```
/*******************************************************************
*
*Cox-Snell residual examination
*
*******************************************************************/

***Model 2
/*load model*/
loc model M2a_HR
cd "C:\data\malaria\results\efron  8 Oct 2015 16_30_08\"
use `model'.dta, clear
estimates use M2a_HR
estimates esample: SpeciesX AGR4_4b EthnicX sexPreg oral_v_dhp if ip==0
/*generate Cox-Snell residuals*/
predict cs, csnell
save "C:\data\malaria\results\26octCoxSnell\M2aHR_coxsnell.dta"
* use "C:\data\malaria\results\26octCoxSnell\M2aHR_coxsnell.dta", clear
stset cs, fail(AdmNext14)
/*generate Nelson-Aalen cumulative hazard estimate*/
sts gen H = na
save "C:\data\malaria\results\26octCoxSnell\M2aHR_coxsnell.dta", replace
 loc model M2a_HR
 /*load symbol for degree into a macro (no smcl character)*/
loc deg =  char(176)
/*plot residuals*/
line H cs cs, sort graphr(color(white) lc(white)) plotr(color(white)) ylab(,nogrid) lpattern(solid dash) lc("153 142 195" "27 158
119") lwidth(thick medium) legend(order(1 "Nelson-Aalen cumulative hazard" 2 "Cox-Snell residual (45`deg' reference line)")
size(small) cols(1)  margin(0 15 0 0)) xtitle(,margin(medsmall)) name(rCS_`model', replace) xsize(10) ysize(10)
/*export*/
graph export "C:\data\malaria\figures\residuals\`model'_coxsnell.emf", as(emf) replace


***Model 3
/*load model*/
loc model M3b_HR
cd "C:\data\malaria\results\efron  8 Oct 2015 21_14_52"
use `model'.dta, clear
estimates use `model'
estimates esample: SpeciesX AGR4_4b EthnicX sexPreg oral_v_dhp if ip==0
/*generate Cox-Snell residuals*/
predict cs, csnell
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta"

stset cs, fail(DiedNext14)

/*generate Nelson-Aalen cumulative hazard estimate*/
sts gen H = na
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta", replace
/*load symbol for degree into a macro (no smcl character)*/
loc deg =  char(176)

/*plot residuals*/
line H cs cs, sort graphr(color(white) lc(white)) plotr(color(white)) ylab(,nogrid) lpattern(solid dash) lc("153 142 195" "27 158
119") lwidth(thick medium) legend(order(1 "Nelson-Aalen cumulative hazard" 2 "Cox-Snell residual (45`deg' reference line)")
size(small) cols(1)  margin(0 15 0 0)) xtitle(,margin(medsmall)) name(rCS_`model', replace) xsize(10) ysize(10)
/*export*/
graph export "C:\data\malaria\figures\residuals/`model'_coxsnell.emf", as(emf) replace

***Model 4
loc model M4a_HR
cd "C:\data\malaria\results\efron  8 Oct 2015 21_14_52"
use `model'.dta, clear
estimates use `model'
estimates esample: SpeciesX AGR4_4b EthnicX sexPreg ivArt if ip==1
predict cs, csnell
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta"

stset cs, fail(DiedNext14)
/*generate Nelson-Aalen cumulative hazard estimate*/
sts gen H = na
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta", replace
/*load symbol for degree into a macro (no smcl character)*/
loc deg =  char(176)
/*plot residuals*/
line H cs cs, sort graphr(color(white) lc(white)) plotr(color(white)) ylab(,nogrid) lpattern(solid dash) lc("153 142 195" "27 158
119") lwidth(thick medium) legend(order(1 "Nelson-Aalen cumulative hazard" 2 "Cox-Snell residual (45`deg' reference line)")
size(small) cols(1)  margin(0 15 0 0)) xtitle(,margin(medsmall)) name(rCS_`model', replace) xsize(10) ysize(10)
/*export*/
graph export "C:\data\malaria\figures\residuals/`model'_coxsnell.emf", as(emf) replace


***TVC models
cd "C:\data\malaria\results\efron 24 Oct 2015 10_47_59"

*Model 2 tv37
loc model M2aTV37_24oct2015
```

```stata
use "MalEps_v1.9.3_M2a_TV37.dta", clear
estimates use `model'
loc varlist _ISpeciesX_2      tv3_ISpeciesX_2      tv7_ISpeciesX_2      ///
            _ISpeciesX_4                                                ///
            _ISpeciesX_5                                                ///
            _IEthnicX_2                                                 ///
            _IEthnicX_3      tv3_IEthnicX_3         tv7_IEthnicX_3       ///
            _IAGR4_4b_1                                                 ///
            _IAGR4_4b_2      tv3_IAGR4_4b_2          tv7_IAGR4_4b_2      ///
            _IAGR4_4b_3                              tv7_IAGR4_4b_3      ///
            _IsexPreg_2                              tv7_IsexPreg_2      ///
            _IsexPreg_3      tv3_IsexPreg_3         tv7_IsexPreg_3       ///
            _Ioral_v_dh_1
estimates esample: `varlist' if ip==0
predict cs, csnell
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta"

stset cs, fail(AdmNext14)
/*generate Nelson-Aalen cumulative hazard estimate*/
sts gen H = na
rename H H_37
rename cs cs_37
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta", replace
/*import model2a CS prediction*/
append using "C:\data\malaria\results\26octCoxSnell\M2aHR_coxsnell.dta", keep(cs H)


/*compare models*/
    *M2 comparison
    loc model m2_coxsnell_AC
    /*Regress Nelson Aalen cumulative hazard and Cox-Snell residual: slope should be 1 (store estimates for plot)*/
    qui: reg cs H        /* Model 2A */
    loc M2a = `:di %9.2f _b[H]'

    qui: reg cs_37 H_37 /* Model 2B */
    loc M2c = `:di %9.2f _b[H_37]'

    /*store highest residual for limit of y axis*/
    qui: su cs_37
    loc ypos `r(max)'

    /*store degree sign in macro (not available in smcl)*/
    loc deg =  char(176)
    /*plot comparison of residuals across models*/
    tw  line H cs cs, sort lc("27 158 119" none) lwidth(thick none) lpattern(dash)  || ///
        line H_37 cs_37 cs_37, sort lpattern(solid solid) ///
            lc("153 142 195" black) lwidth(thick thin) ///
        legend(ring(0) pos(11) lwidth(none) ///
            nobox fc(none) bc(none) lpattern(blank) region(style(none)) ///
            order( ///
                1 "Model 2a Nelson-Aalen cumulative hazard {it:H}({it:r}{sub:cs})= 0 + 0`M2a'{it:r}{sub:cs}" ///
                3 "Model 2c Nelson-Aalen cumulative hazard {it:H}({it:r}{sub:cs})= 0 + 0`M2c'{it:r}{sub:cs}" ///
                4 "Cox-Snell residual (45`deg' reference line)") ///
                    size(vsmall) cols(1) symysize(*.5) ) ///
            xtitle("Cox-Snell residuals from early admission models 2a and 2c", ///
            margin(medsmall)) name("rCS_`model'", replace) xsize(20) ysize(20) ///
            graphr(color(white) lc(white)) plotr(color(white)) ///
            ylab(,nogrid angle(h) format(%9.2f) labsize(small)) ///
            xlab(,format(%9.2f) labsize(small))

    graph export "C:\data\malaria\figures\residuals/`model'_coxsnell.png", as(png) width(1000) height(1000) replace


*Model 3 tv37
loc model M3bTV37_24oct2015
use "MalEps_v1.9.3_M3b_TV37.dta", clear
estimates use `model'
loc varlist _ISpeciesX_2                                               ///
            _ISpeciesX_4                                               ///
            _ISpeciesX_5      tv3_ISpeciesX_5       tv7_ISpeciesX_5     ///
            _IEthnicX_2                                                ///
            _IEthnicX_3                                                ///
            _IAGR4_4b_1                                                ///
            _IAGR4_4b_2      tv3_IAGR4_4b_2          tv7_IAGR4_4b_2     ///
            _IAGR4_4b_3                                                ///
            _IsexPreg_2                                                ///
            _IsexPreg_3                                                ///
            _Ioral_v_dh_1
estimates esample: `varlist' if ip==0
predict cs, csnell
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta"

stset cs, fail(DiedNext14)
sts gen H = na
rename H H_37
rename cs cs_37
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta", replace
```

```
loc model M3bTV37_24oct2015
append using "C:\data\malaria\results\26octCoxSnell/M3b_HR_coxsnell.dta", keep(cs H)

/*compare models*/
    *M3 comparison
    loc model m3_coxsnell_AB
    /*Regress Nelson Aalen cumulative hazard and Cox-Snell residual: slope should be 1 (store estimates for plot)*/
    qui: reg cs H        /* Model 3a */
    loc M3a = `:di %9.2f _b[H]'

    qui: reg cs_37 H_37 /* Model 3c */
    * loc M3c = `:di %9.2f _b[H_37]' /* manual entry as this displays with odd decimal place */
    loc M3c .93
    * di "0`M3a'x and 0`M3c'x"

    /*store highest residual for limit of y axis*/
    qui: su cs_37
    loc ypos `r(max)'

    /*store degree sign in macro (not available in smcl)*/
    loc deg =  char(176)
    /*plot comparison of residuals across models*/
    tw  line H cs cs, sort lc("27 158 119" none) lwidth(thick none) lpattern(dash)  || ///
        line H_37 cs_37 cs_37, sort lpattern(solid solid) ///
            lc("153 142 195" black) lwidth(thick thin) ///
        legend(ring(0) pos(11) lwidth(none) ///
            nobox fc(none) bc(none) lpattern(blank) region(style(none)) ///
            order( ///
                1 "Model 3a Nelson-Aalen cumulative hazard {it:H}({it:r}{sub:cs})= 0 + 0`M3a'{it:r}{sub:cs}" ///
                3 "Model 3c Nelson-Aalen cumulative hazard {it:H}({it:r}{sub:cs})= 0 + 0`M3c'{it:r}{sub:cs}" ///
                4 "Cox-Snell residual (45`deg' reference line)") ///
                    size(vsmall) cols(1) symysize(*.5) ) ///
            xtitle("Cox-Snell residuals from early death models 3a and 3c", ///
            margin(medsmall)) name("rCS_`model'", replace) xsize(20) ysize(20) ///
            graphr(color(white) lc(white)) plotr(color(white)) ///
            ylab(,nogrid angle(h) format(%9.3f) labsize(small)) ///
            xlab(,format(%9.3f) labsize(small))

    graph export "C:\data\malaria\figures\residuals/`model'_coxsnell.png", as(png) width(1000) height(1000) replace
* * Model 3a solograph
* loc deg =  char(176)
* line H cs cs, sort graphr(color(white) lc(white)) plotr(color(white)) ylab(,nogrid) lpattern(solid dash) lc("153 142 195" "27 158 119")
lwidth(thick medium) legend(order(1 "Nelson-Aalen cumulative hazard" 2 "Cox-Snell residual (45`deg' reference line)") size(small)
cols(1)  margin(0 15 0 0)) xtitle(,margin(medsmall)) name("rCS_`model'", replace) xsize(10) ysize(10)

* graph export "C:\data\malaria\figures\residuals/`model'_coxsnell.emf", as(emf) replace

*Model 4 tv37
loc model M4aTV37_24oct2015
use "MalEps_v1.9.3_M4a_TV37.dta", clear
estimates use `model'
loc varlist _ISpeciesX_2                            ///
            _ISpeciesX_4                            ///
            _ISpeciesX_5                            ///
            _IEthnicX_2                             ///
            _IEthnicX_3                             ///
            _IAGR4_4b_1             tv7_IAGR4_4b_1   ///
            _IAGR4_4b_2                             ///
            _IAGR4_4b_3             tv7_IAGR4_4b_3   ///
            _IsexPreg_2                             ///
            _IsexPreg_3                             ///
            _IivArt_1
estimates esample: `varlist' if ip==1
predict mgale, mgale
predict cs, csnell
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta"

stset cs, fail(DiedNext14) id(obsno)
sts gen H = na

rename H H_37
rename cs cs_37
save "C:\data\malaria\results\26octCoxSnell/`model'_coxsnell.dta", replace
loc model M4aTV37_24oct2015
append using "C:\data\malaria\results\26octCoxSnell/M4a_HR_coxsnell.dta", keep(cs H)

/*compare models*/
    *M4 comparison
    loc model m4_coxsnell_AB
    /*Regress Nelson Aalen cumulative hazard and Cox-Snell residual: slope should be 1 (store estimates for plot)*/
    reg cs H        /* Model 3a */
    loc M4a = `:di %9.2f _b[H]'

    reg cs_37 H_37 /* Model 3c */
    loc M4c = `:di %9.2f _b[H_37]'
```

```stata
* di "O`M3a'x and O`M3c'x"

/*store highest residual for limit of y axis*/
qui: su cs_37
loc ypos `r(max)'

/*store degree sign in macro (not available in smcl)*/
loc deg =  char(176)

/*plot comparison of residuals across models*/
tw  line H_37 cs_37 cs_37, sort lc("153 142 195" none) ///
    lwidth(thick none) lpattern(solid)  || ///
    line H cs cs, sort lpattern(dash solid) ///
        lc("27 158 119" black) lwidth(vthick thin) ///
    legend(ring(0) pos(11) lwidth(none) ///
        nobox fc(none) bc(none) lpattern(blank) region(style(none)) ///
        order( ///
            3 "Model 4a Nelson-Aalen cumulative hazard {it:H}({it:r}{sub:cs})= 0 + O`M4a'{it:r}{sub:cs}" ///
            1 "Model 4c Nelson-Aalen cumulative hazard {it:H}({it:r}{sub:cs})= 0 + O`M4c'{it:r}{sub:cs}" ///
            4 "Cox-Snell residual (45`deg' reference line)") ///
                size(vsmall) cols(1) symysize(*.5) ) ///
        xtitle("Cox-Snell residuals from early death models 4a and 4c", ///
        margin(medsmall)) name("rCS_`model'", replace) xsize(20) ysize(20) ///
        graphr(color(white) lc(white)) plotr(color(white)) ///
        ylab(,nogrid angle(h) format(%9.2f) labsize(small)) ///
        xlab(,format(%9.2f) labsize(small))

    graph export "C:\data\malaria\figures\residuals/`model'_coxsnell.png", as(png) width(1000) height(1000) replace

* *Model 4a tv37 solo graph
* loc deg = char(176)
* line H cs cs, sort graphr(color(white) lc(white)) plotr(color(white)) ylab(,nogrid) lpattern(solid dash) lc("153 142 195" "27 158 119")
lwidth(thick medium) legend(order(1 "Nelson-Aalen cumulative hazard" 2 "Cox-Snell residual (45`deg' reference line)") size(small)
cols(1)  margin(0 15 0 0)) xtitle(,margin(medsmall)) name("rCS_`model'", replace) xsize(10) ysize(10)

* graph export "C:\data\malaria\figures\residuals/`model'_coxsnell.emf", as(emf) replace
```