

```

/*****
*Malaria early morbidity and mortality
* Analysis set up do file
*****/

***Set up***
capture log close
version 13.1
set linesize 100
set more off
cd "C:\Users\Carl\Google Drive\MPH\Projects\Malaria project\Data"
loc today = c(current_date)
log using "malariaproject_log_`today'.txt", append text

***Label unlabelled variables***
label variable dod "Date of first discharge"
***label variable DOEnd
label variable Age "Age at date of presentation"
label variable pf "P.falciparum"
label variable pv "P.vivax"
label variable pm "P.malariae"
label variable po "P.ovale"
label variable HbDGr7 "Anaemia at death (< 7g/dL)"
label variable HbDGr5 "Anaemia at death (< 5g/dL)"
label variable Malaria_Last63Gr "Presentations with malaria in the last 2 months"
label variable AGR4 "Age"
label variable Era "ACT Era"
label variable Sex "Sex"
label variable Species "Initial Species"
label variable wbcmin "White Cell Count (minimum)"
label variable wbcmax "White Cell Count (maximum)"
label variable hbmin_Min "Haemoglobin (minimum)"
label variable pltmin "Platelet count (minimum)"
label variable hbmin_First "Haemoglobin (first recorded value)"
label variable hbmin_Last "Haemoglobin (last recorded value)"
label variable aa_any "Amodiaquine+Artesunate"
label variable cq_any "Chloroquine"
label variable cl_any "Clindamycin"
label variable dhp_any "DHA-Piperaquine"
label variable dox_any "Doxycycline"
label variable ivart_any "Iv Artesunate"
label variable ivq_any "Iv Quinine"
label variable oralq_any "Oral Quinine"
label variable pq_any "Primaquine"
label variable sp_any "Sulfadoxine-Pyrimethamine"
label variable PQmgkg_Sum "Sum total dose of Primaquine (mg/kg)"
label variable MalNut "Under-nutrition"
label variable MalNutD "Under-nutrition at death"
label variable op "Outpatient"
label variable Source "Source"
label variable ip "Inpatient"
label variable Bleeding "Bleeding"
label variable EthnicGr "Ethnic Group"

format %12.1f Age
format %12.2f PQmgkg_Sum

```

```
format %9.1f predwt
```

7 day Outcomes

```
recode DiedDay (0/7 = 1) (8/9999 = 0), gen(DiedNext7)
label variable DiedNext7 "Died by 7d"
recode Died_FU (8/9999 = 7), gen(Died_FU7)
label variable Died_FU7 "Died - FollowUp to 7"
```

***Check generation of 7 day outcome variables

```
list DiedDay DiedNext7 Died_FU7 DiedNext14 Died_FU14 if Died_FU14<14
```

***Generate observation id number (for ease of computing totals, etc)

```
gen long obsno = _n
order obsno
label variable obsno "Admissions"
```

***Generate constant in case needed

```
gen constant = 1
label variable obsno "Total admissions"
label define total 1 "Total admissions"
label values constant total
```

***Generate Anemia on admission

```
gen HbAdmGr7 = 1 if hbmin_First<7
recode HbAdmGr7 (.=0)
tab HbAdmGr7 HbDGr7
label variable HbAdmGr7 "Anaemia at admission (< 7g/dL)"
gen HbAdmGr5 = 1 if hbmin_First<5
recode HbAdmGr5 (.=0) if hbmin_First>=5 & hbmin_First<. /* CHECK THAT THIS IS CORRECT */
label variable HbAdmGr5 "Anaemia at admission (< 5g/dL)"
tab HbAdmGr5 HbDGr5
```

***Generate Severe Thrombocytopenia (platelet count < 50,000/uL)

```
gen sevThrom = 1 if pltmin<50
recode sevThrom (.=0) if pltmin>=50 & pltmin~=.
local micro = char(181)
label variable sevThrom "Severe thrombocytopenia (platelet count < 50,000/`micro'L)"
list sevThrom pltmin in 1/10
```

***Generate Log of hb, WBC, Platelets and Primaquine mg/kg

```
gen log10hbmin_f= log10(hbmin_First)
label variable log10hbmin_f "Haemoglobin count (first recorded value; log base 10)"
gen log10wbcmin= log10(wbcmin)
label variable log10wbcmin "White Blood Cell count (minimum; log base 10)"
gen log10pltmin= log10(pltmin)
label variable log10pltmin "Platelet count (minimum; log base 10)"
gen log10PQmgkg_Sum= log10(PQmgkg_Sum)
label variable log10PQmgkg_Sum "Sum total dose of Primaquine (mg/kg; log base 10)"
gen Age_log10= log10(Age)
label variable Age_log10 "Age (years; log base 10)"

gen log2wbcmin= log(wbcmin)/log(2)
label variable log2wbcmin "White Blood Cell count (minimum; log base 2)"
gen log2pltmin= log(pltmin)/log(2)
label variable log2pltmin "Platelet count (minimum; log base 2)"
gen log2PQmgkg_Sum= log(PQmgkg_Sum)/log(2)
```

```
label variable log2PQmgkg_Sum "Sum total dose of Primaquine (mg/kg; log base 2)"
gen Age_log2= log(Age)/log(2)
label variable Age_log2 "Age (years; log base 2)"
```

***Generate quintiles of variable list to check for linearity

/*this code assigns labels based on the min and max of each quintile. For example 1 "100 to 4100" 2 "4110 to 5090" etc */

```
loc q5 wbcmin pltmin/*Designates variables to quintile and label without decimals*/
foreach v of varlist `q5' {
xtile q5_`v' = `v', nq(5)
su q5_`v', meanonly
loc vmin = r(min)
loc vmax = r(max)
forval j = `vmin'/'vmax' {
su `v' if q5_`v'==`j', meanonly
local call `call' `j' "': di %3.0f `=r(min)'' to `: di %3.0f `=r(max)''
}
label define q5_`v' `call', replace
label values q5_`v' q5_`v'
codebook q5_`v'
}
```

```
loc q5 PQmgkg_Sum/*Designates variables to quintile and label with decimals*/
foreach v of varlist `q5' {
xtile q5_`v' = `v', nq(5)
su q5_`v', meanonly
loc vmin = r(min)
loc vmax = r(max)
forval j = `vmin'/'vmax' {
su `v' if q5_`v'==`j', meanonly
local call `call' `j' "': di %3.2f `=r(min)'' to `: di %3.2f `=r(max)''
}
label define q5_`v' `call', replace
label values q5_`v' q5_`v'
codebook q5_`v'
}
label variable q5_PQmgkg_Sum "Sum total dose of primaquine (mg/kg, quintiles)"
label variable q5_wbcmin "White cell count (minimum, quintiles)"
label variable q5_pltmin "Platelet count (minimum, quintiles)"
```

***Generate 'dummy' variable for later Tabout table output macros

```
generate dummy = 1
```

***Generate Female only Pregnancy variable (males are missing)

```
gen pregWom = Preg if Sex==2
label variable pregWom "Pregnant (females only)"
```

***Convert Year to labelled categories starting at 1

```
loc convert Year
foreach v of varlist `convert' {
su `v', meanonly
loc vmin = r(min)
loc vmax = r(max)
loc n 0
forvalues j = `vmin'/'vmax' {
local cat = `++n'
```

```

local convi `convi' "(" `j' "=" `cat' ")"
local def `def' `cat' "`j'"
}

```

```

recode `v' `convi', gen(`v'Cat)
label define `v'Cat `def', replace
label values `v'Cat `v'Cat
label variable `v'Cat "`v'"
codebook `v'Cat
}

```

Define and assign value labels

```

label define SOURCE 1 "OP" 2 "OP to IP" 3 "IP", replace
label define AGR4 1 "< 1 year" 2 "1 to < 5 years" 3 "5 to <15 years" 4 "15+ years", modify
label define yesno 0 "No" 1 "Yes"
label values aa_any cq_any cl_any dhp_any dox_any ivart_any ivq_any oralq_any pq_any sp_any
///
MalNut Bleeding Preg pregWom HbDGr7 HbDGr5 MalNutD VivaxDeath HbAdmGr5 HbAdmGr7
sevThrom ///
MalariaNext365 PFNext365 PVNext365 PMNext365 MIXNext365 AdmNext14 DiedNext14
DiedNext365 DiedNext7 yesno

```

Sort database by hrn, date of admission and date of discharge, in that order

```
sort hrn doa dod
```

*Round age to two decimal places (the current long data format causes difficulties with 'if' statements using scalars where Age < 1, apparently)

```
replace Age = round(Age, .01)
```

*Generate sex variable differentiating between pregnant and not pregnant females

```

gen sexPreg= Sex+Preg
recode sexPreg (1=3) (2=1) (3=2)
lab def sexPreg 1 "Female (not pregnant)" 2 "Female (pregnant)" 3 "Male"
lab val sexPreg sexPreg
lab var sexPreg "Sex and pregnancy status"
codebook sexPreg

```

*Generate combined HRN and MalCluster variable for generating Riskset graphics

```

gen hrnmal = hrn + (MalCluster/10) if MalCluster <10
tempvar maxmal
by hrn: egen `maxmal' = max(MalCluster)
replace hrnmal = hrn +(MalCluster/(`maxmal'+1)) if `maxmal' >=10
list hrnmal if `maxmal' >10

```

```
/*
```

***Generate possible preferred follow up time variables

```

gen FU_Adm = doa + Adm_FU14
format %tdD_m_Y FU_Adm
gen FU_Died = doa + Died_FU14
format %tdD_m_Y FU_Died

```

Generate offset 'begin' and 'end' time variables for subsequent, multiple presentations (may improve stset functionality??)

```

gen begin_m = (MalCluster-1)/1000
gen end_Adm = Adm_FU14 + ((MalCluster-1)/1000)
gen end_D = Died_FU14 + ((MalCluster-1)/1000) */

```

***Generate early exit variables closer to zero for better graphical presentation (equal interval)**

```

gen AdmFU14m = Adm_FU14 + .5
recode AdmFU14m (1=.5)
lab var AdmFU14m "Adm - Follow up to 14 days"
gen DiedFU14m = Died_FU14 + .5
recode DiedFU14m (1=.5)
lab var DiedFU14m "Died - Follow up to 14 days"

gen AdmFU15 = Adm_FU14+1
recode AdmFU15 (1.5=1)
lab var AdmFU15 "Admission: Follow up to 15 days"

gen DiedFU15 = Died_FU14+1
recode DiedFU15 (1.5=1)
lab var DiedFU15 "Died: Follow up to 15 days"

```

***generate estimated date of admission / death**

```

gen doX_adm = doa+AdmFU15
gen doX_died = doa+DiedFU15

```

***Generate pltCat**

```

recode pltmin (20/50=2 "20 to 50"), gen(pltCat)
replace pltCat = 1 if pltmin<20
replace pltCat = 3 if pltmin>50&pltmin<.
list pltmin pltCat
label define pltCat 2 "20 to 50" 1 "< 20" 3 "> 50", replace
label variable pltCat "Platelet count (minimum)"
label variable pltCat "Platelet count ( x 1000s/ $\mu$ L)"

```

***Generate reduced categories of MalPres**

```

recode MalPres (1=1 "1") (2=2 "2") (3/9=3 "3+"), gen(MalPres_cat)
label variable MalPres_cat "Number of malaria events in episode"

```

***Gen white blood cell outside normal range indicator (from Nick)**

```

generate whiteout=.
replace whiteout=1 if Age<0.0192 & (wbcmin<20000 | wbcmax>40000) & wbcmin!=.
replace whiteout=1 if (Age>=0.0192 & Age<0.0385) & (wbcmin<5000 | wbcmax>21000) & wbcmin!=.
replace whiteout=1 if (Age>=0.0385 & Age<0.25) & (wbcmin<5000 | wbcmax>20000) & wbcmin!=.
replace whiteout=1 if (Age>=0.25 & Age<1) & (wbcmin<5000 | wbcmax>15000) & wbcmin!=.
replace whiteout=1 if (Age>=1 & Age<5) & (wbcmin<5000 | wbcmax>12000) & wbcmin!=.
replace whiteout=1 if Age>=5 & (wbcmin<4000 | wbcmax>10000) & wbcmin!=.
replace whiteout=0 if whiteout!=1 & wbcmin!=.
label define whiteout 0 "within normal range" 1 "outside of normal range"
label values whiteout whiteout
tab whiteout
label variable whiteout "WBC count"

```

***Gen white blood cell above, below or within normal range indicator**

```

generate whiteCat = .
replace whiteCat=1 if Age<0.0192 & (wbcmin<20000) & wbcmin!=.
replace whiteCat=2 if Age<0.0192 & (wbcmax>40000) & wbcmin!=.
replace whiteCat=1 if (Age>=0.0192 & Age<0.0385) & (wbcmin<5000) & wbcmin!=.
replace whiteCat=2 if (Age>=0.0192 & Age<0.0385) & (wbcmax>21000) & wbcmin!=.
replace whiteCat=1 if (Age>=0.0385 & Age<0.25) & (wbcmin<5000) & wbcmin!=.
replace whiteCat=2 if (Age>=0.0385 & Age<0.25) & (wbcmax>20000) & wbcmin!=.

```

```

replace whiteCat=1 if (Age>=0.25 & Age<1) & (wbcmin<5000) & wbcmin!=.
replace whiteCat=2 if (Age>=0.25 & Age<1) & (wbcmax>15000) & wbcmin!=.
replace whiteCat=1 if (Age>=1 & Age<5) & (wbcmin<50000) & wbcmin!=.
replace whiteCat=2 if (Age>=1 & Age<5) & (wbcmax>12000) & wbcmin!=.
replace whiteCat=1 if Age>=5 & (wbcmin<4000) & wbcmin!=.
replace whiteCat=2 if Age>=5 & (wbcmax>10000) & wbcmin!=.
replace whiteCat=0 if whiteCat==. & wbcmin!=.
replace whiteCat=0 if whiteCat==1 & whiteout==0
/*The above line is required to ensure whiteCat ranges correspond with whiteout ranges;
although I should confirm sources for these values with Nick Douglas */
label define whiteCat 0 "within normal range" 1 "below normal range" 2 "above normal range"
label values whiteCat whiteCat
tab whiteCat
label variable whiteCat "WBC count"

```

*Generate ACT treatment category (0 = not ACT; 1 = ACT)

```

gen ACT = 0 if TreatGr_First !=.
recode ACT (0 = 1) if TreatGr_First >2 & TreatGr_First<6
label define ACT 0 "not ACT" 1 "ACT" , replace
label values ACT ACT
tab TreatGr_First ACT

```

*Generate treatment mode category (0 = oral; 1 = iv)

```

gen IV = 0 if TreatGr_First !=.
recode IV (0 = 1) if TreatGr_First >4
label define IV 0 "Oral" 1 "IV" , replace
label values IV IV
tab TreatGr_First IV

```

* *Generate initial treatment (0 = Oral not ACT; 1 = Oral ACT; 2 = IV not ACT; 3 = IV ACT) ***

QUESTION: If IVquinine is +/- DHP, then how can we consider as non-ACT?

```

* gen treatCat4 = 0 if TreatGr_First !=.
* recode treatCat4 (0 = 1) if (TreatGr_First>2 & TreatGr_First<5)
* recode treatCat4 (0 = 2) if (TreatGr_First==6)
* recode treatCat4 (0 = 3) if (TreatGr_First==5)
* label define treatCat4 0 "Oral non-ACT" 1 "Oral ACT" 2 "ivQuinine +/-DHP,Cq,S" 3
"ivArtesunate +/-DHP,C " , replace
* label values treatCat4 treatCat4
* tab TreatGr_First treatCat4

```

* *Generate initial treatment (0 = Oral not ACT; 1 = Oral ACT; 2 = IV not ACT; 3 = IV ACT) ***

QUESTION: If IVquinine is +/- DHP, then how can we consider as non-ACT?

```

* gen oralACT = 0 if TreatGr_First !=.
* recode oralACT (0 = 1) if (TreatGr_First>2 & TreatGr_First<5)
* recode oralACT (0 = 2) if TreatGr_First==6
* recode oralACT (0 = 3) if TreatGr_First==5
* label define oralACT 0 "Oral non-ACT" 1 "Oral ACT" 2 "IV (any)" 2 "ivQuinine +/-DHP,Cq,S" 3
"ivArtesunate +/-DHP,C " , replace
* label values oralACT oralACT
* tab TreatGr_First oralACT

```

```

* gen ivACT = 0 if TreatGr_First !=.
* recode ivACT (0 = 1) if TreatGr_First==5
* recode ivACT (0 = 2) if (TreatGr_First<3)
* recode ivACT (0 = 3) if (TreatGr_First>2 & TreatGr_First<5)
* label define ivACT 0 "ivQuinine +/-DHP,Cq,S" 1 "ivArtesunate +/-DHP,C " 2 "Oral non-ACT" 3
"Oral ACT", replace

```

*** label values ivACT ivACT**

*** tab TreatGr_First ivACT**

***renaming variable with too long name**

```
rename Malaria_Last63Gr Mal_Last63Gr
```

***Treatment categories code as per Nick and Ric**

```
gen tgn=.
replace tgn=3 if TreatGr2_First==1 | TreatGr2_First==2
replace tgn=2 if TreatGr1_First==2 & tgn!=3
replace tgn=1 if matchscript==1 & tgn!=2 & tgn!=3
label define tgn 1 "Non-ACT oral first" 2 "ACT oral first" 3 "IV first"
label values tgn tgn
label variable tgn "Initial treatment group"
tab tgn
```

***Generate Species variable omitting P.ovale**

```
gen SpeciesX = Species if Species !=3
label variable SpeciesX "Species"
label copy Species SpeciesX
label values SpeciesX SpeciesX
label define SpeciesX 3 "", modify
```

***Generate AGR4 with age category 4 hard coded as baseline (for convenience)**

```
recode AGR4 (4=0), gen(AGR4_4b)
label copy AGR4 AGR4_4b
label values AGR4_4b AGR4_4b
label variable AGR4_4b "Age"
label define AGR4_4b 1 "< 1 year" 2 "1 to < 5 years" 3 "5 to <15 years" 0 "15+ years
(baseline)", replace
```

***Generate pltCat with age category 4 hard coded as baseline (for convenience)**

```
recode pltCat (3=0), gen(pltCat_3b)
label copy pltCat pltCat_3b
label values pltCat_3b pltCat_3b
label variable pltCat_3b "Platelet count ( x 1000s/ $\mu$ L)"
```

/*****

***Malaria early morbidity and mortality**

*** Tables do file - last modified 5 October 2015**

*** - first run 1. Set up for risk of admission and early death analysis.txt**

*****/

```
capture log close
version 13.1
set linesize 100
set more off
cd "C:\Users\Carl\Google Drive\MPH\Projects\Malaria project\Data\excel"
loc today = c(current_date)
log using "malariaproject_log_`today'.txt", append text
```

***prepare folder for results**

```
local T = c(current_time)
local T = subinstr("`T'", ":", "_", .)
mkdir "table `today' `T'"
cd "table `today' `T'"
```

Table 1a: Characteristics of Patients by Species(export csv for placement in maltab.xlsx)

```
loc dem constant AGR4 sexPreg Ethnic tgn whiteCat HbAdmGr5 pltCat MalNut Malaria_Last63Gr
MalPres_cat Year Era
/*explanatory variables*/
tabout `dem' Species using tables\workfiles\maltable1_Species.csv, replace c(freq row)
f(1) ptotal(none) style(csv)
```

Table 1b: Characteristics of Patients by early outcomestatus (14 days or less) following a malaria episode (export csv for placement in maltab.xlsx)

```
loc group AdmNext14 DiedNext14 /*group variables*/
loc dem constant Species AGR4 sexPreg Ethnic tgn whiteCat HbAdmGr5 pltCat MalNut
Malaria_Last63Gr MalPres_cat Year Era
/*explanatory variables*/
foreach var of varlist `group' {
tabout `dem' `var' using tables\workfiles\maltable1_`var'.csv, replace c(freq row) f(1)
ptotal(none) style(csv) npos(lab)
}

foreach var of varlist `dem' {
tab `var' AdmNext14, row chi
}
```

Table 2Adm: Characteristics of Patients with early re-admission (14 days or less) following a malaria episode (export csv for placement in maltab.xlsx)

```
*AdmNext14==0 (not re-admitted within 14 days)*
loc cont Age hbmin_Min PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin
log10pltmin wbcmin log2wbcmin log10wbcmin
tokenize `cont'
local counter = 0
local filemethod = "replace"
local heading = "h1(nil) h2(nil) h3(|Count | Mean | SD | Median |Min | Max )"
foreach v of varlist `cont' {
if `counter' > 0 {
local filemethod = "append"
local heading = "h1(nil) h2(nil) h3(nil)"
}
label define dummy 1 "`v'", modify
label val dummy dummy
tabout dummy if AdmNext14==0 using tables\workfiles\table2adm0.csv, ///
`filemethod' c(count `v' mean `v' sd `v' median `v' min `v' max `v' ) ///
f(0 lc lc lc lc lc) sum `heading' ///
lines(none) ptotal(none) style(csv)
mac shift
local counter = `counter' + 1
}

*AdmNext14==1 (re-admitted within 14 days)*
loc cont Age hbmin_Min PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin
log10pltmin wbcmin log2wbcmin log10wbcmin
tokenize `cont'
local counter = 0
local filemethod = "replace"
local heading = "h1(nil) h2(nil) h3(|Count | Mean | SD | Median |Min | Max )"
foreach v of varlist `cont' {
if `counter' > 0 {
local filemethod = "append"
```



```

local heading = "h1(nil) h2(nil) h3(nil)"
}
label define dummy 1 "1", modify
label val dummy dummy
tabout dummy if AdmNext14==1 using tables\workfiles\table2adml.csv, ///
`filemethod' c(count `v' mean `v' sd `v' median `v' min `v' max `v' ) ///
f(0 1c 1c 1c 1c 1c) sum `heading' ///
lines(none) ptotal(none) style(csv)
mac shift
local counter = `counter' + 1
}

**ttest vars by AdmNext14*
loc cont Age hbmin_Min PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin
log10pltmin wbcmin log2wbcmin log10wbcmin
loc groupv AdmNext14
foreach v of varlist `cont' {
qui ttest `v', by(`groupv')
di as text " `v' Mean difference by `groupv':"
di %9.1f r(mu_1)-r(mu_2) as text " (95% CI" %9.1f (r(mu_1)-r(mu_2)-(1.96*r(se))) as
text"," as result %9.1f (r(mu_1)-r(mu_2)+(1.96*r(se))) as text "; {it:P-value}:" %9.3f r(p)
as text)"
}

**Mann-Whitney U Test
loc cont PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin log10pltmin
wbcmin log2wbcmin log10wbcmin
loc groupv AdmNext14
foreach v of varlist `cont' {
ranksum `v', by(`groupv')
}

***Ask Julie for help with this - which to use with?

***Table 1 Died: Characteristics of Patients by early death status (14 days or less) following a
malaria episode (export csv for placement in maltab.xlsx)***
loc dem constant Species AGR4 Sex pregWom Ethnic MalNut Malaria_Last63Gr HbAdmGr5
sevThrom q5_wbcmin q5_pltmin Source Year Era TreatGr_First q5_PQmgkg_Sum
tabout `dem' DiedNext14 using tables\workfiles\maltable1_Died.csv, replace c(freq row)
f(1) ptotal(none) style(csv) npos(lab)

foreach var of varlist `dem' {
tab `var' DiedNext14, row chi
}

***Table 2 Died: Characteristics of Patients with early death (14 days or less) following a malaria
episode (export csv for placement in maltab.xlsx)***
*DiedNext14==0 (did not die within 14 days)*
loc cont Age hbmin_Min PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin
log10pltmin wbcmin log2wbcmin log10wbcmin
tokenize `cont'
local counter = 0
local filemethod = "replace"
local heading = "h1(nil) h2(nil) h3(|Count | Mean | SD | Median |Min | Max )"
foreach v of varlist `cont' {
if `counter' > 0 {
local filemethod = "append"
local heading = "h1(nil) h2(nil) h3(nil)"

```

```

}
label define dummy 1 "`1'", modify
label val dummy dummy
tabout dummy if DiedNext14==0 using tables\workfiles\table2d0.csv, ///
`filemethod' c(count `v' mean `v' sd `v' median `v' min `v' max `v' ) ///
f(0 lc lc lc lc lc) sum `heading' ///
lines(none) ptotal(none) style(csv)
mac shift
local counter = `counter' + 1
}

```

DiedNext14==1 (died within 14 days)

```

loc cont Age hbmin_Min PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin
log10pltmin wbcmin log2wbcmin log10wbcmin
tokenize `cont'
local counter = 0
local filemethod = "replace"
local heading = "h1(nil) h2(nil) h3(|Count | Mean | SD | Median |Min | Max )"
foreach v of varlist `cont' {
if `counter' > 0 {
local filemethod = "append"
local heading = "h1(nil) h2(nil) h3(nil)"
}
}
label define dummy 1 "`1'", modify
label val dummy dummy
tabout dummy if DiedNext14==1 using tables\workfiles\table2d1.csv, ///
`filemethod' c(count `v' mean `v' sd `v' median `v' min `v' max `v' ) ///
f(0 lc lc lc lc lc) sum `heading' ///
lines(none) ptotal(none) style(csv)
mac shift
local counter = `counter' + 1
}

```

ttest vars by DiedNext14

```

loc cont Age hbmin_Min PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin
log10pltmin wbcmin log2wbcmin log10wbcmin
loc groupv DiedNext14
foreach v of varlist `cont' {
qui ttest `v', by(`groupv')
di as text "`v' Mean difference by `groupv':"
di %9.1f r(mu_1)-r(mu_2) as text " (95% CI" %9.1f (r(mu_1)-r(mu_2)-(1.96*r(se))) as
text"," as result %9.1f (r(mu_1)-r(mu_2)+(1.96*r(se))) as text "; {it:P-value}:" %9.3f r(p)
as text)"
}

```

*Mann-Whitney U Test

```

loc cont PQmgkg_Sum log2PQmgkg_Sum log10PQmgkg_Sum pltmin log2pltmin log10pltmin
wbcmin log2wbcmin log10wbcmin
loc groupv AdmNext14
foreach v of varlist `cont' {
ranksum `v', by(`groupv')
}

```

***Graph histogram density plots for continuous variables (or is kernel density better? pretty similar)

/*(hbmin_Min is normally distributed; PQmgkg_Sum has an odd distribution suggestive of

```
two distinct treatment groupings - this is especially noticeable if restricted to
AGR4==4, and has some relationship with white blood cell count (eg. second peak is more
prominent in wbcmin>8000))*/
```

```
loc cont Age Age_log10 Age_log2 predwt hbmin_Min pltmin log10pltmin log2pltmin wbcmin
log10wbcmin log2wbcmin
foreach var of varlist `cont' {
  histogram `var', normal dens name("`var'_histo_density",replace) scheme(tufte)
}
```

```
/******
```

```
*
```

```
*EXTRA GRAPHS
```

```
*
```

```
*****/
```

***Graph of initial species by year - note both absolute increase in Pv and mixed diagnoses across study period, and relative to Pf**

```
use "C:\data\malaria\MalEps_v1.9.3_r9aug2015.dta", clear
cd\data\malaria
tempfile original
save `original'
```

```
/*Generate indicators of variables for plotting frequencies */
```

```
g pres_pf = SpeciesX if SpeciesX==1
```

```
g pres_pv = SpeciesX if SpeciesX==2
```

```
g pres_all = constant
```

```
g adm_pf = SpeciesX if AdmNext14==1 & SpeciesX==1
```

```
g adm_pv = SpeciesX if AdmNext14==1 & SpeciesX==2
```

```
g adm_all = constant
```

```
g died_pf = SpeciesX if DiedNext14==1 & SpeciesX==1
```

```
g died_pv = SpeciesX if DiedNext14==1 & SpeciesX==2
```

```
g died_all = constant
```

```
/*Collapse for frequencies of each variable */
```

```
collapse (count)      pres_pf      ///
                        pres_pv      ///
                        pres_all      ///
                        adm_pf        ///
                        adm_pv        ///
                        adm_all        ///
                        died_pf        ///
                        died_pv        ///
                        died_all        ///
                        , by(YearCat)
```

```
/*Colours from colorbrewer2.org */
```

```
loc farb1 = "27 158 119"
```

```
loc farb2 = "217 95 2"
```

```
loc farb3 = "102 194 165"
```

```
loc farb4 = "252 141 98"
```

```
loc farb5 = "179 226 205"
```

```
loc farb6 = "253 205 172"
```

```
tw      line pres_pf Year, sort lc("`farb5'")      || ///
      line pres_pv Year, lc("`farb6'")      || ///
```

```

line adm_pf Year, sort lc("`farb3'") lpattern(dash) || ///
line adm_pv Year, lc("`farb4'") lpattern(dash) || ///
line died_pf Year, sort lc("`farb1'") lpattern(.) || ///
line died_pv Year, lc("`farb2'") lpattern(.) ///
legend(order(1 "{it:P.falciparum}" 2 "{it: P.vivax}"{bf: malaria episodes}" ///
3 "{it:P.falciparum}" 4 "{it: P.vivax}"{bf: early admissions}" ///
5 "{it:P.falciparum}" 6 "{it: P.vivax}"{bf: early deaths}")) ///
col(2) pos(6) ) ///
xlab(2004(1)2013, labsize(small)) xsca(nofextend) ///
xtitle("Year", margin(medsmall)) ///
ytitle(, margin(medsmall)) ylab(,angle(h) nogrid) ///
graphr(color(white) lcolor(white)) plotr(color(white) ) ///
title("Yearly frequency of malaria episodes, early admissions and early deaths", ///
size(medsmall) placement(west) margin(-8 0 0 -3 ) justification(left)) xsize(12)
ysize(10)

/
/*****
* Malaria early morbidity and mortality *
* Preliminary analysis - generating tables and graphs - file last edited - 28 May 2015 *
* - first run do files '1a. Setup', and optionally '1b stvary diagnostics' *
*****/

capture log close
version 13.1
set linesize 100
set more off
cd "C:\Users\Carl\Google Drive\MPH\Projects\Malaria project\Data\results"
loc today = c(current_date)
log using "malariaproject_log_`today'.txt", append text

*TIES
loc ties efron

*prepare folder for results
local T = c(current_time)
local T = subinstr("`T'",":","_",.)
mkdir "`ties' `today' `T'"
cd "`ties' `today' `T'"
mkdir figures
cd figures
mkdir PH
cd ..

keep obsno hrn Age Sex Ethnic AGR4 AdmNext14 DiedNext14 YearCat sexPreg hrnmal AdmFU14m
DiedFU14m whiteCat tgn SpeciesX AdmFU15 DiedFU15

*timer Start

timer clear 1
timer on 1

*** use "C:\Users\Carl\Google Drive\MPH\Internships\Malaria project\Data\File
archive\MalariaEpisodes_vs 1.9.3.dta", clear /*FIRST RUN SET UP */

```

*Outcome / Failure variables

```

loc outcome Adm Died          /* list of outcomes of interest to be analysed
separately */
loc Adm_f early admission      /* full title of 'admission' outcome for graph
display */
loc Died_f early death        /* full title of 'death' outcome for graph display */

```

*Exposures

```

loc commonExp  SpeciesX      ///
                  AGR4        ///
                  sexPreg      ///
                  Ethnic       ///
                  whiteCat     ///
                  tgn          ///

```

*Exposures

```

loc iExp        i.SpeciesX    ///
                  b4.AGR4      ///
                  i.sexPreg    ///
                  i.Ethnic     ///
                  i.whiteCat   ///
                  i.tgn        ///

```

*Model specifications

```

loc model1 ", cluster(hrn)"
loc model2 "i.SpeciesX b4.AGR4 i.sexPreg i.Ethnic i.whiteCat i.tgn, cluster(hrn) `ties'"

```

*save graph style in local macro

```

loc graph_style graphregion(fcolor(white) lcolor(white)) scheme(s2color)
di "`graph_style'"

```

```

foreach outc of loc outcome {

```

*Initiate outcome timer

```

timer clear 2
timer on 2

```

*Copy template result sheet for each outcome

```

copy ..\Template_resTable_v2.xlsx `outc'_resTable.xlsx

```

*Set up for export of data to Excel results worksheet

```

putexcel set "`outc'_resTable.xlsx", modify keepcellformat
putexcel A1 = ("Model 2: stcox `model2' ") /* Title for excel results sheet */ ///
C2 = ("`di proper("`outc'_f'")'")

```

*Create macro references for excel export columns

```

loc nN_Cell      = "C"
loc uHRCCell     = "D"
loc uHRpvalCell  = "E"
loc M2_HRCCell   = "G"
loc M2_HRpvalCell = "H"
loc mfp_HRCCell  = "J"
loc mfp_HRpvalCell = "K"

```

***Start cell for input values**

```
loc vcell = 5
loc varcell = `vcell'
```

***Set up for survival analysis (AdmFU14m and DiedFU14m are currently specified - recoding of follow up time through 0.5 to 14.5)**

```
stset `outc' FU15, fail(`outc' Next14) id(obsno)
loc axismax 15
```

*** *Graph example risk set for outcome (need to fix outpoints and legend to be closed dot, not arrow)**

```
loc Adm_hlstart = 72745
loc Adm_hlend = 72752
loc Died_hlstart = 72745
loc Died_hlend = 72752
loc `outc'rs = ``outc'_hlstart'+1
loc `outc're = ``outc'_hlend'-1
loc hlimit = "if hrnmal>``outc'_hlstart' & hrnmal <``outc'_hlend'"
loc mcols = "black"
loc ts = "_t0"
loc te = "_t"
loc yvar = "hrnmal"
loc textv = ``outc'rs' -.2

twoway sc `yvar' `ts' `hlimit', mc(`mcols') ms(o)
|| ///
pcspike `yvar' `ts' `yvar' `te' `hlimit' & _d==0, mc(`mcols') lcolor(`mcols')
|| ///
pcspike `yvar' `ts' `yvar' `te' `hlimit' & _d==1, lcolor(`mcols')
|| ///
sc `yvar' `te' `hlimit' & _d==1, mc(red) ms(X)
|| ///
sc `yvar' `te' `hlimit' & _d==0, mc(`mcols') ms(o)
///
text(72746.1 0 "(not malaria patient)", size(small) placement(e) color(gray))
///
text(72748.1 0 "(not malaria patient)", size(small) placement(e) color(gray))
///
text(72751.1 0 "(not malaria patient)", size(small) placement(e) color(gray))
///
name("`outc'_egRiskset ``outc'rs'to``outc're'",replace)
///
title("HRN clusters (`outc'_f' riskset example)",size(medsmall))
///
placement(west) margin(-10 0 0 -3) justification(left))
///
ylabel(72746.1(1)72751.1, format(%9.0f)
///
nogrid angle(horizontal) labsize(small))
///
yttitle("Hospital Record Number clusters")
///
xlabel(0(1)`axismax', labsize(small)) yscale(rev)
```

```

                                ///
    xtitle("Time (days) from entry (_t0) until ``outc'_f' or censoring (_t)"
    ///
    , margin(medsmall)) /***/

                                ///
    xline(15, lpattern(shortdash) lc(edkblue) noextend)
    ///
    text(72746 15 "End of two weeks' follow up", size(small) placement(w))
    ///
    legend(on order(1 "entry / exit (censored)" 2 "time at risk" 4 "``outc'_f'"))
    ///
    colfirst notextfirst nostack cols(6) size(small) nobox
    ///
    region(fcolor(white) margin(zero) lcolor(white)) position(12) ring(1))
    ///
    `graph_style' xscale(nofextend)
graph export figures/`outc'_egRiskset``outc'rs'to``outc're'.png, as(png) replace

```

***Loop code over explanatory variables for descriptive statistics

```

foreach v of varlist `commonExp' {

    *Export variable name
    putexcel    A`varcell' = ("`': var label `v'")

```

*Macros for key aspects (min max, n etc)

```

su `v', meanonly
loc vmax = r(max)
loc vmin = r(min)
loc vcat = (`vmax' - `vmin') + 1
if `vcat' < 6 {

    /*alternate spacing for extra categories*/
    loc alt=""
}
else {
    loc alt="alt"
}

loc labname = "`': val label `v'"" /***/
qui: levelsof `v', loc(vl)

```

*Macros for Kaplan-Meier curve and other graphs

```

loc labname = "`': val label `v'"" /***/

tempvar `v'_S /* generating temporary survivor function variable by explanatory
variable to establish scaling */
sts gen ``v'_S' = s, by(`v')
tempvar `v'_F
gen ``v'_F' = 1 - ``v'_S'
su ``v'_F', meanonly
loc fmax = r(max)
loc fmin = r(min)
loc failmax = round(trunc((r(max) * 10))/10,.25)
loc gap = round(`failmax'/5,.05)
loc roundmax = `failmax' - `gap'

```

```

loc mindif = r(max)-`roundmax'
loc med = ""
loc call = ""
if `mindif' > .14 {
    loc med= `roundmax'+ .1
}

loc ordnum = 1
foreach j of loc vl {          /* establishing labels for value categories */
    local call `call' `ordnum' "': label `labname' `j'"
    loc ++ordnum
}

```

*KM survival curve (automatic y axis scaling)

```

sts graph, by(`v') failure                                     ///

    name("`outc' _`v'_KM", replace)                             ///

    title("Probability of failure: "`outc'_f', by `': var label `v'", size(medsmall)
    ///
    placement(west) margin(-8 0 0 -3 ) justification(left))    ///
    xlab(0(1)`axismax', labsize(small)) xmtick(0(1)15)         ///
    xttitle("Days since presentation with malaria", margin(medsmall))
    ///
    ylab(minmax `fmin' `fmax' 0(`gap')`roundmax' `med',
    ///
    add format(%5.3f) nogrid labsize(small) angle(horizontal))
    ///
    legend(on order(`call') colfirst notextfirst nostack cols(6) size(small)
    ///
    nobox region(fcolor(white) margin(zero) lcolor(white)) position(12) ring(1))
    ///
    `graph_style' xscale(nofextend) yscale(nofextend)          ///

    note(" ")
graph export figures/`outc' _`v'_KM.png, as(png) replace

loc adjvar = substr("`commonExp'", "`v'", " ", 1)
loc adjcall
foreach av of varlist `adjvar' {
loc adjcall `adjcall' "':var label `av'", "
}

loc adjcall = substr("`adjcall'", char(34), "", . )           /**/
loc adjcall = substr("`adjcall'",1,length("`adjcall'")-2)

di "Adjusting for `adjcall'"

sts graph, by(`v') failure adjustfor("`adjvar'")              /**/
///
    name("`outc' _`v'_KM_adj", replace)

```



```

///
title("Probability of failure: ``outc'_f', by ``: var label `v', adjusted*",
size(medsmall) ///
placement(west) margin(-8 0 0 -3 ) justification(left))
///
xlab(0(1)`axismax', labsize(small)) xmtick(0(1)15)
///
xtitle("Days since presentation with malaria event", margin(medsmall))
///
ylab(minmax `fmin' `fmax' 0(`gap')`roundmax' `med',
///
add format(%5.3f) nogrid labsize(small) angle(horizontal))
///
legend(on order(`call') colfirst notextfirst nostack cols(6) size(small)
///
nobox region(fcolor(white) margin(zero) lcolor(white)) position(12) ring(1))
///
`graph_style' xscale(nofextend) yscale(nofextend)
///
note(" *adjusted for: `adjcall'")
graph export figures/`outc'_`v'_KM_adj.png, as(png) replace

graph combine `outc'_`v'_KM `outc'_`v'_KM_adj, name("`outc'_`v'_KM_combo", replace)
xsize(20) ysize(10.4) `graph_style'

*Export cumulative incidence to Excel
tab `v' `outc'Next14, row matcell(`v'_`outc'_tab)
mata : st_matrix("`v'_`outc'_N", rowsum(st_matrix("`v'_`outc'_tab"))) /*sums columns
for total N*/
loc r = 1

foreach i of loc vl {
    putexcel B`varcell' = (``: label `labname' `i'``) /**/
    putexcel `nN_Cell'`varcell' = (``:di %6.0fc `v'_`outc'_tab[`r',2] / ``:di %6.0fc (`v'_
`outc'_N[`r',1])' (``:di%-5.2f ((`v'_`outc'_tab[`r',2] / (`v'_`outc'_N[`r',1])) *100)')")

    loc ++r /*increments the row number in stored matrix results */
    loc ++varcell /*increments the row number for output to Excel */
}
}

***Loop code over explanatory variables - Hazard ratios
loc varcell = `vcell'
foreach v in `iExp' {
    ***Univariable unadjusted model (results for each outcome output to excel worksheets
per variable in folder 'Results')
    stcox `v', `ties'
    matrix vHR = r(table)'
    local names: rownames vHR
    loc r = 1
    foreach n of loc names {
        loc vr `=substr("`n'",1,1)' /**/
        loc br `=substr("`n'",2,1)' /**/

        di "`vr'"
        di "`br'"
    }
}

```

```

if "`br'" == "b" {
    putexcel                `uHRCcell'`varcell' = ("1.00 (reference)")
                                ///
                                `uHRpvalCell'`varcell' = ("-")

}

if "`br'" == "o" {
    putexcel                `uHRCcell'`varcell' = ("(omitted)")
                                ///
                                `uHRpvalCell'`varcell' = ("-")

}

if "`br'" == "." {
    putexcel                `uHRCcell'`varcell' = ("`:di%3.2f vHR[`r',1]' (
                                `:di%3.2f vHR[`r',5]', `:di%3.2f vHR[`r',6]')")
                                ///
                                `uHRpvalCell'`varcell' = ("`: di subinword("`: di
                                %4.3f vHR[`r',4]'", "0.000", "< 0.001", 1)')")

}

loc ++r
loc ++varcell
di "r = `r'; varcell = `varcell'"
}

}

```

```
/* end of univariable loop */
```

***Plot failure rate for Year with Era marker

```

loc `outc'_var YearCat                                /*define list of explanatory variables*/
foreach v of varlist ``outc'_var' {
    su `v', meanonly
    loc vmax = r(max)
    loc eramarker = ""
    set varabbrev off
    loc Adm_era_mark = 22.75
    loc Died_era_mark = 0.55

    strate `v', per(10000) graph cluster(hrn)
                                ///
    name("`outc'_YearEra_strate", replace)
                                ///
    title("Rate of ``outc'_f' per 10,000 patient-days, by Year & ACT Era",
                                ///
                                size(medsmall) placement(west) margin(-10 0 0 -3) justification(left))
                                ///
    m(o) mc(black) ciopts(lc(black) ls(p2other))
                                ///
    xlabel(#`vmax', value label labsize(small))
                                ///
    xtitle("`": var label `v'""', margin(medsmall)) /****/
                                ///
    ylabel(, nogrid angle(horizontal) labsize(small)) ytitle("")
                                ///
    xline(3.4, lpattern(shortdash) lc(blue) noextend)
                                ///
    text("`outc'_era_mark' 5.7 "ACT usage commences in April 2006", size(small)
                                ///

```

```

justification(left))

addplot(pcarrowi ``outc'_era_mark' 4 ``outc'_era_mark' 3.6 (3), mc(black)
      ///
      msiz(medsmall) mfc(black) lc(black))
      ///

legend(off)
      ///

xscale(nofextend) yscale(nofextend) `graph_style'

graph export figures/`outc'_Year-Era_stratel0k.png, as(png) replace
}

timer off 2
timer list 2
di "Time to process data for `outc': " r(t1)/60 "minutes"
} /* end of outcome loop */

timer off 1
timer list 1
di "Time to process complete do-file: " r(t1)/60 "minutes"

/*****
* Malaria early morbidity and mortality *
* Risk of Admission as inpatient within 14 days of presentation - 9 December 2014 *
* - first run do files '1a...' (Setup) and '1b...' (stvary diagnostics) *
*****/

*Set up log and working directory
capture log close
version 13.1
set linesize 100
set more off
cd "C:\Users\Carl\Google Drive\MPH\Projects\Malaria project\Data\results"
loc today = c(current_date)
log using "malariaproject_log_`today'.txt", append text

*local macro to establish method of Cox model ties handling
loc ties efron

* prepare folder for results
local T = c(current_time)
local T = substr("`T'", ":", "_", ".")
mkdir "`ties' `today' `T'"
cd "`ties' `today' `T'"
mkdir figures
cd figures
mkdir PH
cd ..

*timer Start

```

```
timer clear 1
timer on 1
```

*** Admission

*Logistic regression

*m1a

```
logistic ip i.SpeciesX i.Ethnic ib4.AGR4 i.sexPreg, vce(cluster hrn)
estimates store M1a_OR_v2
/* store model for later retrieval */
estimates save M1a_OR_v2
linktest
```

*m1b

```
logistic ip i.SpeciesX i.Ethnic ib4.AGR4 i.sexPreg i.whiteCat, vce(cluster hrn)
estimates store M1b_OR /* store
model for later retrieval */
estimates save M1b_OR
linktest
```

* *M1a and M1b lrtest: Doesn't work - uneven observation duh

* lrtest M1a_OR M1b_OR

*Cox PH regression

```
stset AdmFU15, fail(AdmNext14) id(obsno)
gen oral_v_dhp = 1 if TreatGr_First==4
replace oral_v_dhp =0 if TreatGr_First == 2
tab oral_v_dhp TreatGr_First
```

*m2a: risk of admission within 15 days in those who were not admitted immediately, and on oral or dhp

```
stcox i.SpeciesX ib4.AGR4 i.Ethnic i.sexPreg i.oral_v_dhp if ip==0, cluster(hrn) efron
estimates store M2a_HR /* store
model for later retrieval */
estimates save M2a_HR
linktest, cluster(hrn) efron
```

*m2b: as above with wcc, limited to those with laboratory data

```
stcox i.SpeciesX ib4.AGR4 i.Ethnic i.sexPreg i.oral_v_dhp i.whiteCat if ip==0,
cluster(hrn) efron
estimates store M2b_HR /* store
model for later retrieval */
estimates save M2b_HR
linktest, cluster(hrn) efron
```

* lrtest M2a_HR M2b_HR

*Mann-Whitney U-test

```
ranksum MalPres, by(oral_v_dhp)
ranksum MalPres, by(oral_v_dhp) porder
median MalPres, by(oral_v_dhp) exact
```

***Death

```
stset DiedFU15, fail(DiedNext14) id(obsno)
```

*m3a: risk of death by day 15 in those who were not initially admitted, including oral / dhp

first treatment

```
stcox i.SpeciesX ib4.AGR4 i.Ethnic i.sexPreg i.oral_v_dhp if ip==0, cluster(hrn) efron
estimates store M3a_HR /* store
model for later retrieval */
estimates save M3a_HR
linktest, cluster(hrn) efron
```

***m3b: with WBC count normality**

```
stcox i.SpeciesX ib4.AGR4 i.Ethnic i.sexPreg i.oral_v_dhp i.whiteCat if ip==0,
cluster(hrn) efron
estimates store M3b_HR /* store
model for later retrieval */
estimates save M3b_HR
linktest, cluster(hrn) efron
```

*** m4a: risk of death by day 15 limited to those who were admitted immediately & rx'd IV treatment first**

```
gen ivArt = 1 if TreatGr_First ==5
replace ivArt = 0 if TreatGr_First ==6
lab copy TreatGr_First ivArt
label define ivArt 1 "ivArtesunate +/-DHP,Cq,SP" 0 "ivQuinine +/-DHP,Cq,SP", replace
label values ivArt ivArt
lab var ivArt "IV treatment"
codebook ivArt
```

```
stcox i.SpeciesX ib4.AGR4_4b i.Ethnic i.sexPreg i.ivArt if ip==1, cluster(hrn) efron
estimates store M4a_HR /* store
model for later retrieval */
estimates save M4a_HR
linktest, cluster(hrn) efron
```

***m4b: with WBC count normality**

```
stcox i.SpeciesX ib4.AGR4 i.Ethnic i.sexPreg i.ivArt i.whiteCat if ip==1, cluster(hrn)
efron
estimates store M4b_HR /* store
model for later retrieval */
estimates save M4b_HR
linktest, cluster(hrn) efron
```

```
timer off 1
timer list 1
```

```
/******
*Multivariable Fractional Polynomial regression
* Drawing on do-file of Julie Simpson and Nick Douglas
*****/
```

```
capture log close
version 13.1
set linesize 100
set more off
cd "C:\data\malaria\results"
loc today = c(current_date)
log using "malariaproject_log_`today'.txt", append text
local T = c(current_time)
local T = subinstr("`T'", ":", "_", .)
```

```
capture: drop agegraph
```

```
egen agegraph = cut (Age), at (0 (0.04) 60.04)
sort Age agegraph
```

*Generate variable excluding 1st and 99th percentiles

```
su Age, d
loc agep1 r(p1)
loc agep99 r(p99)
gen Age99p = 1 if Age > `agep1' & Age < `agep99'
codebook Age99p
su Age if Age99p==.

hist Age if Age99p==.
hist Age if Age99p==1

tw hist Age if Age99p==1, freq width(1) fc("216 179 101") lc("black") lwidth(vvthin) || hist
Age if Age99p==., fc("90 180 172") lc("black") lwidth(vvthin) freq width(.5)
xtitle(,margin(medsmall)) ytitle(,margin(medsmall)) plotr(color(white)) graphr(color(white)
lc(white)) ylab(,nogrid angle(h) format(%9.0fc)) ///
legend(order(1 "146 days {&le} Age {&le} 58 years" ///
2 "Age {&lt; 146 days {&union} 58 years {&lt; Age") rows(2) pos(6)) ///
|| pcarrowi 14000 0.4 12500 0.4 "1st percentile", lc("black") lwidth(vvthin) msymbol(i)
mlabcolor(black) mc(black) mlwidth(vthin) mlabpos(1) ///
|| pcarrowi 14000 58 1000 58 "99th percentile", lc("black") lwidth(vvthin) msymbol(i)
mlabcolor(black) mc(black) mlwidth(vthin) mlabpos(1) ///
name(age_histo_percentiles)
```

* Admission

* MFP without age in 1st or 99th percentile

```
xi: mfp logistic AdmNext14 i.SpeciesX i.EthnicX Age i.sexPreg if Age99p==1, cluster(hrn)
df(2, Age: 4)

qui: adjust _IEthnicX_2 _IEthnicX_3 _IsexPreg_2 _IsexPreg_3, by(agegraph SpeciesX) pr ci
replace
```

* ***Graph the results***

```
twoway (rarea ub lb agegraph if SpeciesX==4 & ///
agegraph>0.019, fcolor(gray) fintensity(50) lcolor(white) ///
lwidth(none)) (line pr agegraph if SpeciesX==4 & agegraph>0.019, ///
lcolor(gray) lwidth(thick) lpattern(solid)) (rarea ub lb agegraph ///
if SpeciesX==5 & agegraph>0.20, fcolor(dkorange) fintensity(50) ///
lcolor(white) lwidth(none)) (line pr agegraph if SpeciesX==5 & ///
agegraph>0.15, lcolor(dkorange) lwidth(thick) lpattern(solid)) ///
(rarea ub lb agegraph if SpeciesX==1 & agegraph>0.019, ///
fcolor("147 30 17") fintensity(50) lcolor(white) lwidth(none)) ///
(line pr agegraph if SpeciesX==1 & agegraph>0.019, lcolor("147 30 17") ///
lwidth(thick) lpattern(solid)) (rarea ub lb agegraph if SpeciesX==2 & ///
agegraph>0.019, fcolor("21 155 2") fintensity(50) lcolor(white) ///
lwidth(none)) (line pr agegraph if SpeciesX==2 & agegraph>0.019, ///
lcolor("21 155 2") lwidth(thick) lpattern(solid)), ///
ytitle(Probability of early admission) ytitle(, margin(medium)) ///
ylabel(, nogrid) ymtick(, nogrid) xtitle(Age (years)) ///
xtitle(, margin(medium)) ///
title("Probability of early admission by {it:Plasmodium} species and age*", span ///
```

```

size(medlarge) margin(medium)) ///
legend(on order(4 "{it:P. vivax}" (95% CI)" 2 "{it:P. falciparum}" (95% CI)" 6 "{it:P.
malariae}" (95% CI)" 8 "Mixed (95% CI)") ///
colfirst notextfirst nostack cols(2) size(small) nobox ///
region(fcolor(white) margin(medium) lcolor(white)) bmargin(zero) ///
position(2) ring(0)) graphregion(fcolor(white) lcolor(white) ///
ifcolor(white) ilcolor(white)) plotregion(fcolor(white) ///
lcolor(white) ifcolor(white) ilcolor(white)) ///
note(" *adjusted for ethnicity, sex and pregnancy status;" "Age excludes observations below
1st percentile and above 99th percentile", span) ///
name(fp_age_Adm_1, replace)

xi: mfp logistic DiedNext14 i.SpeciesX i.EthnicX Age i.sexPreg if Age99p==1, cluster(hrn)
df(2, Age: 5)

qui: adjust _IethnicX_2 _IethnicX_3 _IsexPreg_2 _IsexPreg_3, by(agegraph SpeciesX) pr ci
replace

* ***Graph the results***
twoway (rarea ub lb agegraph if SpeciesX==4 & ///
agegraph>0.019, fcolor(gray) fintensity(50) lcolor(white) ///
lwidth(none)) (line pr agegraph if SpeciesX==4 & agegraph>0.019, ///
lcolor(gray) lwidth(thick) lpattern(solid)) (rarea ub lb agegraph ///
if SpeciesX==5 & agegraph>0.20, fcolor(dkorange) fintensity(50) ///
lcolor(white) lwidth(none)) (line pr agegraph if SpeciesX==5 & ///
agegraph>0.15, lcolor(dkorange) lwidth(thick) lpattern(solid)) ///
(rarea ub lb agegraph if SpeciesX==1 & agegraph>0.019, ///
fcolor("147 30 17") fintensity(50) lcolor(white) lwidth(none)) ///
(line pr agegraph if SpeciesX==1 & agegraph>0.019, lcolor("147 30 17") ///
lwidth(thick) lpattern(solid)) (rarea ub lb agegraph if SpeciesX==2 & ///
agegraph>0.019, fcolor("21 155 2") fintensity(50) lcolor(white) ///
lwidth(none)) (line pr agegraph if SpeciesX==2 & agegraph>0.019, ///
lcolor("21 155 2") lwidth(thick) lpattern(solid)), ///
ytitle(Probability of early death) ytitle(, margin(medium)) ///
ylabel(, nogrid) ymtick(, nogrid) xtitle(Age (years)) ///
xtitle(, margin(medium)) ///
title("Probability of early death by {it:Plasmodium} species and age*", span) ///
size(medlarge) margin(medium)) ///
legend(on order(4 "{it:P. vivax}" (95% CI)" 2 "{it:P. falciparum}" (95% CI)" 6 "{it:P.
malariae}" (95% CI)" 8 "Mixed (95% CI)") ///
colfirst notextfirst nostack cols(2) size(small) nobox ///
region(fcolor(white) margin(medium) lcolor(white)) bmargin(zero) ///
position(2) ring(0)) graphregion(fcolor(white) lcolor(white) ///
ifcolor(white) ilcolor(white)) plotregion(fcolor(white) ///
lcolor(white) ifcolor(white) ilcolor(white)) ///
note(" *adjusted for ethnicity, sex and pregnancy status;" "Age excludes observations below
1st percentile and above 99th percentile", span) ///
name(fp_age_Died_1, replace)

/*****
*
*Model 1 regression diagnostics
*
*****/

```

***Model 1**

```
use "C:\data\malaria\MalEps_v1.9.3_r5oct2015.dta"
```

```
logistic ip i.SpeciesX i.EthnicX i.AGR4_4b i.sexPreg, cluster(hrn)
```

***diagnostics**

```
predict r if e(sample), resid /* predict Pearson residuals */
```

```
predict dbeta if e(sample), dbeta /* Pregibon's delta-beta */
```

```
predict phat if e(sample) /* predicted probability */
```

```
logistic ip i.SpeciesX i.EthnicX i.AGR4_4b i.sexPreg if Preg==0, cluster(hrn)
```

```
predict r_np if e(sample), resid
```

```
predict phat_np if e(sample)
```

***Colours**

```
loc farb1 "27 158 119"
```

```
loc farb2 "217 95 2"
```

```
loc farb3 "117 112 179"
```

```
loc farb4 "231 41 138"
```

```
loc farb5 "102 166 30"
```

***Graph Pearson residual by probability, for ethnic background, sex and pregnancy status**

```
tw sc r phat if SpeciesX==1, mc("`farb1'") || sc r phat if SpeciesX==2, mc("`farb2'") || sc r  
phat if SpeciesX==4, mc("`farb3'") || sc r phat if SpeciesX==5, mc("`farb4'") by(EthnicX  
sexPreg, title(,size(small))) legend(order(1 "{it: P.falciparum}" 2 "{it: P.vivax}" 3 "{it: P  
.malariae}" 4 "mixed") title("{it: Plasmodium} species",size(medsmall)) rows(1)) ylab(-  
10(5)10,nogrid angle(h) labsize(small)) yline(0, lc(black)) yline(5, lc(red)) yline(-  
5,lc(red)) xtitle(,margin(medsmall)) xlab(0(.2)1,labsize(small)) graphr(color(white)  
lc(white)) plotr(color(white))
```

```
/******
```

```
*
```

***Proportional Hazards Assessment**

```
*
```

```
*****/
```

*** *create EthnicX with Highland as baseline reference**

```
* codebook Ethnic
```

```
* recode Ethnic (1=3) (2=1) (3=2), gen(EthnicX)
```

```
* codebook EthnicX
```

```
* label copy Ethnic EthnicX
```

```
* label variable EthnicX EthnicX
```

```
* codebook EthnicX
```

```
* label values EthnicX EthnicX
```

```
* label define EthnicX 3 "Non Papuan" 1 "Highland" 2 "Lowland", replace
```

```
* codebook EthnicX
```

```
* tab Ethnic EthnicX
```

```
* tab Ethnic EthnicX, missing
```

```
* label variable EthnicX "Ethnicity"
```

*** *Create AGR5X - with age 15+ as baseline reference, and including < 7d as a category**


```

* codebook AGR4
* codebook SpeciesX
* codebook sexPreg
* codebook Ethnic
* codebook AGR4
* gen AGR5X = AGR4+2
* recode AGR5X (6=1)
* codebook AGR5X
* replace AGR5X=2 if AgeGr7d==0
* codebook AGR5X
* label copy AGR4 AGR5X
* label values AGR5X AGR5X
* label define AGR5X 3 "8 days to < 1 year" 4 "1 to < 5 years" 5 "5 to <15 years" 1 "15+ years" 2
"0 to 7 days", replace
* codebook AGR5X
* label variable AGR5X "Age"

```

```

* stcox i.SpeciesX i.EthnicX i.AGR5X i.sexPreg if ip==0 & AgeGr7d==1, cluster(hrn) tvc(SpeciesX
EthnicX AGR5X sexPreg) texp(_t>3)

```

```

use "C:\data\malaria\MalEps_v1.9.3_r5oct2015.dta", clear

```

```

**M2AHR

```

```

***Model for hazard ratio of admission in outpatients on oral treatment (ie. risk of admission after
first day of follow up)

```

```

*** Variables are Species (omitting Ovale), Age group (4 categories), Ethnic group, combined sex
and pregnancy status, and oral treatment

```

```

use "C:\data\malaria\results\efron 8 Oct 2015 16_30_08\M2a_HR.dta", clear

```

```

stset AdmFU15, fail(AdmNext14)

```

```

/* STORED MODEL WITH GENERATED SCALED SCHOENFELD RESIDUALS

```

```

loc model M2a_HR

```

```

loc cond if ip==0

```

```

stcox i.SpeciesX i.AGR4_4b i.EthnicX i.sexPreg i.oral_v_dhp `cond', allbaselevels vsquish
cluster(hrn) efron cformat(%6.2f) nolog

```

```

predict `i', scaledsch

```

```

*/

```

```

loc model M2a_HR

```

```

***Combination Graphs

```

```

*Species (SpeciesX)

```

```

use "C:\data\malaria\results\efron 8 Oct 2015 16_30_08\M2a_HR.dta", clear

```

```

running sch1 _t if _d == 1, gen(smooth_sch1 ) nodraw
running sch2 _t if _d == 1, gen(smooth_sch2 ) nodraw
running sch3 _t if _d == 1, gen(smooth_sch3 ) nodraw
running sch4 _t if _d == 1, gen(smooth_sch4 ) nodraw
running sch5 _t if _d == 1, gen(smooth_sch5 ) nodraw
running sch6 _t if _d == 1, gen(smooth_sch6 ) nodraw
running sch7 _t if _d == 1, gen(smooth_sch7 ) nodraw
running sch8 _t if _d == 1, gen(smooth_sch8 ) nodraw
running sch9 _t if _d == 1, gen(smooth_sch9 ) nodraw
running sch10 _t if _d == 1, gen(smooth_sch10) nodraw

```

```

running sch11 _t if _d == 1, gen(smooth_sch11) nodraw
running sch12 _t if _d == 1, gen(smooth_sch12) nodraw
running sch13 _t if _d == 1, gen(smooth_sch13) nodraw
running sch14 _t if _d == 1, gen(smooth_sch14) nodraw
running sch15 _t if _d == 1, gen(smooth_sch15) nodraw
running sch16 _t if _d == 1, gen(smooth_sch16) nodraw
gen smooth_esca1 = exp(smooth_sch1 )
gen smooth_esca2 = exp(smooth_sch2 )
gen smooth_esca3 = exp(smooth_sch3 )
gen smooth_esca4 = exp(smooth_sch4 )
gen smooth_esca5 = exp(smooth_sch5 )
gen smooth_esca6 = exp(smooth_sch6 )
gen smooth_esca7 = exp(smooth_sch7 )
gen smooth_esca8 = exp(smooth_sch8 )
gen smooth_esca9 = exp(smooth_sch9 )
gen smooth_esca10 = exp(smooth_sch10)
gen smooth_esca11 = exp(smooth_sch11)
gen smooth_esca12 = exp(smooth_sch12)
gen smooth_esca13 = exp(smooth_sch13)
gen smooth_esca14 = exp(smooth_sch14)
gen smooth_esca15 = exp(smooth_sch15)
gen smooth_esca16 = exp(smooth_sch16)

loc model M2a_HR
loc var Species
tw line smooth_esca1 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca3 _t, sort lwidth(0.5) lc("117 112 179") || ///
line smooth_esca4 _t, sort lwidth(0.5) lc("231 41 138") || ///
line smooth_esca2 _t, sort lwidth(0.5) lc("217 95 2") ///
name(`var'_PHtest, replace) ///
legend(order(1 "{it: P.falciparum}" (ref.)" 4 "{it: P.vivax}" (p < 0.0001)" 2 "{it: P.
malariae}" (p = 0.458)" 3 "mixed (p = 0.044)") pos(3) col(1) textwidth(20) forcesize)
///
xtitle("time (days following presentation)", margin(medsmall))
ytitle("exponentiated scaled Schoenfeld residuals", margin(medsmall)) subtitle("`var'")
xmtick(2(1)15) graphr(color(white) lc(white)) plotr(color(white)
lc(white)) ylab(, angle(h) labsize(medsmall) nogrid format(%9.1f)) xlab(2 "1" 8
"7" 15 "14", labsize(medsmall)) ysca(log) xsize(20) ysize(12) xsca(nofextend)
ylab(1, add)

* graph export "C:\data\malaria\figures\PH test/\`var'PHtest_`model'.png",
as(png) replace width(800) height(600)

```

*Age (AGR4_4b)

```

loc var Age group
loc vars AGR4
tw line smooth_esca6 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca7 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_esca8 _t, sort lwidth(0.5) lc("117 112 179") || ///
line smooth_esca5 _t, sort lwidth(0.5) lc("231 41 138") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "0 to < 1 year (p = 0.131)" 2 "1 to < 5 years (p = 0.010)" 3 "5 to <15
(p = 0.0008 )" 4 "15+ (ref.)") pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log) xsize(20)

```

```
ysize(12) xsca(nofextend) ylab(1, add)
```

```
* graph export "C:\data\malaria\figures\PH test\/`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)
```

*Ethnic

```
loc var Ethnic group
loc vars EthnicX
tw line smooth_escala9 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_escala10 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_escala11 _t, sort lwidth(0.5) lc("117 112 179") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "Highland (ref.)" 2 "Lowland (p = 0.272)" 3 "non-Papuan (p < 0.0001)")
pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white) lc(white))
plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid format(%9
.1f)) xlab(2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log) xsize(20) ysize(12)
xsca(nofextend) ylab(1, add)
```

```
* graph export "C:\data\malaria\figures\PH test\/`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)
```

*Sex and Pregnancy

```
loc var Sex and pregnancy status
loc vars sexPreg
tw line smooth_escala12 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_escala13 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_escala14 _t, sort lwidth(0.5) lc("117 112 179") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "Female (not pregnant; ref.)" 2 "Female (pregnant; p = 0.013)" 3
"Male (p = 0.001)") pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log) xsize(20)
ysize(12) xsca(nofextend) ylab(1, add)
```

```
* graph export "C:\data\malaria\figures\PH test\/`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)
```

*Oral treatment

```
loc var Oral treatment
loc vars oralDHP
tw line smooth_escala15 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_escala16 _t, sort lwidth(0.5) lc("217 95 2") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "oral quinine (ref.)" 2 "DHP (p = 0.378)") pos(3) col(1)
textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white) lc(white))
plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid format(%9
.1f)) xlab(2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log) xsize(20) ysize(12)
xsca(nofextend) ylab(1, add)
```

```
* graph export "C:\data\malaria\figures\PH test\/`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)
```

```
loc model M2a_HR
graph combine Species_PHtest AGR4_PHtest sexPreg_PHtest EthnicX_PHtest
oralDHP_PHtest, col(1) graphr(color(white) lc(white)) plotr(color(white)) xcommon
```

```

ysize(20) xsize(12) name(PH_`model',replace) note("Global PH test:  $\chi^2$  133.04, df
= 11, p < 0.0001", size(tiny)) iscale(0.4)
loc model M2a_HR
graph export "C:\data\malaria\figures\PH test\PH_`model'.emf", as(emf) replace

```

*Illustrative PH test with 95% CI - following Royston Parmar in Flexible Parametric Survival Analysis (chapter 7 "Cox with model time-dependent effects")

***Vivax

```

use "C:\data\malaria\results\efron 8 Oct 2015 16_30_08\M2a_HR.dta", clear
loc model M2a_HR
loc v sch2
loc outc Adm
loc v_name vivax
* running `v' _t if _d==1, gen(`v'_smooth) gense(`v'_smooth_se)
nodraw /* generate smoothed Schoenfeld residual and associated
SE */
* gen `v'_smooth_e =
exp(`v'_smooth) /* gen
exponentiated smoothed Schoenfeld residual */
* gen `v'_smooth_e_lci = exp(`v'_smooth -
1.96*`v'_smooth_se) /* lower 95% CI for exp. smth. Sch.
residuals */
* gen `v'_smooth_e_uci = exp(`v'_smooth +
1.96*`v'_smooth_se) /* upper 95% CI for exp. smth.
Sch. residuals */
tw rarea `v'_smooth_e_lci `v'_smooth_e_uci _t, pstyle(ci) sort fc("253
205 172") lc("253 205 172") || /// /*Plot exp smth Sch residual
CI area */
line `v'_smooth_e _t, sort clpattern(solid) lc("217 95 2")
|| /// /* plot exp smth Sch residual estimate */
function y = 1, lpattern(solid) range(2 15) lc("27 158 119")
|| /// /*plot null / baseline value of 1 */
function y = 0.92, lpattern(shortdash) range(2 15) lc(black)
/// /* plot estimated HR for variable */
name(M2_PH_Adm_vivax, replace)
/// /* graph
options */
legend(order(2 "smoothed residuals (95 %CI)" 3 "{it:P.falciparum}"
(reference) "
4 "estimated HR 0.92 (95% CI 0.85, 1.00)") colfirst notextfirst
nostack cols(1) size(small) ///
nobox region(fcolor(white) margin(zero) lcolor(white)) position(12)
ring(1)) ///
yttitle("Exponentiated scaled Schoenfeld residuals", margin(medsmall))
///
title("Species: {it:P.vivax} relative to {it:P.falciparum}",
///
size(medsmall) ) ///
xttitle("Time (days) since presentation with malaria")
///
ylabel(, nogrid angle(h) labsize(small))
///
xlab(2 "1" 8 "7" 15 "14") xmtick(1(1)15) xscale(nofextend)
yscale(log) ///
graphhr(color(white) lc(white)) plotr(color(white) lc(white))

```

```

graph export "C:\data\malaria\figures\PH test\focusPH_`model'_pv.emf",
as(emf) replace

**OralDHP
loc model M2a_HR
loc v sch16
loc outc Adm
loc v_name DHP
* running `v' _t if _d==1, gen(`v'_smooth) gense(`v'_smooth_se)
nodraw          /* generate smoothed Schoenfeld residual and associated
SE */
* gen `v'_smooth_e =
exp(`v'_smooth)                                /* gen
exponentiated smoothed Schoenfeld residual */
* gen `v'_smooth_e_lci = exp(`v'_smooth -
1.96*`v'_smooth_se)                          /* lower 95% CI for exp. smth. Sch.
residuals */
* gen `v'_smooth_e_uci = exp(`v'_smooth +
1.96*`v'_smooth_se)                          /* upper 95% CI for exp. smth.
Sch. residuals */
tw rarea `v'_smooth_e_lci `v'_smooth_e_uci _t, pstyle(ci) sort fc("253
205 172")    lc("253 205 172")    ||    ///    /*Plot exp smth Sch residual
CI area */
line `v'_smooth_e _t, sort clpattern(solid) lc("217 95 2")    ||
///    /* plot exp smth Sch residual estimate */
function y = 1, lpattern(solid) range(2 15) lc("27 158 119")    ||
///    /*plot null / baseline value of 1 */
function y = 0.60, lpattern(shortdash) range(2 15) lc(black)
///    /* plot estimated HR for
variable */
name(M2_PH_Adm_DHP, replace)
///    /* graph
options */
legend(order(2 "smoothed residuals (95 %CI)" 3 "oral quinine(reference)"
///
4 "estimated HR 0.60 (95% CI 0.55, 0.66)") colfirst notextfirst
nostack cols(1) size(small)    ///
nobox region(fcolor(white) margin(zero) lcolor(white)) position(12)
ring(1))    ///
yttitle("Exponentiated scaled Schoenfeld residuals", margin(medsmall))
///
title("Oral treatment, DHP relative to quinine",    ///
size(medsmall) )    ///
xttitle("Time (days) since presentation with malaria")
///
ylabel(, nogrid angle(h) labsize(small))
///
xlab(2 "1" 8 "7" 15 "14") xmtick(1(1)15) xscale(nofextend)
yscale(log)    ///
graphhr(color(white) lc(white)) plotr(color(white) lc(white))

graph export "C:\data\malaria\figures\PH test\focusPH_`model'_DHP.emf",
as(emf) replace
graph combine M2_PH_Adm_vivax M2_PH_Adm_DHP, col(1) graphr(color(white)
lc(white)) plotr(color(white)) ysize(20) xsize(12)
name(PH_M2combo_PvDHP,replace) xcommon
loc model M2a_HR

```

```
graph export "C:\data\malaria\figures\PH test/'model'_combo_PvDHP.emf",
as(emf) replace
```

*M3BHR

*** risk of death by day 15 in those who were not initially admitted, including oral / dhp first treatment

*** Variables are Species (omitting Ovale), Age group (4 categories), Ethnic group (omitting non-Papuans), combined sex and pregnancy status, and oral treatment

```
stset DiedFU15, fail(DiedNext14) id(obsno)
```

```
use "C:\data\malaria\results\efron 8 Oct 2015 21_14_52\M3b_HR.dta", clear
```

```
/* STORED MODEL WITH GENERATED SCALED SCHOENFELD RESIDUALS
```

```
loc model M3b_HR
```

```
stcox i.SpeciesX i.AGR4_4b i.EthnicX i.sexPreg i.oral_v_dhp if ip==0 , allbaselevels
vsquish cluster(hrn) efron cformat(%6.2f) nolog
```

```
predict `i'*, scaledsch
*/
```

```
loc model M3b_HR
```

```
running sch_`model'1 _t if _d == 1, gen(smooth_sch1 ) nodraw
running sch_`model'2 _t if _d == 1, gen(smooth_sch2 ) nodraw
running sch_`model'3 _t if _d == 1, gen(smooth_sch3 ) nodraw
running sch_`model'4 _t if _d == 1, gen(smooth_sch4 ) nodraw
running sch_`model'5 _t if _d == 1, gen(smooth_sch5 ) nodraw
running sch_`model'6 _t if _d == 1, gen(smooth_sch6 ) nodraw
running sch_`model'7 _t if _d == 1, gen(smooth_sch7 ) nodraw
running sch_`model'8 _t if _d == 1, gen(smooth_sch8 ) nodraw
running sch_`model'9 _t if _d == 1, gen(smooth_sch9 ) nodraw
running sch_`model'10 _t if _d == 1, gen(smooth_sch10) nodraw
running sch_`model'11 _t if _d == 1, gen(smooth_sch11) nodraw
running sch_`model'12 _t if _d == 1, gen(smooth_sch12) nodraw
running sch_`model'13 _t if _d == 1, gen(smooth_sch13) nodraw
running sch_`model'14 _t if _d == 1, gen(smooth_sch14) nodraw
running sch_`model'15 _t if _d == 1, gen(smooth_sch15) nodraw
running sch_`model'16 _t if _d == 1, gen(smooth_sch16) nodraw
gen smooth_esca1 = exp(smooth_sch1 )
gen smooth_esca2 = exp(smooth_sch2 )
gen smooth_esca3 = exp(smooth_sch3 )
gen smooth_esca4 = exp(smooth_sch4 )
gen smooth_esca5 = exp(smooth_sch5 )
gen smooth_esca6 = exp(smooth_sch6 )
gen smooth_esca7 = exp(smooth_sch7 )
gen smooth_esca8 = exp(smooth_sch8 )
gen smooth_esca9 = exp(smooth_sch9 )
gen smooth_esca10 = exp(smooth_sch10)
gen smooth_esca11 = exp(smooth_sch11)
gen smooth_esca12 = exp(smooth_sch12)
gen smooth_esca13 = exp(smooth_sch13)
gen smooth_esca14 = exp(smooth_sch14)
gen smooth_esca15 = exp(smooth_sch15)
gen smooth_esca16 = exp(smooth_sch16)
```

```
loc model M3b_HR
```

***Combinable Graphs

***Species (SpeciesX)**

```

loc var Species
tw line smooth_esca1 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca2 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_esca3 _t, sort lwidth(0.5) lc("117 112 179") || ///
line smooth_esca4 _t, sort lwidth(0.5) lc("231 41 138") ///
name(`var'_PHtest, replace) ///
legend(order(1 "{it: P.falciparum}" (ref.)" 2 "{it: P.vivax}" (p = 0.303)" 3 "{it: P.
malariae}" (p = 0.424)" 4 "mixed" (p = 0.021)")) pos(3) col(1) textwidth(20)
forcesize) ///
xtitle("time (days following presentation)", margin(medsmall))
ytitle("exponentiated scaled Schoenfeld residuals", margin(medsmall)) subtitle("`var'")
xmtick(2(1)15) graphr(color(white) lc(white)) plotr(color(white)
lc(white)) ylab(, angle(h) labsize(medsmall) nogrid format(%9.1f)) xlab(1 "0" 2
"1" 8 "7" 15 "14", labsize(medsmall)) ysca(log) xsize(20) ysize(12)
xsca(nofextend) ylab(1, add)

* graph export "C:\data\malaria\figures\PH test/\`var'PHtest_`model'.png",
as(png) replace width(800) height(600)

```

***Age (AGR4_4b)**

```

loc var Age group
loc vars AGR4
tw line smooth_esca6 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca7 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_esca8 _t, sort lwidth(0.5) lc("117 112 179") || ///
line smooth_esca5 _t, sort lwidth(0.5) lc("231 41 138") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "0 to < 1 year" (p = 0.426)" 2 "1 to < 5 years" (p = 0.026)" 3 "5 to
<15" (p = 0.452)" 4 "15+ (ref.)")) pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

* graph export "C:\data\malaria\figures\PH test/\`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)

```

***Ethnic**

```

loc var Ethnic group
loc vars EthnicX
tw line smooth_esca9 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca10 _t, sort lwidth(0.5) lc("217 95 2") ///
non-Papuans excluded: line smooth_esca11 _t, sort lwidth(0.5) lc("117 112
179")
name(`vars'_PHtest, replace) ///
legend(order(1 "Highland (ref.)" 2 "Lowland" (p = 0.345)" 3 "non-Papuan (no
deaths)")) pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

* graph export "C:\data\malaria\figures\PH test/\`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)

```

***Sex and Pregnancy**


```

loc var Sex and pregnancy status
loc vars sexPreg
tw line smooth_escal2 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_escal3 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_escal4 _t, sort lwidth(0.5) lc("117 112 179") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "Female (not pregnant; ref.)" 2 "Female (pregnant; p = 0.446)" 3
"Male (p = 0.615)") pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

```

*** graph export "C:\data\malaria\figures\PH test\'vars'PHtest_'model'.png",
as(png) replace width(800) height(600)**

***Oral treatment**

```

loc var Oral treatment
loc vars oralDHP
tw line smooth_escal5 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_escal6 _t, sort lwidth(0.5) lc("217 95 2") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "oral quinine (ref.)" 2 "DHP (p = 0.145)") pos(3) col(1)
textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

```

*** graph export "C:\data\malaria\figures\PH test\'vars'PHtest_'model'.png",
as(png) replace width(800) height(600)**

```

loc model M3b_HR
graph combine Species_PHtest AGR4_PHtest sexPreg_PHtest EthnicX_PHtest
oralDHP_PHtest, col(1) graphr(color(white) lc(white)) plotr(color(white)) xcommon
ysize(20) xsize(12) name(PH_`model',replace) note("Global PH test: {&chi} 20.20, df =
10, p < 0.0274", size(tiny)) iscale(0.4)
loc model M3b_HR
graph export "C:\data\malaria\figures\PH test\PH_`model'.emf", as(emf) replace

```

***Illustrative PH test with 95% CI - following Royston Parmar in Flexible Parametric Survival Analysis (chapter 7 "Cox with model time-dependent effects")**

*****Vivax**

```

use "C:\data\malaria\results\efron 8 Oct 2015 21_14_52\M3b_HR.dta", clear
loc model M3b_HR
loc v sch_`model'2
loc outc Died
loc v_name vivax
running `v' _t if _d==1, gen(`v'_smooth) gense(`v'_smooth_se) nodraw
/* generate smoothed Schoenfeld residual and associated SE */
gen `v'_smooth_e = exp(`v'_smooth)
/* gen exponentiated
smoothed Schoenfeld residual */
gen `v'_smooth_e_lci = exp(`v'_smooth - 1.96

```



```

*`v'_smooth_se)                                /* lower 95% CI for exp. smth. Sch.
residuals */
gen `v'_smooth_e_uci = exp(`v'_smooth + 1.96
*`v'_smooth_se)                                /* upper 95% CI for exp. smth. Sch.
residuals */
tw rarea `v'_smooth_e_lci `v'_smooth_e_uci _t, pstyle(ci) sort fc("253
205 172")    lc("253 205 172")    ||    ///    /*Plot exp smth Sch residual
CI area */
line `v'_smooth_e _t, sort clpattern(solid) lc("217 95 2")
||    ///    /* plot exp smth Sch residual estimate */
function y = 1, lpattern(solid) range(_t) lc("27 158 119")
||    ///    /*plot null / baseline value of 1 */
function y = 1.46, lpattern(shortdash) range(_t) lc(black)
///    /* plot estimated HR for variable */
name(M3_PH_Died_vivax, replace)
///    /* graph

options */
legend(order(2 "smoothed residuals (95 %CI)" 3 "{it:P.falciparum}"
(reference)"
4 "estimated HR 1.46 (95% CI 0.85, 2.51)") colfirst notextfirst
nostack cols(1) size(small)    ///
nobox region(fcolor(white) margin(zero) lcolor(white)) position(12)
ring(1))    ///
yttitle("Exponentiated scaled Schoenfeld residuals", margin(medsmall))
///
title("Species: {it:P.vivax} relative to {it:P.falciparum}",
///
size(medsmall) )    ///
xttitle("Time (days) since presentation with malaria")
///
ylabel(10(10)36.6 0.2 "0.2" 0.5 "0.5" 1 2 3 5, add nogrid angle(h)
labsize(small))    ///
xlab(1 "0" 2 "1" 8 "7" 15 "14") xmtick(1(1)15) xscale(nofextend)
yscale(log)    ///
graphr(color(white) lc(white)) plotr(color(white) lc(white))

graph export "C:\data\malaria\figures\PH test\focusPH_`model'_pv.emf",
as(emf) replace

**OralDHP
loc model M3b_HR
loc v sch_`model'16
loc outc Died
loc v_name DHP
running `v' _t if _d==1, gen(`v'_smooth) gense(`v'_smooth_se) nodraw
/* generate smoothed Schoenfeld residual and associated SE */
gen `v'_smooth_e = exp(`v'_smooth)
/* gen exponentiated

smoothed Schoenfeld residual */
gen `v'_smooth_e_lci = exp(`v'_smooth - 1.96
*`v'_smooth_se)                                /* lower 95% CI for exp. smth. Sch.
residuals */
gen `v'_smooth_e_uci = exp(`v'_smooth + 1.96
*`v'_smooth_se)                                /* upper 95% CI for exp. smth. Sch.
residuals */
tw rarea `v'_smooth_e_lci `v'_smooth_e_uci _t, pstyle(ci) sort fc("253
205 172")    lc("253 205 172")    ||    ///    /*Plot exp smth Sch residual

```

```

CI area */
line `v'_smooth_e _t, sort clpattern(solid) lc("217 95 2")      ||
///      /* plot exp smth Sch residual estimate */
function y = 1, lpattern(solid) range(_t) lc("27 158 119")      ||
///      /*plot null / baseline value of 1 */
function y = 0.97, lpattern(shortdash) range(_t) lc(black)
///      /* plot estimated HR for

variable */
name(M3_PH_Died_DHP, replace)

options */
legend(order(2 "smoothed residuals (95 %CI)" 3 "oral quinine (reference)"
///
4 "estimated HR 0.97 (95% CI 0.50, 1.86)") colfirst notextfirst
nostack cols(1) size(small) ///
nobox region(fcolor(white) margin(zero) lcolor(white)) position(12)
ring(1)) ///
yttitle("Exponentiated scaled Schoenfeld residuals", margin(medsmall))
///
title("Oral treatment: DHP relative to quinine", ///
size(medsmall) ) ///
xtitle("Time (days) since presentation with malaria")
///
ylabel(10(10)24.7 0.003 "0.003" 0.1 "0.1" 0.5 "0.5" 1 2 3 5, add nogrid
angle(h) labsize(small)) ///
xlab(1 "0" 2 "1" 8 "7" 15 "14") xmtick(1(1)15) xscale(nofextend)
yscale(log) ///
graphr(color(white) lc(white)) plotr(color(white) lc(white))

graph export "C:\data\malaria\figures\PH test\focusPH_`model'_DHP.emf",
as(emf) replace
graph combine M3_PH_Died_vivax M3_PH_Died_DHP, col(1) graphr(color(white)
lc(white)) plotr(color(white)) ysize(20) xsize(12)
name(PH_M3combo_PvDHP,replace) xcommon
loc model M3b_HR
graph export "C:\data\malaria\figures\PH test/`model'_combo_PvDHP.emf",
as(emf) replace

```

*M4AHR:

***risk of death by day 15 limited to those who were admitted immediately & rx'd IV treatment first

*** Variables are Species (omitting Ovale), Age group (4 categories), Ethnic group, combined sex and pregnancy status, and IV treatment

```
use "C:\data\malaria\results\efron 8 Oct 2015 21_14_52\M4a_HR.dta", clear
```

```
/* STORED MODEL WITH GENERATED SCALED SCHOENFELD RESIDUALS
```

```
loc model M4a_HR
```

```
stcox i.SpeciesX i.AGR4_4b i.EthnicX i.sexPreg i.ivArt if ip==1 , allbaselevels vsquish
```

```
cluster(hrn) efron cformat(%6.2f) nolog
```

```
predict `i'*, scaledsch
```

```
*/
```

```
loc model M4a_HR
```

```
running sch_`model'1 _t if _d == 1, gen(smooth_sch1 ) nodraw
```

```
running sch_`model'2 _t if _d == 1, gen(smooth_sch2 ) nodraw
```

```
running sch_`model'3 _t if _d == 1, gen(smooth_sch3 ) nodraw
```

```

running sch_`model'4 _t if _d == 1, gen(smooth_sch4 ) nodraw
running sch_`model'5 _t if _d == 1, gen(smooth_sch5 ) nodraw
running sch_`model'6 _t if _d == 1, gen(smooth_sch6 ) nodraw
running sch_`model'7 _t if _d == 1, gen(smooth_sch7 ) nodraw
running sch_`model'8 _t if _d == 1, gen(smooth_sch8 ) nodraw
running sch_`model'9 _t if _d == 1, gen(smooth_sch9 ) nodraw
running sch_`model'10 _t if _d == 1, gen(smooth_sch10) nodraw
running sch_`model'11 _t if _d == 1, gen(smooth_sch11) nodraw
running sch_`model'12 _t if _d == 1, gen(smooth_sch12) nodraw
running sch_`model'13 _t if _d == 1, gen(smooth_sch13) nodraw
running sch_`model'14 _t if _d == 1, gen(smooth_sch14) nodraw
running sch_`model'15 _t if _d == 1, gen(smooth_sch15) nodraw
running sch_`model'16 _t if _d == 1, gen(smooth_sch16) nodraw
gen smooth_esca1 = exp(smooth_sch1 )
gen smooth_esca2 = exp(smooth_sch2 )
gen smooth_esca3 = exp(smooth_sch3 )
gen smooth_esca4 = exp(smooth_sch4 )
gen smooth_esca5 = exp(smooth_sch5 )
gen smooth_esca6 = exp(smooth_sch6 )
gen smooth_esca7 = exp(smooth_sch7 )
gen smooth_esca8 = exp(smooth_sch8 )
gen smooth_esca9 = exp(smooth_sch9 )
gen smooth_esca10 = exp(smooth_sch10)
gen smooth_esca11 = exp(smooth_sch11)
gen smooth_esca12 = exp(smooth_sch12)
gen smooth_esca13 = exp(smooth_sch13)
gen smooth_esca14 = exp(smooth_sch14)
gen smooth_esca15 = exp(smooth_sch15)
gen smooth_esca16 = exp(smooth_sch16)

```

```
loc model M4a_HR
```

***Combinable Graphs

*Species (SpeciesX)

```

loc var Species
tw line smooth_esca1 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca2 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_esca3 _t, sort lwidth(0.5) lc("117 112 179") || ///
line smooth_esca4 _t, sort lwidth(0.5) lc("231 41 138") ///
name(`var'_PHtest, replace) ///
legend(order(1 "{it: P.falciparum}" (ref.)" 2 "{it: P.vivax}" (p = 0.792)" 3 "{it: P.
malariae}" (p = 0.170)" 4 "mixed (p = 0.395)") pos(3) col(1) textwidth(20) forcesize)
///
xtitle("time (days following presentation)", margin(medsmall))
ytitle("exponentiated scaled Schoenfeld residuals", margin(medsmall)) subtitle("`var'")
xmtick(2(1)15) graphr(color(white) lc(white)) plotr(color(white)
lc(white)) ylab(, angle(h) labsize(medsmall) nogrid format(%9.1f)) xlab(2 "1" 8
"7" 15 "14", labsize(medsmall)) ysca(log) xsize(20) ysize(12) xsca(nofextend)
ylab(1, add)

```

```

* graph export "C:\data\malaria\figures\PH test/\`var'_PHtest_`model'.png",
as(png) replace width(800) height(600)

```

*Age (AGR4_4b)

```

loc var Age group
loc vars AGR4

```

```

tw line smooth_esca6 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca7 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_esca8 _t, sort lwidth(0.5) lc("117 112 179") || ///
line smooth_esca5 _t, sort lwidth(0.5) lc("231 41 138") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "0 to < 1 year (p = 0.080)" 2 "1 to < 5 years (p = 0.129)" 3 "5 to <
15 (p = 0.0005)" 4 "15+ (ref.)") pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

```

*** graph export "C:\data\malaria\figures\PH test/\`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)**

***Ethnic**

```

loc var Ethnic group
loc vars EthnicX
tw line smooth_esca9 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca10 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_esca11 _t, sort lwidth(0.5) lc("117 112 179") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "Highland (ref.)" 2 "Lowland (p = 0.517)" 3 "non-Papuan (p = 0.
115)") pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

```

*** graph export "C:\data\malaria\figures\PH test/\`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)**

***Sex and Pregnancy**

```

loc var Sex and pregnancy status
loc vars sexPreg
tw line smooth_esca12 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca13 _t, sort lwidth(0.5) lc("217 95 2") || ///
line smooth_esca14 _t, sort lwidth(0.5) lc("117 112 179") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "Female (not pregnant; ref.)" 2 "Female (pregnant, p = 0.629)" 3
"Male (p = 0.106)") pos(3) col(1) textwidth(20) forcesize) ///
xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

```

*** graph export "C:\data\malaria\figures\PH test/\`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)**

***Oral treatment**

```

loc var IV treatment
loc vars ivArt
tw line smooth_esca15 _t, sort lwidth(0.5) lc("27 158 119") || ///
line smooth_esca16 _t, sort lwidth(0.5) lc("217 95 2") ///
name(`vars'_PHtest, replace) ///
legend(order(1 "IV quinine (ref.)" 2 "IV artesunate (p = 0.965)") pos(3) col(1)
textwidth(20) forcesize) ///

```

```

xtitle("time (days following presentation)", margin(medsmall)) ytitle(" ",
margin(medsmall)) subtitle("`var'") xmtick(2(1)15) graphr(color(white)
lc(white)) plotr(color(white) lc(white)) ylab(, angle(h) labsize(medsmall) nogrid
format(%9.1f)) xlab(1 "0" 2 "1" 8 "7" 15 "14", labsize(medsmall)) ysca(log)
xsize(20) ysize(12) xsca(nofextend) ylab(1, add)

```

```

* graph export "C:\data\malaria\figures\PH test\/`vars'PHtest_`model'.png",
as(png) replace width(800) height(600)

```

```
loc model M4a_HR
```

```

graph combine Species_PHtest AGR4_PHtest sexPreg_PHtest EthnicX_PHtest ivArt_PHtest,
col(1) graphr(color(white) lc(white)) plotr(color(white)) xcommon ysize(20) xsize(12)
name(PH_`model',replace) note("Global PH test:  $\chi^2$  24.48, df = 11, p < 0.0108",
size(tiny)) iscale(0.4)

```

```
loc model M4a_HR
```

```
graph export "C:\data\malaria\figures\PH test\PH_`model'.emf", as(emf) replace
```

* Illustrative PH test with 95% CI - following Royston Parmar in Flexible Parametric Survival Analysis (chapter 7 "Cox with model time-dependent effects")

*** Vivax

```
use "C:\data\malaria\results\efron 8 Oct 2015 21_14_52\M4a_HR.dta", clear
```

```
loc model M4a_HR
```

```
loc v sch_`model'2
```

```
loc outc Adm
```

```
loc v_name vivax
```

```
running `v' _t if _d==1, gen(`v'_smooth) gense(`v'_smooth_se) nodraw /* gen smoothed
```

```
Schoenfeld residual and associated SE */
```

```
gen `v'_smooth_e = exp(`v'_smooth) /* gen exponentiated
```

```
smoothed Schoenfeld residual */
```

```
gen `v'_smooth_e_lci = exp(`v'_smooth - 1.96*`v'_smooth_se) /* lower 95% CI for exp.
```

```
smth. Sch. residuals */
```

```
gen `v'_smooth_e_uci = exp(`v'_smooth + 1.96*`v'_smooth_se) /* upper 95% CI for exp.
```

```
smth. Sch. residuals */
```

```
tw rarea `v'_smooth_e_lci `v'_smooth_e_uci _t, pstyle(ci) sort fc("253 205 172")
```

```
lc("253 205 172") || /// /*Plot exp smth Sch residual CI area */
```

```
line `v'_smooth_e _t, sort clpattern(solid) lc("217 95 2") || /// /*
```

```
plot exp smth Sch residual estimate */
```

```
function y = 1, lpattern(solid) range(_t) lc("27 158 119") || ///
```

```
/*plot null / baseline value of 1 */
```

```
function y = 1.26, lpattern(shortdash) range(_t) lc(black) /// /* plot
```

```
estimated HR for variable */
```

```
name(M4_PH_Died_vivax, replace) ///
```

```
/* graph options */
```

```
legend(order(2 "smoothed residuals (95 %CI)" 3 "{it: P.falciparum} (reference)"
```

```
///
```

```
4 "estimated HR 1.26 (95% CI 0.97, 1.64)") colfirst notextfirst nostack cols(1)
```

```
size(small) ///
```

```
nobox region(fcolor(white) margin(zero) lcolor(white)) position(12) ring(1))
```

```
///
```

```
ytitle("Exponentiated scaled Schoenfeld residuals", margin(medsmall)) ///
```

```
title("Species: {it:P.vivax} relative to {it:P.falciparum}", ///
```

```
size(medsmall) ) ///
```

```
xtitle("Time (days) since presentation with malaria") ///
```

```
ylabel(2(2)6 0.4 "0.4" 1, nogrid angle(h) labsize(small))
```

```
///
```

```
xlab(1 "0" 2 "1" 8 "7" 15 "14") xmtick(1(1)15) xscale(nofextend) yscale(log)
```

```
///
```

```
graphr(color(white) lc(white)) plotr(color(white) lc(white))
```

```

graph export "C:\data\malaria\figures\PH test\focusPH_`model'_pv.emf", as(emf) replace

**ivArt
loc model M4a_HR
loc v sch_`model'16
loc outc Died
loc v_name ivArt
running `v' _t if _d==1, gen(`v'_smooth) gense(`v'_smooth_se) nodraw /* gen smoothed
Schoenfeld residual and associated SE */
gen `v'_smooth_e = exp(`v'_smooth) /* gen exponentiated
smoothed Schoenfeld residual */
gen `v'_smooth_e_lci = exp(`v'_smooth - 1.96*`v'_smooth_se) /* lower 95% CI
for exp. smth. Sch. residuals */
gen `v'_smooth_e_uci = exp(`v'_smooth + 1.96*`v'_smooth_se) /* upper 95% CI
for exp. smth. Sch. residuals */
tw rarea `v'_smooth_e_lci `v'_smooth_e_uci _t, pstyle(ci) sort ///
fc("253 205 172") lc("253 205 172") || /// /*Plot exp
smth Sch residual CI area */
line `v'_smooth_e _t, sort clpattern(solid) lc("217 95 2") || /// /* plot exp
smth Sch residual estimate */
function y = 1, lpattern(solid) range(_t) lc("27 158 119") || /// /*plot null /
baseline value of 1 */
function y = 2.64, lpattern(shortdash) range(_t) lc(black) /// /* plot
estimated HR for variable */
name(M4_PH_Died_ivArt, replace) /// /* graph
options */
legend(order(2 "smoothed residuals (95 %CI)" 3 "IV quinine (reference)"
///
4 "estimated HR 2.64 (95% CI 1.83, 3.82)") colfirst notextfirst nostack cols(1)
///
size(small) nobox region(fcolor(white) margin(zero) lcolor(white)) position(12)
ring(1)) ///
ytitle("Exponentiated scaled Schoenfeld residuals", margin(medsmall))
///
title("Intravenous treatment: artesunate relative to quinine",
///
size(medsmall) )
///
xtitle("Time (days) since presentation with malaria")
///
ylabel(2(2)10 0.5 "0.5" 1 15, nogrid angle(h) labsize(small))
///
xlab(1 "0" 2 "1" 8 "7" 15 "14") xmtick(1(1)15) xscale(nofextend) yscale(log)
///
graphr(color(white) lc(white)) plotr(color(white) lc(white))

graph export "C:\data\malaria\figures\PH test\focusPH_`model'_ivArt.emf", as(emf) replace

graph combine M4_PH_Died_vivax M4_PH_Died_ivArt, col(1) graphr(color(white) lc(white))
///
plotr(color(white)) ysize(20) xsize(12) name(PH_M4combo_PvArt,replace) xcommon
loc model M4a_HR
graph export "C:\data\malaria\figures\PH test/`model'_combo_PvArt.emf", as(emf) replace

```

```

/*****

```

```
*
*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
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             ///
             _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, 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 "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) 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
*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(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 + 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) xszsize(10) ysize(10)
```

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

```
/******
*
*Incorporation of time-varying coefficients into models 2, 3 and 4
*
*****/
```

***Set up log and working directory**

```
capture log close
version 13.1
set linesize 100
set more off
```

```
cd "C:\data\malaria\results"
loc today = c(current_date)
log using "malariaproject_log_`today'.txt", append text
```

***cox model ties handling**

```
loc ties efron
```

*** prepare folder for results**

```
local T = c(current_time)
local T = substr("`T'",":","_",.)
mkdir "`ties' `today' `T'"
cd "`ties' `today' `T'"
```

*****note '3' and '7' refer to days following presentation (ie. _t = 4 and _t = 8, respectively)**

***Model 2**

```
/*load data*/
```

```
use "C:\data\malaria\MalEps_v1.9.3_r5oct2015.dta", clear
```

```
/*create indicator variables*/
```

```
xi i.SpeciesX i.EthnicX i.AGR4_4b i.sexPreg i.oral_v_dhp
```

```
stset AdmFU15, fail(AdmNext14) id(obsno)
```

```
/*split time*/
```

```
stsplitt new, at(4 8) /* Splitting time (see note aboe about t4 and t8 above) */
```

```
loc varlist _ISpeciesX_2 /// /*List of variables to split */
             _ISpeciesX_4 ///
```

```

_ISpeciesX_5      ///
_IEthnicX_2       ///
_IEthnicX_3       ///
_IAGR4_4b_1       ///
_IAGR4_4b_2       ///
_IAGR4_4b_3       ///
_IsexPreg_2       ///
_IsexPreg_3       ///
_Ioral_v_dh_1

```

```
/*generate interaction term*/
```

```

foreach i of varlist `varlist' {
gen tv3`i' = `i' * (new==4)
gen tv7`i' = `i' * (new==8)
}

```

```
/*List of variables for model including interactions with time */
```

```

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

```

```
stcox `varlist' if ip==0, efron allbaselevels vsquish cluster(hrn) cformat(%6.2f)
```

```
/*save and store estimates and scaled Schoenfeld residuals for later access*/
```

```
estimates
```

```
estimates store M2aTV37_24oct2015
```

```
estimates save M2aTV37_24oct2015
```

```
predict sch_M2aTV37*, sca
```

```
save MalEps_v1.9.3_M2a_TV37.dta
```

```
linktest, cluster(hrn) efron
```

```
estat phtest, d
```

```
lincom _b[_ISpeciesX_2]+_b[tv3_ISpeciesX_2]+_b[tv7_ISpeciesX_2], eform
```

```
lincom _b[_ISpeciesX_2]+_b[tv3_ISpeciesX_2], eform
```

```
*Model 3
```

```
set more off
```

```
*load data
```

```
use "C:\data\malaria\MalEps_v1.9.3_r5oct2015.dta", clear
```

```
/*create indicator variables*/
```

```
xi i.SpeciesX i.EthnicX i.AGR4_4b i.sexPreg i.oral_v_dhp
```

```
stset DiedFU15, fail(DiedNext14) id(obsno)
```

```
/*split time*/
```

```
stsplot new, at(4 8)
```

```

loc varlist _ISpeciesX_2      ///
             _ISpeciesX_4      ///
             _ISpeciesX_5      ///

```

```

_IEthnicX_2    ///
_IEthnicX_3    ///
_IAGR4_4b_1    ///
_IAGR4_4b_2    ///
_IAGR4_4b_3    ///
_IsexPreg_2    ///
_IsexPreg_3    ///
_Ioral_v_dh_1

```

```

foreach i of varlist `varlist' {
gen tv3`i' = `i' * (new==4)
gen tv7`i' = `i' * (new==8)
}

```

```
/*List of variables for model including interactions with time */
```

```

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

```

```
/*run model*/
```

```
stcox `varlist' if ip==0 , efron allbaselevels vsquish cluster(hrn) cformat(%6.2f) nolog
```

```
/*save and store estimates and scaled Schoenfeld residuals for later access*/
```

```
estimates
```

```
estimates store M3bTV37_24oct2015
```

```
estimates save M3bTV37_24oct2015
```

```
predict sch_M3bTV37*, sca
```

```
save MalEps_v1.9.3_M3b_TV37.dta
```

```
linktest, cluster(hrn) efron
```

```
estat phtest, d
```

```
*Model 4
```

```
/*load data*/
```

```
use "C:\data\malaria\MalEps_v1.9.3_r5oct2015.dta", clear
```

```
/*create indicator variables*/
```

```
xi i.SpeciesX i.EthnicX i.AGR4_4b i.sexPreg i.ivArt
```

```
/*declare survival time*/
```

```
stset DiedFU15, fail(DiedNext14) id(obsno)
```

```
/*split time*/
```

```
stsplot new, at(8)
```

```
/*list of variables to create potential splits for*/
```

```

loc varlist _ISpeciesX_2    ///
             _ISpeciesX_4    ///
             _ISpeciesX_5    ///
             _IEthnicX_2    ///
             _IEthnicX_3    ///

```

```

_IAGR4_4b_1    ///
_IAGR4_4b_2    ///
_IAGR4_4b_3    ///
_IsexPreg_2    ///
_IsexPreg_3    ///
_IivArt_1

```

```

foreach i of varlist `varlist' {
gen tv7`i' = `i' * (new==8)
}

```

```
/*list of variables including TVCs*/
```

```

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

```

```
*run Cox model with TVCs
```

```
stcox `varlist' if ip==1 , efron allbaselevels vsquish cluster(hrn) cformat(%6.2f) nolog
```

```
*store results for later access
```

```
estimates
```

```
estimates store M4aTV37_24oct2015
```

```
estimates save M4aTV37_24oct2015
```

```
predict sch_M4aTV37*, sca
```

```
save MalEps_v1.9.3_M4a_TV37.dta
```

```
linktest, cluster(hrn) efron
```

```
estat phtest, d
```

```
****Coefficient plots
```

```
*Model 2
```

```
cd "C:\data\malaria\results\efron 24 Oct 2015 10_47_59\"
```

```
use "C:\data\malaria\results\efron 24 Oct 2015 10_47_59\MalEps_v1.9.3_M2a_TV37.dta", clear
```

```
estimates use M2aTV37_24oct2015.ster
```

```
estimates esample: ///
```

```

_IISpeciesX_2    ///
tv3_IISpeciesX_2    ///
tv7_IISpeciesX_2    ///
_IISpeciesX_4    ///
_IISpeciesX_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

```

label variable _ISpeciesX_2 "{it:P.vivax}"
label variable _ISpeciesX_4 "{it:P.malariae}"
label variable _ISpeciesX_5 "mixed"
label variable _IEthnicX_2 "Lowland"
label variable _IEthnicX_3 "non-Papuan"
label variable _IAGR4_4b_1 "0 to {<} 1"
label variable _IAGR4_4b_2 "1 to {<} 5 "
label variable _IAGR4_4b_3 "5 to {<} 15"
label variable _IsexPreg_2 "female (pregnant)"
label variable _IsexPreg_3 "male"
label variable _Ioral_v_dh_1 "DHP"

```

```

label variable tv3_ISpeciesX_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_ISpeciesX_4 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_ISpeciesX_5 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IEthnicX_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IEthnicX_3 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IAGR4_4b_1 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IAGR4_4b_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IAGR4_4b_3 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IsexPreg_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IsexPreg_3 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_Ioral_v_dh_1 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"

```

```

label variable tv7_ISpeciesX_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_ISpeciesX_4 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_ISpeciesX_5 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IEthnicX_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IEthnicX_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IAGR4_4b_1 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IAGR4_4b_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IAGR4_4b_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IsexPreg_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IsexPreg_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_Ioral_v_dh_1 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"

```

```

coefplot      (M2a_24oct2015,      mc("241 163 64")  ciopts(lc("241 163 64")))
              ///

```



```

label(multivariable model 2) )
                                     ///
(M2aTV37_24oct2015, mc("153 142 195") ciopts(lc("153 142 195")))
                                     ///
label("model 2 with time interaction")
                                     ///
, eform baselevels xline(1, lc("27 158 119"))
                                     ///
order(  _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)
                                     ///
headings(_ISpeciesX_2 = "{it:P.falciparum}" (reference)"
                                     ///
      _IEthnicX_2 = "Highland (reference)"
                                     ///
      _IAGR4_4b_1 = " {&ge} 15 (reference)"
                                     ///
      _IsexPreg_2 = "female, pregnant (reference)"
                                     ///
      _Ioral_v_dh_1 = "oral quinine (reference)"
                                     ///
coeflabels(,labsize(small)) legend(cols(1))
                                     ///
graphr(color(white) lc(white) margin(2 2 0 0)) plotr(color(white) lc(white))
      ///
grid(within glwidth(thin)) ysize(20) xsize(15)
      ///
xtitle("Hazard Ratio", margin(medsmall)) xlab(,labsize(small))
      ///
xmlab(1 "reference",add tlc("27 158 119") labcolor("27 158 119"))
      ///
subtitle("Early admission in outpatients on oral treatment",
      ///
      size(medium) margin(-30 0 2 0))
      ///
note("Note: {it:t} refers to analysis time in days since presentation with a malaria
episode; " ///
" i.e. time is split at day 3 and/or day 7 following presentation, where
specified." ///
, margin(-37 0 0 2) size(vsmall) )

graph export "C:\data\malaria\figures\Model2_compare24oct2015.emf", as(emf) replace

```

****Graph piece-wise regression of model 2 incorporating split at days 3 and 7 following the day of presentation**

estimates

```

matrix M2tv = r(table)'
di "Day 0 to Day 3: HR" %9.2f M2tv[1,1] %9.2f M2tv[1,5] %9.2f M2tv[1,6]
di "Day 3 to Day 7: HR" %9.2f M2tv[2,1] %9.2f M2tv[2,5] %9.2f M2tv[2,6]
di "Day 7 to Day 14: HR" %9.2f M2tv[3,1] %9.2f M2tv[3,5] %9.2f M2tv[3,6]
local hr1 = M2tv[1,1]

```

```

local hr2 = M2tv[2,1]
local hr3 = M2tv[3,1]
local hr1_lci = M2tv[1,5]
local hr1_uci = M2tv[1,6]
local hr2_lci = M2tv[2,5]
local hr2_uci = M2tv[2,6]
local hr3_lci = M2tv[3,5]
local hr3_uci = M2tv[3,6]
di "Day 0 to Day 3: " %9.2f `hr1' %9.2f `hr1_lci' %9.2f `hr1_uci'
di "Day 3 to Day 7: " %9.2f `hr2' %9.2f `hr2_lci' %9.2f `hr2_uci'
di "Day 7 to Day 14:" %9.2f `hr3' %9.2f `hr3_lci' %9.2f `hr3_uci'
twoway      function y = `hr1', range(2 4) lwidth(thick) lpattern(solid) lc("217 95 2")
||      ///
      function y = `hr2', range(4 8) lwidth(thick) lpattern(solid) lc("217 95 2")
||      ///
      function y = `hr3', range(8 15) lwidth(thick) lpattern(solid) lc("217 95 2")
||      ///
      function y = `hr1_lci', range(2 4) lpattern(dash) lc("253 205 172")
||      ///
      function y = `hr2_lci', range(4 8) lpattern(dash) lc("253 205 172")
||      ///
      function y = `hr3_lci', range(8 15) lpattern(dash) lc("253 205 172")
||      ///
      function y = `hr1_uci', range(2 4) lpattern(dash) lc("253 205 172")
||      ///
      function y = `hr2_uci', range(4 8) lpattern(dash) lc("253 205 172")
||      ///
      function y = `hr3_uci', range(8 15) lpattern(dash) lc("253 205 172")
||      ///
      function y = 1, lwidth(thick) lpattern(solid) range(2 15) lc("27 158 119")
||      ///
      function y = 0.92, lpattern(solid) range(2 15) lc("247 247 247") lwidth(thick)
      ///
      legend(order(10 "{it:P.falciparum}" (reference)"
      ///
      11 "{it:P.vivax}" multivariable model 2, HR 0.92" ///
      1  "{it:P.vivax}" model 2 with time interaction, HR (95% CI)"
      ///
      pos(6) col(1))
      ///

xtitle("Time (days) since presentation with malaria", margin(medsmall))
///
ytitle("Hazard Ratio", margin(medsmall))
///
ylab(`hr1' `hr2' `hr3' 0.65 1 2, nogrid angle(h) labsize(small) format(%9.2f))
///
xlab(2 "1" 4 "3" 8 "7" 15 "14", labsize(small)) xmtick(1(1)15)
///
xscale(nofextend) yscale(log fextend) ///
graphhr(color(white) lc(white)) plotr(color(white) lc(white))

*Model 3
cd "C:\data\malaria\results\efron 24 Oct 2015 10_47_59\"
use "C:\data\malaria\results\efron 24 Oct 2015 10_47_59\MalEps_v1.9.3_M3b_TV37.dta", clear
estimates use M3bTV37_24oct2015.ster

```

estimates esample: ///

```

_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

```

label variable _ISpeciesX_2 "{it:P.vivax}"
label variable _ISpeciesX_4 "{it:P.malariae}"
label variable _ISpeciesX_5 "mixed"
label variable _IEthnicX_2 "Lowland"
label variable _IEthnicX_3 "non-Papuan"
label variable _IAGR4_4b_1 "0 to {&lt;} 1"
label variable _IAGR4_4b_2 "1 to {&lt;} 5 "
label variable _IAGR4_4b_3 "5 to {&lt;} 15"
label variable _IsexPreg_2 "female (pregnant)"
label variable _IsexPreg_3 "male"
label variable _Ioral_v_dh_1 "DHP"

```

```

label variable tv3_ISpeciesX_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_ISpeciesX_4 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_ISpeciesX_5 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IEthnicX_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IEthnicX_3 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IAGR4_4b_1 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IAGR4_4b_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IAGR4_4b_3 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IsexPreg_2 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_IsexPreg_3 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"
label variable tv3_Ioral_v_dh_1 "{it:t}{sub:3}{&rarr}{it:t}{sub:7}"

```

```

label variable tv7_ISpeciesX_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_ISpeciesX_4 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_ISpeciesX_5 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IEthnicX_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IEthnicX_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IAGR4_4b_1 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IAGR4_4b_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IAGR4_4b_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IsexPreg_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_IsexPreg_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
label variable tv7_Ioral_v_dh_1 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"

```

```

coefplot      (M3b_24oct2015,      mc("241 163 64")  ciopts(lc("241 163 64"))
              ///
              label(multivariable model 3) )
              ///
              (M3bTV37_24oct2015, mc("153 142 195") ciopts(lc("153 142 195"))
              ///
              label("model 3 with time interaction"))
              ///
              , eform baselevels xline(1, lc("27 158 119"))
              ///
order(      _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)
              ///

headings(_ISpeciesX_2 = "{it:P.falciparum}" (reference)"
              ///
              _IEthnicX_2 = "Highland (reference)"
              ///
              _IAGR4_4b_1 = " {&ge;} 15 (reference)"
              ///
              _IsexPreg_2 = "female, pregnant (reference)"
              ///
              _Ioral_v_dh_1 = "oral quinine (reference)"
              ///
              coeflabels(,labsize(small)) legend(cols(1))
              ///
              graphr(color(white) lc(white) margin(2 2 0 0)) plotr(color(white) lc(white))
              ///
              grid(within glwidth(thin)) ysize(20) xsize(15)
              ///
              xtitle("Hazard Ratio", margin(medsmall))      xlab(,labsize(small))
              ///
              xlabel(1 "reference",add tlc("27 158 119") tlength(*8) labcolor("27 158 119")
              tlwidth(medium)) ///
              subtitle("Early death in outpatients on oral treatment",
              ///
              size(medium) margin(-30 0 2 0))
              ///
note("Note: {it:t} refers to analysis time in days since presentation with a malaria
episode; " ///
"      i.e. time is split at day 3 and/or day 7 following presentation, where
specified." ///
, margin(-37 0 0 2) size(vsmall) )

graph export "C:\data\malaria\figures\Model3_compare24oct2015.emf", as(emf) replace

*Model 4 comparison of with and without time split
cd "C:\data\malaria\results\efron 24 Oct 2015 10_47_59\"
use "C:\data\malaria\results\efron 24 Oct 2015 10_47_59\MalEps_v1.9.3_M4a_TV37.dta", clear
estimates use M4aTV37_24oct2015.ster

```

```
estimates esample: ///
```

```
_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
```

```
label variable _ISpeciesX_2 "{it:P.vivax}"  
label variable _ISpeciesX_4 "{it:P.malariae}"  
label variable _ISpeciesX_5 "mixed"  
label variable _IEthnicX_2 "Lowland"  
label variable _IEthnicX_3 "non-Papuan"  
label variable _IAGR4_4b_1 "0 to {&lt;} 1"  
label variable _IAGR4_4b_2 "1 to {&lt;} 5 "  
label variable _IAGR4_4b_3 "5 to {&lt;} 15"  
label variable _IsexPreg_2 "female (pregnant)"  
label variable _IsexPreg_3 "male"  
* label variable _Ioral_v_dh_1 "DHP"  
label variable _IivArt_1 "artesunate"
```

```
label variable tv7_ISpeciesX_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_ISpeciesX_4 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_ISpeciesX_5 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IEthnicX_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IEthnicX_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IAGR4_4b_1 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IAGR4_4b_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IAGR4_4b_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IsexPreg_2 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IsexPreg_3 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
* label variable tv7_Ioral_v_dh_1 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"  
label variable tv7_IivArt_1 "{it:t}{sub:7}{&rarr}{it:t}{sub:14}"
```

```
***Graph
```

```
coefplot (M4a_24oct2015, mc("241 163 64") ciopts(lc("241 163 64"))  
///  
          label(multivariable model 4) )  
          ///  
          (M4aTV37_24oct2015, mc("153 142 195") ciopts(lc("153 142 195"))  
          ///  
          label("model 4 with time interaction"))  
          ///  
          , eform baselevels xline(1, lc("27 158 119"))  
          ///  
order( _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)
    ///
headings(_ISpeciesX_2 = "{it:P.falciparum}" (reference)"
///
    _IEthnicX_2 = "Highland (reference)"
    ///
    _IAGR4_4b_1 = " {&ge} 15 (reference)"
    ///
    _IsexPreg_2 = "female, pregnant (reference)"
    ///
    _IivArt_1 = "IV quinine (reference)"
    ///
    coeflabels(,labsize(small)) legend(cols(1))
    ///
    graphr(color(white) lc(white) margin(2 2 0 0)) plotr(color(white) lc(white))
    ///
    grid(within glwidth(thin)) ysize(20) xsize(15)
    ///
xtitle("Hazard Ratio", margin(medsmall))      xlab(,labsize(small))
///
xmlab(1 "reference",add tlc("27 158 119"))
///
tlength(*8) labcolor("27 158 119") tlwidth(medium)
subtittle("Early death in outpatients on intravenous treatment",
///
size(medium) margin(-30 0 2 0))
///
note("Note: {it:t} refers to analysis time in days since presentation with a malaria
episode; " ///
"          i.e. time is split at day 3 and/or day 7 following presentation, where
specified." ///
, margin(-37 0 0 2) size(vsmall) )

graph export "C:\data\malaria\figures\Model3_compare24oct2015.emf", as(emf) replace

```