Codes

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\*2012

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

clear all

\*directory

cd "G:\Diarrhoea Project\Data Set\Bangladesh MICS6 SPSS Datasets"

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\*DATA MERGE

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

use "hh" , clear

sort HH1 HH2

save "hh" , replace

use "wm" , clear

sort HH1 HH2 LN

save "wm" , replace

use "bh" , clear

sort HH1 HH2 LN

save "bh" , replace

use "ch" , clear

sort HH1 HH2 LN

save "ch" , replace

merge m:1 HH1 HH2 using hh.dta

keep if \_merge == 3

drop \_merge

save "ch1" , replace

merge using wm.dta

tab \_merge

keep if \_merge == 3

save "ch" , replace

drop \_merge

\*outcome and key predictor

svy: tab CA1

gen had\_diarrhea = .

replace had\_diarrhea = 1 if CA1==1

replace had\_diarrhea = 0 if CA1==2

replace had\_diarrhea = . if CA1==8

replace had\_diarrhea = . if CA1==9

label define diar 1 "Yes" 0 "No"

label value had\_diarrhea diar

svy: tab had\_diarrhea, count

svy: tab had\_diarrhea, count cellwidth(15) format(%15.2g)

drop if had\_diarrhea == .

save "ch1" , replace

svy: tab had\_diarrhea, count cellwidth(15) format(%15.2g)

\*Age.

svy: tab CAGE\_11

svy: tab CAGE\_11 had\_diarrhea, count cellwidth(15) format(%15.2g) row

svy: tab CAGE\_11 had\_diarrhea,cellwidth(15) format(%15.2g) row

\*child sex.

svy: tab HL4 had\_diarrhea, row

svy: tab HL4 had\_diarrhea, count cellwidth(15) format(%15.2g) row

\*Residence.

svy: tab HH6

gen area1=HH6

recode area1 1=1

recode area1 2/4=2

recode area1 5=3

label define area1 1 "Rural" 2 "Urban" 3 "Tribal"

label values area area1

svy: tab area had\_diarrhea, row

svy: tab area had\_diarrhea, count cellwidth(15) format(%15.2g) row

\*Division.

svy: tab HH7

svy:tab HH7 had\_diarrhea, row

svy: tab HH7 had\_diarrhea, count cellwidth(15) format(%15.2g) row

\*Education.

svy: tab melevel

recode melevel 9=.

svy: tab melevel had\_diarrhea, row

svy: tab melevel had\_diarrhea, count cellwidth(15) format(%15.2g) row

\*household sex.

svy: tab HHSEX had\_diarrhea, row

svy: tab HHSEX had\_diarrhea, count cellwidth(15) format(%15.2g) row

\*Type of toilet facility.

svy: tab WS11

gen TF1=WS11

recode TF1 11/23=1

recode TF1 31/95=2

recode TF1 96=3

recode TF1 99=.

label define TF1 1 "improved" 2 "unimproved" 3 "other"

label values TF TF1

svy: tab TF had\_diarrhea, row

svy: tab TF had\_diarrhea, count cellwidth(15) format(%15.2g) row