

```

/*****
*
*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)

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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
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]`

qui: su cs_37
loc ypos `r(max)`

loc deg = char(176)
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

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```

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 "O`M3a'x and O`M3c'x"
qui: su cs_37
loc ypos `r(max)`

loc deg = char(176)
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) symsize(*.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
*correlation between Nelson Aalen cumulative hazard and Cox-Snell residual (should be 1)
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]\'
* di "O`M3a'x and O`M3c'x"
qui: su cs_37
loc ypos `r(max)\'

loc deg = char(176)
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(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 + 0
        `M4a' {it:r}{sub:cs}" ///
        1 "Model 4c Nelson-Aalen cumulative hazard {it:H}({it:r}{sub:cs})= 0 + 0
        `M4c' {it:r}{sub:cs}" ///
        4 "Cox-Snell residual (45`deg' reference line)" ///
        size(vsmall) cols(1) symsize(*.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) labszsize(small)) ///  
xlab(,format(%9.2f) labszsize(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
```