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Subject: Malawi prevalence at national, regional, & cluster scale

Posted by [Ansmi25](#) on Thu, 12 Jul 2018 20:29:25 GMT

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Hello. I am trying to calculate malaria prevalence at national, region, and cluster scales. I noticed that when I calculate regions by microscopy my values are slightly different than those presented in the Malawi MIS 2017 final report. Could someone please assist me in understanding why my values are different (Freq: 266.7, 1060.2, & 1151.6)? I'd also appreciate any guidance on how to correctly code by cluster.

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\*Parasitemia (vis RDT) in children 6-59 months

cap gen rdtmalpos=0

cap replace rdtmalpos=(HML35==1)

cap lab var rdtmalpos "Parasitemia (via RDT) in children 6-59 months"

\*Parasitemia (vis microscopy) in children 6-59 months

cap gen micmalpos=0

cap replace micmalpos=(HML32==1)

cap lab var micmalpos "Parasitemia (via microscopy) in children 6-59 months"

\*Weighting

gen wgt = hv005/1000000

\*Proportion of children 6-59 months old with malaria infection (RDT)

tab rdtmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml35==0|hml35==1)

[iweight=wgt]

tab micmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml32==0|hml32==1)

[iweight=wgt]

\*RDT by region

tab rdtmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml35==0|hml35==1) & hv024==1

[iweight=wgt]

tab rdtmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml35==0|hml35==1) & hv024==2

[iweight=wgt]

tab rdtmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml35==0|hml35==1) & hv024==3

[iweight=wgt]

\*Mic by region

tab micmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml32==0|hml32==1) &

hv024==1 [iweight=wgt]

tab micmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml32==0|hml32==1) &

hv024==2 [iweight=wgt]

tab micmalpos if hc1>=6 & hc1<=59 & hv103==1 & hml33==0 & (hml32==0|hml32==1) &

hv024==3 [iweight=wgt]