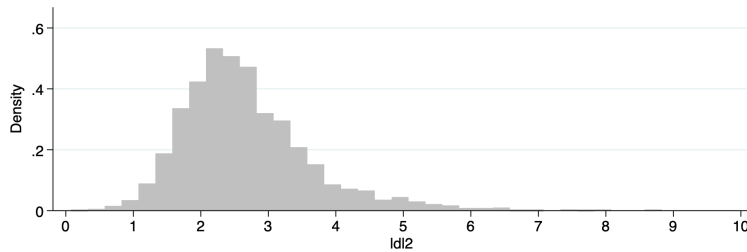
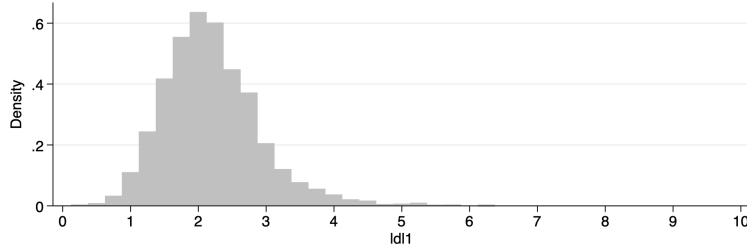
ldl1				
Percentiles		Smallest		
1%	.833	.123		
5%	1.164	.273		
10%	1.372	.322	Obs	2,784
25%	1.6945	.412	Sum of Wgt.	2,784
50%	2.1195		Mean	2.195147
		Largest	Std. Dev.	.7253906
75%	2.581	5.667		
90%	3.073	5.803	Variance	.5261915
95%	3.512	5.829	Skewness	.9833921
99%	4.441	6.274	Kurtosis	5.316994
ldl2				
Percentiles		Smallest		
1%	.977	.077		
5%	1.431	.337		
10%	1.634	.408	Obs	2,784
25%	2.028	.434	Sum of Wgt.	2,784
50%	2.509		Mean	2.670523
		Largest	Std. Dev.	.9806975
75%	3.129	7.839		
90%	3.886	7.925	Variance	.9617677

95%	4.525	8.611	Skewness	1.33667
99%	5.884	8.823	Kurtosis	6.399398

```

.
. hist ldl1, xlabel(0/10) width(.25) name(s1, replace)
(bin=25, start=.123, width=.25)
. hist ldl2, xlabel(0/10) width(.25) name(s2, replace)
(bin=35, start=.077, width=.25)
. graph combine s1 s2, name(s0, replace) ycommon cols(1)
. graph export s0.png, replace
(file s0.png written in PNG format)

```



We model the marginal distributions of the 2 variables: $f(ldl_1), f(ldl_2)$. We consider skew-normal models. This means that $Z = G(Y)$ follows a standard skew-normal distribution.

$$G(y) = (y - \mu)/\sigma$$

$$g(y) = 1/\sigma$$

$$f_Z(z) = 2F_N(\alpha z)f_N(z)$$

where $F_N(z)$ and $f_N(z)$ are the standard normal CDF and PDF, respectively.

Estimate the 2 models' parameters and plot the densities over the sample histograms. Are the data suggesting that the skewness parameter α is different from 0?

```

. local G = "(ldl1-{mu})/exp({theta})"
. local g = "1 / exp({theta})"
. local f1 = "normal({alpha}*`G`)"
. local f2 = "normalden(`G`)*`g`"
. mlexp (log(2*`f1`*`f2`))
initial:      log likelihood = -9998.109
alternative:  log likelihood = -4801.7168
rescale:      log likelihood = -4801.7168
rescale eq:   log likelihood = -3154.1605
Iteration 0:  log likelihood = -3154.1605
Iteration 1:  log likelihood = -2945.0724
Iteration 2:  log likelihood = -2924.1425
Iteration 3:  log likelihood = -2920.4731
Iteration 4:  log likelihood = -2920.4395
Iteration 5:  log likelihood = -2920.4395
Maximum likelihood estimation
Log likelihood = -2920.4395      Number of obs      =      2,784

```

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]

/alpha	2.611656	.1571988	16.61	0.000	2.303552	2.91976
/mu	1.406456	.0213084	66.00	0.000	1.364692	1.44822
/theta	.0690262	.0198467	3.48	0.001	.0301275	.107925

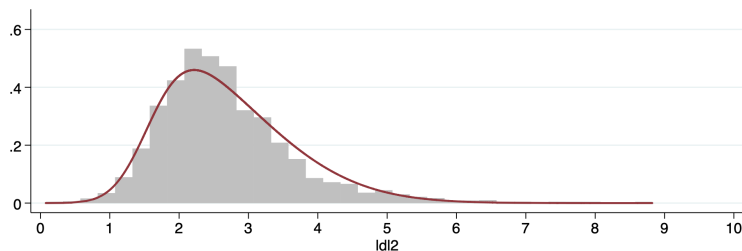
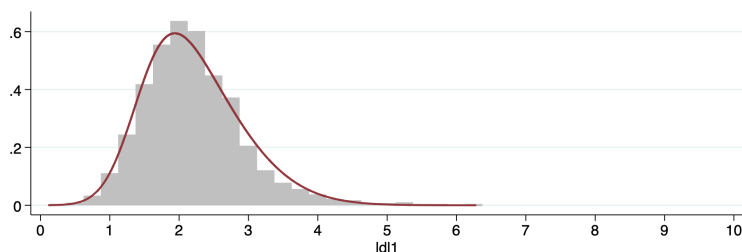
```
. gen fhat_ldl1 = 2*normal(_b[/alpha]*(ldl1-_b[/mu])/exp(_b[/theta]))*normalden((ldl1-_b[/mu])/exp(_b[/theta]))/exp(_b[/theta])
> theta])
. tw (hist ldl1, width(.25)) (line fhat_ldl1 ldl1, sort), name(s1, replace) xlabel(0/10) legend(off)
.
. local G = "(ldl2-{mu})/exp({theta})"
. local g = "1 / exp({theta})"
. local f1 = "normal({alpha}*`G`)"
. local f2 = "normalden(`G`)*`g`"
. mlexp (log(2*`f1`*`f2`))
initial:      log likelihood = -13823.944
alternative:  log likelihood = -5798.7897
rescale:     log likelihood = -5072.3055
rescale eq:  log likelihood = -4031.7673
Iteration 0:  log likelihood = -4031.7673
Iteration 1:  log likelihood = -3868.3234
Iteration 2:  log likelihood = -3860.2447 (not concave)
Iteration 3:  log likelihood = -3675.2321
Iteration 4:  log likelihood = -3651.3767
Iteration 5:  log likelihood = -3649.0576
Iteration 6:  log likelihood = -3649.036
Iteration 7:  log likelihood = -3649.036
```

Maximum likelihood estimation

Log likelihood = -3649.036 Number of obs = 2,784

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
/alpha	3.524436	.1928855	18.27	0.000	3.146387	3.902484
/mu	1.561897	.0223357	69.93	0.000	1.518119	1.605674
/theta	.3920594	.0175325	22.36	0.000	.3576964	.4264223

```
. gen fhat_ldl2 = 2*normal(_b[/alpha]*(ldl2-_b[/mu])/exp(_b[/theta]))*normalden((ldl2-_b[/mu])/exp(_b[/theta]))/exp(_b[/theta])
> theta])
. tw (hist ldl2, width(.25)) (line fhat_ldl2 ldl2, sort), name(s2, replace) xlabel(0/10) legend(off)
.
. graph combine s1 s2, name(p6, replace) ycommon cols(1)
. graph export p6.png, replace
(file p6.png written in PNG format)
```



Exercise 4

We consider the joint distribution of ldl_1 and ldl_2

$$f(ldl_1, ldl_2) = f(ldl_2|ldl_1)f(ldl_1)$$

We assume that $f(ldl_1)$ and $f(ldl_2|ldl_1)$ are skew-normal. Allow all parameters of $f(ldl_2|ldl_1)$ to depend on ldl_1 . Estimate the model's parameters. Remember to constrain the bounded parameters.

```
. local f1 = "normal({alpha1}*(ldl1-{beta1})/exp({theta1}))"
. local f2 = "normalden((ldl1-{beta1})/exp({theta1}))/exp({theta1})"
.
. local f3 = "normal({alpha2: _cons ldl1}*(ldl2-{beta2: _cons ldl1})/exp({theta2: _cons ldl1}))"
. local f4 = "normalden((ldl2-{beta2: _cons ldl1})/exp({theta2: _cons ldl1}))/exp({theta2: _cons ldl1})"
.
. // The code above is equivalent to the (probably more familar) code below, but it's more compact
. // and easier to read. The output of the code above is easier to read, too.
. // local f3 = "normal(({alpha20}+{alpha21}*ldl1)*(ldl2-({beta20}+{beta21}*ldl1))/exp({theta20}+{theta21}*ldl1))"
. // local f4 = "normalden((ldl2-({beta20}+{beta21}*ldl1))/exp({theta20}+{theta21}*ldl1))/exp({theta20}+{theta21}*ldl1)"
.
. mlexp(log(2*f1*f2) + log(2*f3*f4))
initial:      log likelihood = -23822.053
alternative:  log likelihood = -10600.506
rescale:      log likelihood = -10018.378
rescale eq:   log likelihood = -7185.9278
Iteration 0:  log likelihood = -7185.9278 (not concave)
Iteration 1:  log likelihood = -6701.0692
Iteration 2:  log likelihood = -6388.4497 (not concave)
Iteration 3:  log likelihood = -6266.5071
Iteration 4:  log likelihood = -6179.0375
Iteration 5:  log likelihood = -6171.9849
Iteration 6:  log likelihood = -6171.8148
Iteration 7:  log likelihood = -6171.8146
```

Maximum likelihood estimation

Log likelihood = -6171.8146 Number of obs = 2,784

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
alpha1						
_cons	2.611652	.1571985	16.61	0.000	2.303549	2.919756
beta1						
_cons	1.406457	.0213085	66.00	0.000	1.364693	1.44822
theta1						
_cons	.0690259	.0198467	3.48	0.001	.0301271	.1079246
alpha2						
ldl1	-1.154094	.1203596	-9.59	0.000	-1.389995	-.9181938
_cons	5.912853	.3713762	15.92	0.000	5.184969	6.640737
beta2						
ldl1	.6225221	.0290767	21.41	0.000	.5655327	.6795114
_cons	.3965575	.0557818	7.11	0.000	.2872271	.5058879
theta2						
ldl1	.0917335	.0204176	4.49	0.000	.0517159	.1317512
_cons	.0259962	.0464537	0.56	0.576	-.0650512	.1170437

```
. mlexp, coeflegend // Display the legend for the model's coefficients, so that we know how to reference them
```

Maximum likelihood estimation

Log likelihood = -6171.8146 Number of obs = 2,784

	Coef.	Legend
alpha1		
_cons	2.611652	_b[alpha1:_cons]
beta1		

	_cons	1.406457	_b[beta1:_cons]
theta1	_cons	.0690259	_b[theta1:_cons]
alpha2	ldl1	-1.154094	_b[alpha2:ldl1]
	_cons	5.912853	_b[alpha2:_cons]
beta2	ldl1	.6225221	_b[beta2:ldl1]
	_cons	.3965575	_b[beta2:_cons]
theta2	ldl1	.0917335	_b[theta2:ldl1]
	_cons	.0259962	_b[theta2:_cons]

Draw a scatterplot of ldl_2 versus ldl_1 . Do the results above agree with the plot? Make a qualitative assessment.

Plot the estimated conditional density $\hat{f}(ldl_2|ldl_1)$ for ldl_1 values of 2, 3, and 5 mmol/L. Again, make a qualitative assessment of the plot.

```
. tw (scatter ldl2 ldl1, msize(tiny) msym(Oh)), name(p7, replace)
. graph export p7.png, replace
(file p7.png written in PNG format)

.
. gen fhat_y2 = 2 * normal((_b[alpha2:_cons]+_b[alpha2:ldl1]*2)*(ldl2-(_b[beta2:_cons]+_b[beta2:ldl1]*2))/exp((_b[theta2
> :_cons]+_b[theta2:ldl1]*2))) * ///
> normalden((ldl2-(_b[beta2:_cons]+_b[beta2:ldl1]*2))/exp((_b[theta2:_cons]+_b[theta2:ldl1]*2)))/exp((_b[theta2:_cons]+_
> b[theta2:ldl1]*2))

.
. gen fhat_y3 = 2 * normal((_b[alpha2:_cons]+_b[alpha2:ldl1]*3)*(ldl2-(_b[beta2:_cons]+_b[beta2:ldl1]*3))/exp((_b[theta2
> :_cons]+_b[theta2:ldl1]*3))) * ///
> normalden((ldl2-(_b[beta2:_cons]+_b[beta2:ldl1]*3))/exp((_b[theta2:_cons]+_b[theta2:ldl1]*3)))/exp((_b[theta2:_cons]+_
> b[theta2:ldl1]*3))

.
. gen fhat_y5 = 2 * normal((_b[alpha2:_cons]+_b[alpha2:ldl1]*5)*(ldl2-(_b[beta2:_cons]+_b[beta2:ldl1]*5))/exp((_b[theta2
> :_cons]+_b[theta2:ldl1]*5))) * ///
> normalden((ldl2-(_b[beta2:_cons]+_b[beta2:ldl1]*5))/exp((_b[theta2:_cons]+_b[theta2:ldl1]*5)))/exp((_b[theta2:_cons]+_
> b[theta2:ldl1]*5))

.
. tw (line fhat_y2 fhat_y3 fhat_y5 ldl2, sort lc(blue purple red)), name(p8, replace) legend(rows(1))
. graph export p8.png, replace
(file p8.png written in PNG format)
```

