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/*******
*Model 1 regression diagnostics
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*Model 1
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("`farb1'") || 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))
*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) || ///
    {\tt 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)) yline(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 */
                       /* p = 1.000 */
estat gof
/* 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" ))
                                                                                                          111
                                                                           111
    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
*Explore extremes of the Pearson residuals amongst subgroups
codebook hrn if r_mfpD > 5 &r_mfpD~=. /* 1,384/182,292 episodes */
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tab EthnicX sexPreg if r_mfpD > 5 &r_mfpD~=. /*doesn't appear to differ much between nonPreg females and males*/
bysort EthnicX: tab SpeciesX AGR4 if r > 5 &r~=.
bysort DiedNext14: tab AGR4 SpeciesX if r>5&r~=. /* mostly did not die; those who did mostly older (15+); it seems <1 years quite
well predicted (but then again, many some excluded with no 1st percentile...) but Pv death in 1 to <5 overestimated */
/*Poorly predicted*/
tab Year sexPreg if r_mfpD > 10 & AGR4==2 & EthnicX==3 /* 2 female non-Papuans infants aged 1 to <5, in 2005/2006 w/ mixed infection */