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/******
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```
*
*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) labszsize(small)) yline(0, lc(black)) yline(5, lc(red)) yline(-
5,lc(red)) xtitle(,margin(medsmall)) xlab(0(.2)1,labszsize(small)) graphr(color(white)
lc(white)) plotr(color(white))
```

*MFP model - admission

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

```
df(2, Age: 4)
```

```
predict r_mfpA, resid
```

```
codebook hrn
```

```
predict phat_mfpA if e(sample)
```

```
tw sc r_mfpA phat_mfpA if Species==1, mc( "27 158 119") ms(Oh) || ///
```

```
sc r_mfpA phat_mfpA if Species==2, mc("217 95 2") ms(Oh) || ///
```

```
sc r_mfpA phat_mfpA if Species==4 , mc("117 112 179") ms(Oh) || ///
```

```
sc r_mfpA phat_mfpA if Species==5 , mc("231 41 138") ms(Oh) || ///
```

```
pcarrowi 9.7 0.25 9.7 0.15 (3) "341 Highland males aged 20 with falciparum infection,
receiving ", mc(black) lc(black) mlabcolor(black) text(9.4 0.26 "various courses of
treatment (mostly DHP, 44.5%) and presenting" "across each year and month between 2004
and 2013", j(left) place(4) size(small)) ylab(,nogrid) yline(0,lc(black))
```

```
ylab(5,lc(gray)) yline(-5,lc(gray)) graphr(color(white) lc(white)) plotr(color(white))
legend(order(1 "{it: P. falciparum}" 2 "{it: P.vivax}" 3 "{it: P.malariae}" 4 "mixed" ))
```

```

    xtitle("Pr(early admission), MFP model", margin(medsmall)) ytitle(Pearson's residuals,
    margin(medsmall))
tab Ethnic AGR4 if r > 5 &r~=.
tab Ethnic SpeciesX if r > 5 &r~=.

graph export "C:\data\malaria\Final\figures\mfpA_residualsPfPv.png", as(png) replace

*MFP model - Death
xi: mfp logistic DiedNext14 i.SpeciesX i.EthnicX Age i.sexPreg if Age99p==1, cluster(hrn)
df(2, Age: 4)
linktest, cluster(hrn) /* hat^2: z -0.39 p = 0.697 */
estat gof /* p = 1.000 */
/* the above suggest adequate fit, inspite of the appearance of below */
estimates
predict r_mfpD, resid
codebook hrn
predict phat_mfpD if e(sample)

tw sc r_mfpD phat_mfpD if Species==1, mc( "27 158 119") ms(Oh) || ///
sc r_mfpD phat_mfpD if Species==2, mc("217 95 2") ms(Oh) || ///
sc r_mfpD phat_mfpD if Species==4 , mc("117 112 179") ms(Oh) || ///
sc r_mfpD phat_mfpD if Species==5 , mc("231 41 138") ms(Oh) ///
ylab(,nogrid) yline(0,lc(black)) yline(5,lc(gray)) ///
xlab(0(.005).03) ///
graphr(color(white) lc(white)) plotr(color(white)) ///
legend(order(1 "{it: P. falciparum}" 2 "{it: P.vivax}" 3 "{it: P.malariae}" 4 "mixed" ))
///
xtitle("Pr(early death), MFP model", margin(medsmall)) ///
ytitle(Pearson's residuals, margin(medsmall))

graph export "C:\data\malaria\Final\figures\mfpD_residualsPfPv.png", as(png) replace

```