```
1   //  program no.:    #01
2   //  program:    2024_01_10_ALERT_Analysis_final.do
3   //  task:       Preparing HMIS and ALERT datasets
4   //  project:    ALERT Study
5   //  Requestor:  Claudia/Manuela/ALERT
6   //  author:     Joseph\10th January, 2024
7   //  #0
8   //  programme setup
9
10  frames reset
11  clear
12  **# ALERT DATASET
13  **# Loading clean dataset
14
15  cd "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\"
16
17  use allcountries16Apr24clean.dta, clear
18
19  **# Dates
20  *Creating a stata readable date
21      gen date = dofc(q1date)
22      format date %td
23  *Converting date into stata weeks of the year
24      gen weeks = wofd(date)
25      format weeks %tw
26
27      gen months = mofd(date)
28      format months %tm
29
30      gen qtr3 = qofd((date))
31      format qtr3 %tq
32
33  **# WOMAN LEVEL
34  **# Number of records/Deliveries
35      gen NRecords = 1
36      ta NRecords, mi
37
38  **# Bookmark #15
39          label define country 1 " Benin" 2 "Malawi" 3 "Tanzania" 4 "Uganda"
40          label values count country
41
42  **# Number of records by hospital by months
43
44  *Cleaning and keeping only 30 months from July 2021 to December 2023
45  x
46  *Bennin
47  gen perprotocol = 1 if count==1 & inrange(month,7,13)
48  replace perprotocol = 2 if count==1 & inrange(month,14,19)
49  replace perprotocol = 3 if count==1 & inrange(month,20,26)
50  replace perprotocol = 4 if count==1 & inrange(month,27,31)
51  replace perprotocol = 5 if count==1 & inrange(month,32,38)
52
53  *Malawi
54  replace perprotocol = 1 if count==2 & inrange(month,7,14)
55  replace perprotocol = 2 if count==2 & inrange(month,15,21)
56  replace perprotocol = 3 if count==2 & inrange(month,22,27)
57  replace perprotocol = 4 if count==2 & inrange(month,28,33)
58  replace perprotocol = 5 if count==2 & inrange(month,34,38)
59
60  *Tanzania
61  replace perprotocol = 1 if count==3 & inrange(month,7,13)
62  replace perprotocol = 2 if count==3 & inrange(month,14,19)
63  replace perprotocol = 3 if count==3 & inrange(month,20,27)
64  replace perprotocol = 4 if count==3 & inrange(month,28,32)
65  replace perprotocol = 5 if count==3 & inrange(month,33,38)
66
```

```
67
68  *Uganda
69  replace perprotocol = 1 if count==4 & inrange(month,7,13)
70  replace perprotocol = 2 if count==4 & inrange(month,14,18)
71  replace perprotocol = 3 if count==4 & inrange(month,19,25)
72  replace perprotocol = 4 if count==4 & inrange(month,26,31)
73  replace perprotocol = 5 if count==4 & inrange(month,32,36)
74
75  xx
76
77
78  drop if months==. | hospn==29 | months==m(2020m6) | !inrange(month,7,36)
79  duplicates tag hospn month, gen(dups) // Checking for multiple months
80  drop dups
81
82  xxx - perprotocol#
83  drop if perprotocol==.
84
85  **Anonymised hospital names
86  replace hosp = "Benin-Hospital-1" if hospn==11
87  replace hosp = "Benin-Hospital-2" if hospn==12
88  replace hosp = "Benin-Hospital-3" if hospn==13
89  replace hosp = "Benin-Hospital-4" if hospn==14
90  replace hosp = "Malawi-Hospital-1" if hospn==21
91  replace hosp = "Malawi-Hospital-2" if hospn==22
92  replace hosp = "Malawi-Hospital-3" if hospn==23
93  replace hosp = "Malawi-Hospital-4" if hospn==24
94  replace hosp = "Tanzania-Hospital-1" if hospn==31
95  replace hosp = "Tanzania-Hospital-2" if hospn==32
96  replace hosp = "Tanzania-Hospital-3" if hospn==33
97  replace hosp = "Tanzania-Hospital-4" if hospn==34
98  replace hosp = "Uganda-Hospital-1" if hospn==41
99  replace hosp = "Uganda-Hospital-2" if hospn==42
100 replace hosp = "Uganda-Hospital-3" if hospn==43
101 replace hosp = "Uganda-Hospital-4" if hospn==44
102
103 gen hp =.
104 replace hp = 1 if hospn==11
105 replace hp = 2 if hospn==12
106 replace hp = 3 if hospn==13
107 replace hp = 4 if hospn==14
108 replace hp = 5 if hospn==21
109 replace hp = 6 if hospn==22
110 replace hp = 7 if hospn==23
111 replace hp = 8 if hospn==24
112 replace hp = 9 if hospn==31
113 replace hp = 10 if hospn==32
114 replace hp = 11 if hospn==33
115 replace hp = 12 if hospn==34
116 replace hp = 13 if hospn==41
117 replace hp = 14 if hospn==42
118 replace hp = 15 if hospn==43
119 replace hp = 16 if hospn==44
120
121 *Creating the 6-months periofs
122 egen period = cut(month), group(5) label //1 missing value created
123
124 tab month period
125
126 // recode month (min/5= 0 "1-5 Months") (6/10=1 "6-10 Months") (11/15=2 "11-15 Months") (16/20=3
    "16-20 Months") (21/25=4 "21-25 Months") (26/30=5 "26-30 Months") (31/35=6 "31-35 Months"),
    gen(period) label(periodz)
127 // collapse (sum) NRecords, by(period hospn)
128
129 recode month (min/12= 0 "1-6 Months") (13/18=1 "7-12 Months") (19/24=2 "13-18 Months") (25/30=3
    "19-24 Months") (31/36=4 "25-30 Months"), gen(time2) label(period)
```

```
// collapse (sum) NRecords, by(period hospn)

egen time3 = cut(month), group(5) label //1 missing value created

**# Randomisation
gen group = 1 if hospn==11 | hospn==21 | hospn==31 | hospn==41
replace group = 2 if hospn==12 | hospn==22 | hospn==32 | hospn==42
replace group = 3 if hospn==13 | hospn==23 | hospn==33 | hospn==43
replace group = 4 if hospn==14 | hospn==24 | hospn==34 | hospn==44


**# Intervention
gen hosp1_intervention = month>=13 //jan2022
gen hosp2_intervention = month>=19 //jul2022
gen hosp3_intervention = month>=25 //jan2023
gen hosp4_intervention = month>=31 //jul2023

gen intervention = 0
replace intervention = 1 if hosp1_intervention==1
replace intervention = 2 if hosp1_intervention==1 & hosp2_intervention==1
replace intervention = 3 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1
replace intervention = 4 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1 &
 hosp4_intervention==1

label define intervention 0 "No intervention" 1 "Hosp 1" 2 "Hosp 1,2" 3 "Hosp 1,2,3" 4 "Hosp
1,2,3,4"
label values intervention intervention
tab intervention


**# Treatment variable
ren time2 time
generate byte has_been_treated1 = 0
replace has_been_treated1 = 1 if time ==1 & group ==1 ///
    | time ==2 & inlist(group, 1,2) | time ==3 & inlist(group,1,2,3) | time ==4

generate byte has_been_treated2 = 0
replace has_been_treated2 = 1 if time3 ==1 & group ==1 ///
    | time3 ==2 & inlist(group, 1,2) | time3 ==3 & inlist(group,1,2,3) | time3 ==4


. table hospn time, statistic(mean has_been_treated1) nototal
. table hospn time3, statistic(mean has_been_treated2) nototal

ren has_been_treated2 treat


//PER PROTOCOL ANALYSIS
generate byte has_been_treated3 = 0
replace has_been_treated3 = 1 if perprotocol ==2 & group ==1 ///
    | perprotocol ==3 & inlist(group, 1,2) | perprotocol ==4 & inlist(group,1,2,3) | perprotocol ==
5


**# Table 1
**# Number of records by hospital by months
// collapse (sum) NRecords, by(hosp period)
// sort hosp period, stable
// drop months

**# Table 1 Baseline data
// keep alert_id hospnam q1date todaydate q2ref q2aqta q2bwhe q3age q4grav q7ces q8anc q9aga
q10syp q11hiv q12acom q12bcom q12ccom q12dcom q12ecom q12fcom q12gcom q12hcom q12icom q12lcom
q12mcom q12ncom q13onq q13aind___1 q13aind___2 q13aind___3 q13aind___4 q13aind___5 q13aind___6
q14acervix q15aug q16fet q17pret q17adex q17cdos q25babies country count hosp hospn hosp2 year
month week
```

```
189
190  **# Age
191  tab q3age
192  recode q3age (min/14 = 1 "<15") (15/19 = 2 "15-19") (20/24 = 3 "20-24") (25/29 = 4 "25-29") (30/34
     = 5 "30-34") (35/39=6 "35-39") (40/50=7 "40+") , gen(agemum) label(MaternalAge)
193
194  **# Referral status
195  tab1 q2ref q2aqta q2bwhe
196  recode q2ref 0=1 if q2aqta!=.
197  recode q2ref 0=1 if q2bwhe!=.
198  label define q2ref 0 "Woman not referred into facility" 1 "Woman referred into facility"
199  label value q2ref q2ref
200
201  recode q2bwhe .=4
202  label define q2bwhe_ 4 "Woman not referred into facility", modify
203
204  **# gravidity
205  recode q4grav (1 = 1 "1") (2 = 2 "2") (3 = 3 "3") (4/5 = 4 "4-5") (6/8 = 5 "6-8") (9/15 = 6 "9+") ,
      gen(gravidity) label(gravidity)
206
207  **# parity
208  recode q6par (.0 = 0 "Nulliparous") (2 = 1 "1") (3/4 = 3 "3") (5/15 = 4 "5+") , gen(parity) label(parity)
209
210  **# Previous CS
211  tab q7ces
212
213  **# ANC visits
214  tab q8anc
215  recode q8anc (min/3 = 1 "<4") (4/14 = 4 "4+") , gen(ancno) label(ancno)
216
217  **# TESTS AT ANC
218  label define tests 1 "Positive" 2 "Negative" 3 "Not done"
219  foreach var q10syph q11hiv {
220  tab q10syph
221
222  tab q11hiv
223
224  **# Antenatal complications
225  tab1 q12acom q12bcom q12ccom q12dcom q12ecom q12fcom q12gcom q12hcom q12icom q12kcom q12lcom q12mcom q12ncom
226
227
228  **# Labour and birth
229  tab q13onq
230
231  **# Indication for induction of labour
232  tab1 q13aind___1 q13aind___2 q13aind___3 q13aind___4 q13aind___5 q13aind___6
233
234  **# Start of labour
235  sort id
236  merge 1:1 id using "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
     paper\TimeofLabour.dta", keep(time) nogen
237
238  drop if _merge==3
239
240  drop _merge
241  **# Augumentation of labour
242
243
244  **# Fetal heartbeat at admission
245
246
247  **# Preterm labour
248
249  // q3age conts %5.1f \ agemum  cat %5.1f \ q2ref bin \ q2aqta cat \ q2bwhe cat \ q4grav conts
     %5.1f \ gravidity cat \ q6par conts %5.1f \ parity cat \ q7ces bin \ ancno cat \ q10syp cat \
     q11hiv cat \ q12acom bin \ q12bcom bin \ q12ccom bin \ q12dcom bin \ q12ecom bin \ q12fcom bin \
```

```
    q12gcom bin \ q12hcom bin \ q12icom bin \ q12kcom bin \ q12lcom bin \ q12mcom bin \ q12ncom bin \
    q13onq cat \ q13aind___1 bin \ q13aind___2 bin \ q13aind___3 bin \ q13aind___4 bin \ q13aind___5
    bin \ timeofday cat \ q15aug  bin
250
251
252 table1, by(count) vars( q3age conts %5.1f \ agemum  cat \ q2ref bin \ q2aqta cat \ q2bwhe cat \
    q4grav conts %5.1f \ gravidity cat \ q6par conts %5.1f \ parity cat \ q7ces bin \ ancno cat \
    q12acom bin \ q12bcom bin \ q12ccom bin \ q12dcom bin \ q12ecom bin \ q12fcom bin \ q12gcom bin \
    q12hcom bin \ q12icom bin \ q12kcom bin \ q12lcom bin \ q12mcom bin \ q12ncom bin \ q13onq cat \
    timeofday cat \ q15aug  bin) format(%2.1f) onecol missing saving(Results_Table1.xlsx, sheet(
    "Table1", replace))
253
254 table1, by(treat) vars( q3age conts %5.1f \ agemum  cat \ q2ref bin \ q2aqta cat \ q2bwhe cat \
    q4grav conts %5.1f \ gravidity cat \ q6par conts %5.1f \ parity cat \ q7ces bin \ ancno cat \
    q12acom bin \ q12bcom bin \ q12ccom bin \ q12dcom bin \ q12ecom bin \ q12fcom bin \ q12gcom bin \
    q12hcom bin \ q12icom bin \ q12kcom bin \ q12lcom bin \ q12mcom bin \ q12ncom bin \ q13onq cat \
    timeofday cat \ q15aug  bin) format(%2.1f) onecol missing saving(Results_Table1.xlsx, sheet(
    "Table1a", replace))
255
256
257
258 *#############################################################################
259 *Prepare new variables that indicate number of missing or other property of interest
260 *#############################################################################
261 **ADMISSION STANDARDS AND PROCEDURES
262 **INDICATOR 1 - appropriate admission standards and procedures
263 **Ind 1 Q1,2,3,4,8,9,10,11,12
264
265 foreach p in q1date q2ref q3age q4grav q8anc q9dob q9aga q10syp /*
266     */ q11hiv q12acom q12bcom q12ccom q12dcom /*
267     */ q12ecom q12fcom q12gcom q12hcom q12icom {
268     gen `p'_ = !missing(`p')
269     gen `p'_m = `p'_*100 //multiply by 100 to make percentages in the table
270     drop `p'_
271     //replace `p'_m = . //if babynr!="1"
272 }
273
274 **Ind 1 Q2
275 gen q2aqta_m = .
276 replace q2aqta_m = 100 if q2ref==1 & q2aqta!=. //& babynr=="1"
277 replace q2aqta_m = 0 if q2ref==1 & q2aqta==. //& babynr=="1"
278
279 **Ind 1 Q5
280 gen q5out_m = .
281 replace q5out_m = 100 if q4grav>1 & q4grav!=. & q5out!=. //& babynr=="1"
282 replace q5out_m = 0 if q4grav>1 & q4grav!=. & q5out==. //& babynr=="1"
283
284 **Ind 1 Q6
285 gen q6par_m = .
286 replace q6par_m = 100 if q4grav>1 & q4grav!=. & q6par!=. //& babynr=="1"
287 replace q6par_m = 0 if q4grav>1 & q4grav!=. & q6par==. //& babynr=="1"
288
289 **Ind 1 Q7
290 gen q7ces_m = .
291 replace q7ces_m = 100 if q4grav>1 & q4grav!=. & q7ces!=. //& babynr=="1"
292 replace q7ces_m = 0 if q4grav>1 & q4grav!=. & q7ces==. //& babynr=="1"
293
294 **Summary of indicator 1
295 gen ind1_sum = (q1date_m+q2ref_m+q2aqta_m+q3age_m+q4grav_m+q5out_m+q6par_m+q7ces_m+ /*
296     */ q8anc_m+q9dob_m+q9aga_m+q10syp_m+q11hiv_m+ /*
297     */ q12acom_m+q12bcom_m+q12ccom_m+q12dcom_m+q12ecom_m+q12fcom_m+ /*
298     */ q12gcom_m+q12hcom_m+q12icom_m)/22
299
300
301 **INDICATOR 2 - Fetal heart on admission
302 **Ind 2: fetal check at admission done
```

```
gen q16fet_p = .
replace q16fet_p = 1 if (q16fet==1 | q16fet==2) //& babynr=="1"
replace q16fet_p = 0 if (q16fet==3 | q16fet==.) //& babynr=="1"
ta q16fet_p
**INDICATOR 3 - fetal monitoring done and documented in 1st stage of labour
gen q18_0fhmeas_p = .
replace q18_0fhmeas_p = 1 if q18_0fhmeas==1 //& babynr=="1"
replace q18_0fhmeas_p = 0 if (q18_0fhmeas==0 | q18_0fhmeas==.) //& babynr=="1"
ta q18_0fhmeas_p
**INDICATOR 4 - fetal monitoring done in 2nd stage
gen q21secfet_p = .
replace q21secfet_p = 1 if q21secfet==1 //& babynr=="1"
replace q21secfet_p = 0 if (q21secfet==0 | q21secfet==.) //& babynr=="1"

**EMERGENCY PREPAREDNESS
**Ind 5: Decision to delivery time in case of Caesarean section
gen del_time = minutes(q23birth-q22etimedec) // Decision to delivery time in case of Caesarean
section

***THIS INDICATOR NEEDS CHECKING AGAIN
// replace del_time = . if del_time < 0 // make negative time missing
 gen emergencycs = .
// replace emergencycs = 100 if (q19ddec==2 | q22ddec==3) & del_time<45 & del_time!=.
// replace emergencycs = 0 if (q19ddec==2 | q22ddec==3) & del_time!=. // THIS REPLACES THE ABOVE

**Ind 6: Resuscitation for babies with APGAR < 7
gen resapg = .
replace resapg = 1 if q32resc==1 & q30apg<7
replace resapg = 0 if q32resc!=1 & q30apg<7

**RESPONSIVENESS FOCUSED
**INDICATOR 7 - Companionship
**Ind 7a: Was a companion present during labour
gen q39comp1_p = 0
replace q39comp1_p = 1 if q39comp1==1

** 7b: Companion during birth
gen q39comp2_p = 0
replace q39comp2_p = 1 if q39comp2==1


**ACTIVE MANAGEMENT OF THIRD STAGE/EARLY NEWBORN CARE
**Ind 8: Breastfeeding within 1 h
gen q36breast_p = 0
replace q36breast_p = 1 if q36breast==1 & q27out ==1

**QUALITY IMPROVEMENT
**Ind 9: Fresh stillbirth with a positive heartbeat at admission
gen freshheart = .
replace freshheart = 1 if q16fet==1 & q27out==2
replace freshheart = 0 if q16fet!=1 & q27out==2

*SEVERE MATERNAL OUTCOMES
**Definition from protocol paper
gen sevmatout=.
recode sevmatout .=1 if q42kperint==1 //hysterectomy
recode sevmatout .=1 if q42jperint==1 //laparotomy for ruptured uterus
recode sevmatout .=1 if q42iperint==1 //blood transfusion
recode sevmatout .=1 if q49==3 // 3 referred to ICU or higher level facility
recode sevmatout .=0
tab sevmat

label variable ind1_sum "Appropriate admission standards and procedures"
label variable q16fet_p "Fetal heart check at admission done"
label variable q18_0fhmeas_p "Fetal monitoring done and documented in 1st stage of labour"
label variable q21secfet_p "Fetal monitoring done in 2nd stage "
```

```
label variable resapg "Resuscitation for babies with APGAR < 7"
label variable q39comp1_p "Companion present during labour"
label variable q39comp2_p "Companion present during birth"
label variable q36breast_p "Breastfeeding within 1 hour"
label variable freshheart "Fresh stillbirth with a positive heartbeat at admission"
label variable sevmat"Severe maternal outcomes"
label variable emergencycs "Decision to delivery time in case of Caesarean section"

table1, by(count) vars(ind1_sum contn \q16fet_p bin \q18_0fhmeas_p bin \ q21secfet_p bin \
q39comp1_p bin  \ q39comp2_p bin \ sevmat bin  ) format(%9.1fc) missing onecol saving(
Results_Table1.xlsx, sheet("Table2_process", replace))

table1, by(treat) vars(ind1_sum contn \q16fet_p bin \q18_0fhmeas_p bin \ q21secfet_p bin \
q39comp1_p bin  \ q39comp2_p bin \ sevmat bin ) format(%9.1fc) missing onecol saving(Results_Table1
.xlsx, sheet("Table2b_process", replace))
x
**# MAIN STUDY OUTCOMES

*MATERNAL MORBIDITY - hysterectomy, laparotomy, blood transfusion, adm to intensive care, referral
to higher facility

gen matmorb=.
lab var matmorb "Severe Maternal morbidity"
recode matmorb .=1 if (q42j==1|q42k==1|q42iperint==1|q49==3) //|q49==4)
recode matmorb .=0
lab def matmorb 1 "severe maternal morbidity" 0 "none"
lab val matmorb matmorb


table1, by(count) vars(matmorb bin ) format(%9.1fc) missing onecol saving(Results_Table1.xlsx,
sheet("Table3", replace))

table1, by(treat) vars(matmorb bin) format(%9.1fc) missing onecol saving(Results_Table1.xlsx, sheet
("Table3b", replace))
x
**# BABY LEVEL
//  use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\UG\2023_09_04_UG.dta", clear

*Reshaping to long
    run "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\ALERT
do-files\OneDrive_1_04-09-2023\1b. Reshaping (wide to long).do"


svyset hospn

*INTRAPARTUM SB (based on visual identification) *this should be run after reshaping? or add
numbers from baby 1, 2, 3?
gen ipsb=.
recode ipsb .=1 if q27out==2
recode ipsb .=0 if (q27out==1|q27out==3|q27out==.)

*gen stillbirthrate=prop(ipsb)/1000
*gen proplarger = (_N-_n)/_N

*denominator is live births and stillbirths BIRTHS
*live births from q27out
gen births=.
recode births .=1 if (q27out==1|2|3)
tab births

*do reshape

*1 FRESH STILLBIRTH RATE
gen fsb=.
lab var fsb "Fresh stillbirths"
```

```
recode fsb .=1 if q27out==2
recode fsb .=0 if (q27out==1|3)
label define fsb 1 "fresh stillbirth" 0 "macerated or live births"
label val fsb fsb

// svy: tab fsb, subpop(if country1==1) percent  ci format (%2.1f)
// svy: tab fsb, subpop(if country1==2) percent  ci format (%2.1f)
// svy: tab fsb, subpop(if country1==3) percent  ci format (%2.1f)
// svy: tab fsb, subpop(if country1==4) percent  ci format (%2.1f)

*2. In-facility early perinatal mortality
*Number of fresh stillbirths (as above) and up-to discharge neonatal deaths per 1000 live and stillbirths (composite indicator)
ren eperi eperi_old
gen eperi=.
lab var eperi "early perinatal mortality"
recode eperi .=1 if q27out==2
recode eperi .=1 if (q27out==1|q27out==.) & (q44status==1|q44status==.) & q45status==3
*recode eperi .=1 if (q27out==1|q27out==.) & q44status==2 & (q45status==3|q45status==4|q45status==5|q45status==.)
recode eperi .=1 if (q27out==1|q27out==.) & q44status==2
recode eperi .=1 if (q27out==1|q27out==.) & (q45status==3)
*recode eperi .=1 if (q27out==1|q27out==.) & (q45status==3|q45status==4)

recode eperi .=0
tab eperi
tab eperi q27out, mi
tab eperi q44status, mi
tab eperi q45status, mi


gen eperi2=.
lab var eperi2 "early perinatal mortality"
recode eperi2 .=1 if q27out==2
recode eperi2 .=1 if (q27out==1|q27out==.) & (q44status==1|q44status==.) & q45status==3
*recode eperi .=1 if (q27out==1|q27out==.) & q44status==2 & (q45status==3|q45status==4|q45status==5|q45status==.)
recode eperi2 .=1 if (q27out==1|q27out==.) & q44status==2
recode eperi2 .=1 if (q27out==1|q27out==.) //& (q45status==3|q45status==4)
recode eperi2 .=0
tab eperi2
tab eperi2 q27out, mi
tab eperi2 q44status, mi
tab eperi2 q45status, mi
*3. Fetal distress (neonates with Apgar <7 at 5 min out 1000 live births and stillbirths)
gen lowapgar =.
lab var lowapgar "low apgar score (<7)"
recode lowapgar .=0 if q30apg>=7
recode lowapgar .=1 if q30apg <7
tab q30apg lowapg, m
label define lowapg 1 "apgar <7" 0 "apgar≥7"
lab val lowapg lowapgar

*3. Neonatal seizures (number of neonates diagnosed with seizures per 1000 live and stillbirths)
gen seizures=.
recode seizures .=1 if (q46b==1)
recode seizures .=0
tab seizures
label define seizures 1 "seizures" 0 "no seizures"
lab val seizures seizures
prop seizures, percent
// svy: tab seizures, subpop(if country1==1) percent  ci format (%2.1f)
// svy: tab seizures, subpop(if country1==2) percent  ci format (%2.1f)
// svy: tab seizures, subpop(if country1==3) percent  ci format (%2.1f)
// svy: tab seizures, subpop(if country1==4) percent  ci format (%2.1f)

```

```
487
488  *CAESAREAN SECTIONS
489  gen CS=.
490  lab var CS "Caesarean section"
491  recode CS .=1 if q24mode ==2
492  recode CS .=0 if q24mode!=2
493  tab CS q24mode
494  lab def CS 1 "CS" 0 "Vaginal birth"
495  lab val CS CS
496  // svy: tab CS, subpop(if country1==1) percent  ci format (%2.1f)
497  // svy: tab CS, subpop(if country1==2) percent  ci format (%2.1f)
498  // svy: tab CS, subpop(if country1==3) percent  ci format (%2.1f)
499  // svy: tab CS, subpop(if country1==4) percent  ci format (%2.1f)
500
501  *DETECTION OF FETAL DISTRESS
502  *q41icomp
503  gen fetdist=q41icomp
504  lab var fetdist "fetal distress"
505
506  *TIME TO DECISION FOR CS
507  *What is the variable?
508  // gen del_time = minutes(q23birth-q22etimedec) // Decision to delivery time in case of Caesarean
     section
509  // replace del_time = . if del_time < 0 // make negative time missing
510  *gen emergencycs = .
511  *replace emergencycs = 100 if (q19ddec==2 | q22ddec==3) & del_time<45 & del_time!=.
512  *replace emergencycs = 0 if (q19ddec==2 | q22ddec==3) & del_time!=.
513  *check variable q19ddec 2 & 3
514  *del_time
515  ta del_time
516
517  recode q36breast (1=1 "<1 hr") (2=2 "1 - 24hrs") (3=3 "1-6 days") (4=4 "7+ days") (5=5 "Unknown")
     if q27out==1, gen(breastfed2) label(breastfed)
518
519  **# NEONATAL DEATH
520  gen neonataldeath=.
521  lab var neonataldeath "neonatal death"
522  recode neonataldeath .=1 if (q27out==1|q27out==.) & (q44status==1|q44status==.) & inrange(q45status
     ,3,4)
523  *recode eperi .=1 if (q27out==1|q27out==.) & q44status==2 &
     (q45status==3|q45status==4|q45status==5|q45status==.)
524  recode neonataldeath .=1 if (q27out==1|q27out==.) & q44status==2
525  recode neonataldeath .=1 if (q27out==1|q27out==.) & (q45status==3|q45status==4)
526  recode neonataldeath .=0
527  tab neonataldeath
528  tab neonataldeath q27out, mi
529  tab neonataldeath q44status, mi
530  tab neonataldeath q45status, mi
531  tab neonataldeath eperi, mi
532
533  *NEONATAL NEARMISS
534  gen neonatal_nearmiss = cond((q27out==1 & q45status==1 & q28weight<=1750 | q30apg<=7 | q9aga<=33),1
     ,0)
535  tab neonatal_nearmiss
536
537  *PRETERM BIRTH
538  gen preterm = inrange(q9aga,28,37) //& q27out==1
539  label variable preterm "preterm birth"
540  ta preterm
541  *SGA
542  tostring q29sex, gen(sex)
543  gen bwt_kg = q28weight/1000
544  gen gest_age = q9aga*7
545  egen sga = classify_sga(bwt_kg), gest_age(gest_age) sex(sex) sexcode(male=2, female=1)
546  label variable sga "small for gestational age"
547
```

```
label define sga_labels  -2 "Severely Small for Gestational Age (<3rd centile)" -1 "Small for Gestational Age (<10th centile)"  0 "Appropriate for Gestational Age (10th to 90th centile)" 1 "Large for Gestational Age (>90th centile)", modify
drop sex

tab sga,mi


*LBW
recode q28weight (min/2499 = 1 "<2500g") (2500/4500 = 2 "normal birthweight (2500 - 4500g)") (4501/9000 = 3 "macrosomia (>4500)"), gen(bwt) label(bwt)
ta bwt, mi

**# SVN
**# Small and Vulnerable newborn
gen svn = cond((preterm==1 | sga<0 | bwt==1),1,0)

label variable svn "Small and Vulnerable Newborn"

*TABLES
table1, by(count) vars(fsb bin\eperi bin\lowapg bin\seizures bin\CS bin\fetdist bin \ breastfed cat \q9aga conts %5.1f \ preterm bin \ q28weight conts %5.1f\ bwt cat) format(%9.1fc) missing onecol saving(Results_Table1.xlsx, sheet("Table3c", replace))

*table by Treatment arm

table1, by(treat) vars(fsb bin\eperi bin\lowapg bin\seizures bin\CS bin\fetdist bin \ breastfed cat \q9aga conts %5.1f \ preterm bin \ q28weight conts %5.1f\ bwt cat)  format(%9.1fc) missing onecol saving(Results_Table1.xlsx, sheet("Table3d", replace))



**# Labour information and process measurement
**# First stage
*First stage labour monitoring documented
gen firststage = !missing(dur_stage1)
lab var firststage "First stage of labour monitoring documented"
*Duration of first stage in hours
sum dur_stage1
lab var dur_stage1 "Duration of first stage in hours"

*Fetal heart beat meassured at 1st stage
tab q18_0fhmeas
lab var q18_0fhmeas "Fetal heart beat meassured at 1st stage"

*Fetal heart abnormality found - 1st stage
recode  q18anom 2=.
ta q18anom , nol
lab var q18anom "Fetal heart abnormality found - 1st stage"

*Senior midwife informed at 1st stage
 ta q19binfo
 lab var q19binfo "Senior midwife informed at 1st stage"

*Doctor informed at 1 stage
 ta q19cdoc
lab var q19cdoc "Doctor informed at 1 stage"

*Decision made at 1st stage
tab q19ddec
lab var q19ddec "Decision made at 1st stage"

*Duration of decision at 1st stage in minutes
tab decbir_tim
lab var decbir_tim "Duration of decision at 1st stage in minutes"

```

```
**# Second stage
tab q20sec
lab var q20sec "Second stage of labour monitoring documented"


//  (firststage bin \ dur_stage1 conts \ q18_0fhmeas bin \ q18anom bin \ q19binfo bin \ q19cdoc bin \ q19ddec cat \ decbir_tim conts \ q20sec bin \ dur_stage2 conts \ q21secfet bin \ q22path bin \ q22binfo bin \ q22cdoc bin \ q22ddec cat \ decbir_tim2 conts \ lol conts \ adm_birth conts \ los conts \ q24mode cat \ q24indi___1 bin \  q24indi___2 bin \  q24indi___3 bin \  q24indi___4 bin \ q24indi___5 bin \  q24indi___6bin \  q24indi___7 bin \  q24indi___8 bin \  q24indi___9 bin \ q24indi___10 bin \   q24indi___11 bin \   q24indi___12 bin \   q24indi___13 bin \   q24indi___14 q24indi___15 bin)

*Duration of second stage in hours
sum dur_stage2
lab var dur_stage2 "Duration of second stage in hours"

*Fetal heart beat meassured at first stage
tab q21secfet
lab var q21secfet "Fetal heart beat meassured at first stage"

*Fetal heart anormally
ta q22path
lab var q22path "Fetal heart abnormality found - 2nd stage"

*Senior midwife informed
 ta q22binfo
 lab var q22binfo "Senior midwife informed a 2nd stage"

*Doctor informed
 ta q22cdoc
lab var q22cdoc "Doctor informed at 2nd stage"

*Decision made
tab q22ddec
lab var q22ddec "Decision made at 2nd stage"

*Duration of decision at 1st stage in minutes
tab decbir_tim2
lab var decbir_tim2 "Duration of decision at 1st stage in minutes"

**# Length of labour in hours
ta lol
lab var lol "Length of labour in hours"

**# Time from Admission to birth in hours
sum adm_birth //hours
ta adm_birth
lab var adm_birth "Time from Admission to birth in hours"

**# Length of stay in facility (hours)
sum los, detail
lab var los "Length of stay in facility (hours)"

*Mode of delivery
tab q24mode
lab var q24mode "Mode of delivery"

*Indication of operative birth
tab1 q24indi___1 q24indi___2 q24indi___3 q24indi___4 q24indi___5 q24indi___6 q24indi___7 q24indi___8 q24indi___9 q24indi___10 q24indi___11 q24indi___12 q24indi___13 q24indi___14 q24indi___15

table1, by(count) vars(firststage bin \ dur_stage1 conts \ q18_0fhmeas bin \ q18anom bin \ q19binfo bin \ q19cdoc bin \ q19ddec cat \ decbir_tim conts \ q20sec bin \ dur_stage2 conts \ q21secfet bin \ q22path bin \ q22binfo bin \ q22cdoc bin \ q22ddec cat \ decbir_tim2 conts \ lol conts \
```

```
adm_birth conts \ los conts \ q24mode cat \ q24indi___1 bin \  q24indi___2 bin \  q24indi___3 bin
\  q24indi___4 bin \  q24indi___5 bin \  q24indi___6 bin \  q24indi___7 bin \  q24indi___8 bin \
q24indi___9 bin \   q24indi___10 bin \   q24indi___11 bin \   q24indi___12 bin \   q24indi___13 bin
 \   q24indi___14 bin \ q24indi___15 bin)  format(%9.1fc) missing onecol saving(Results_Table1.xlsx
, sheet("Table2b", replace))

table1, by(treat) vars(firststage bin \ dur_stage1 conts \ q18_0time cat \ q18anom bin \ q19binfo bin \ q19cdoc bin \ q19ddec cat
 \ decbir_tim1 conts \ q20sec bin \ dur_stage2 conts \ q21secfet bin \ q22path bin \ q22binfo bin \ q22cdoc bin \
q22ddec cat \ decbir_tim2 conts \ lol conts \ adm_birth conts \ los conts \ q24mode cat \
q24indi___1 bin \ q24indi___2 bin \ q24indi___3 bin \ q24indi___4 bin \ q24indi___5 bin \ q24indi___6 bin \ q24indi___7
 bin \ q24indi___8 bin \ q24indi___9 bin \   q24indi___10 bin \   q24indi___11 bin \   q24indi___12 bin \   q24indi___13
 bin \   q24indi___14 bin \ q24indi___15 bin) format(%9.1fc) missing onecol saving(Results_Table1.xlsx, sheet(
"Table2", replace))
*/

**Ind 6: Resuscitation for babies with APGAR < 7
gen resapg2 = .
replace resapg2 = 1 if q32res==1 & q30apg<7
replace resapg2 = 0 if q32res!=1 & q30apg<7

**ACTIVE MANAGEMENT OF THIRD STAGE/EARLY NEWBORN CARE
**Ind 8: Breastfeeding within 1 h
gen q36breast_p2 = 0
replace q36breast_p2 = 1 if q36bfe==1 & q27out == 1

**QUALITY IMPROVEMENT
**Ind 9: Fresh stillbirth with a positive heartbeat at admission
gen freshheart2 = .
replace freshheart2 = 1 if q16fet==1 & q27out==2
replace freshheart2 = 0 if q16fet!=1 & q27out==2
label variable resapg2 "Resuscitation for babies with APGAR < 7"
label variable q36breast_p2 "Breastfeeding within 1 hour"
label variable freshheart2 "Fresh stillbirth with a positive heartbeat at admission"

*Mode of delivery
tab q24mode
lab var q24mode "Mode of delivery"


table1, by(count) vars(resapg2 bin \ q36breast_p2 bin \ freshheart2 bin \ q24mode cat ) format(%9.1fc) missing onecol saving(
Results_Table1.xlsx, sheet("Table2_process_baby", replace))

table1, by(treat) vars(resapg2 bin \ q36breast_p2 bin \ freshheart2 bin \ q24mode cat ) format(%9.1fc) missing onecol saving(
Results_Table1.xlsx, sheet("Table2b_process_baby", replace))







x
**# regression
// outcome 1 - fsb Fresh stillbirths
// outcome 2 - eperi early perinatal mortality
// outcome 3 - lowapg low apgar score (<7)
// outcome 4 - seizures seizures
// outcome 5 - CS Caesarean section
// outcome 6 - matmorb Severe Maternal morbidity //Maternal
// outcome 7 - fetdist fetal distress
// outcome 8 - Responsiveness //Maternal
// outcome 9 - Mistreatment //Maternal
// outcome 10 - q36breast_p2 Breastfeeding



gen time2 = time3
```

```
**# FRESH STILLBIRTHS
tempname memhold
**# Bookmark #2
postfile `memhold' hospn treat_beta treat_se pvalue using "outcomex.dta", replace
forval j=11/44 {
capture noisily melogit q20sec i.treat i.time2 i.group if hospn==`j' || group: , or
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

postfile `memhold' hosp treat_beta treat_se pvalue using "outcome5a.dta", replace
forval j=11/44 {
capture noisily xtlogit CS i.period i.treat if hosp==`j', pa i(id2) corr(exchangeable) vce(robust)
or
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc


Applied

gen id = alert_id
replace id = subinstr(id, "-", "", .)
replace id = subinstr(id, "/", "", .)

alert_id
344-504613
344-5-04613
344-504613
344-5-04613

alert_id
111-5-00980
1115-00980
111-5-00980
1115-00980

gen id2 = real(id)
gen last5 = substr(alert_id, strlen(alert_id) - 4, 5)
gen last

tempname memhold
postfile `memhold' hospn treat_beta treat_se pvalue using "outcome5a.dta", replace

forval j=1/16 {
    capture noisily {
        xtgee CS i.treat if hp==`j', i(id2) family(binomial 1) link(log) ///
                corr(exchangeable) vce(robust)
                *set trace on
                matrix b = e(b)
```

```
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see')
                }

}
postclose `memhold'


tempname memhold
postfile `memhold' hospn treat_beta treat_se pvalue using "outcome5a.dta", replace

* Loop through each hospital to fit the model and store results
forval j=1/16 {
    * Check if there is data for the current hospital
    count if hp == `j'
    if r(N) > 0 {
        capture noisily {
            xtgee CS i.treat if hp==`j', i(id2) family(binomial 1) link(log) ///
                corr(exchangeable) vce(robust)
            if _rc == 0 {
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])

                * Calculate p-value (assuming z-test)
                local z = `beta' / `see'
                local pvalue = 2 * (1 - normal(abs(`z')))

                post `memhold' (`j') (`beta') (`see') (`pvalue')
            }
        }
    }
}

postclose `memhold'

* Display the results
use "outcome5a.dta", clear
list



. table hospn time2, statistic(sum NRecords )
. table hospn time2, statistic(sum fsb )
. table hospn time2, statistic(mean fsb )

gen type = .
recode type .=1 if q27out==1
recode type .=2 if fsb==1
tab type
tab q27out fsb
gen type2 =.
recode type2 .=1 if q27out==1
recode type2 .=2 if eperi==1
mean fsb if inrange(type,1,2), over(hospn)
mean eperi if inrange(type2,1,2), over(hospn)
mean lowapg , over(hospn)
mean seizures, over(hospn)
mean CS, over(hospn)
mean matmorb, over(hospn)
mean fetdist, over(hospn)
mean fetdist, over(hospn)
mean q36breast_p2, over(hospn)
```

```
847
848  tabstat q36breast_p2, statistic(mean) by(hospn)
849
850  use "C:\Users\eidejwai\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
     plan\2023_09_04_DATA\outcome4.dta", clear
851
852  label define hospn 11 "1.1 DeZone Come-Grand Popo" 12 "1.2 Centre et Dépt Zou-Collines" 13 "1.3
     Centre National Hubert Maga" 14 "1.4 Policlinique Bon Samaritan" 21 "2.1 Mchinji" 22 "2.2 Ntcheu D"
      23 "2.3 Mitundu Rural" 24 "2.4 St Gabriels" 31 "3.1 Ndanda" 32 "3.2 Mkomaindo" 33 "3.3 Nachingwea"
      34 "3.4 Newala district" 41 "4.1 Jinja Regional" 42 "4.2 Kamuli Mission " 43 "4.3 Iganga Referral"
      44 "4.4 Bugiri General"
853  lab val hospn hospn
854  label var CS_rate "CS Rate"
855  label var hospn "Hospital"
856  label var pvalue "P-value"
857  label var var13 "P-value"
858
859  replace pvalue = round(pvalue,0.0001)
860
861  format %9.4f pvalue
862
863  **# Forest Plot
864  metan treat_beta treat_se, eform fixedi ///
865      lcols(hospn CS_rate) astext (60) favours (Other modes of delivery # CS mode of delivery) rcols(
     var13)   textsize(120) boxsca(80) xsize(8) ysize(6) ///
866      t1(Difference between CS rate by hospital) ///
867      caption("Adjusted for time")
868
869  *Collapsing to obtain numbers per month and hospital
870  collapse (sum) LBW Alive FSB MSB Singleton Twin Triplet SVD CS Vacuum Forceps Breech, by(months
     month hospnam)
871  drop if month==.
872  frame put hospnam month months LBW Alive FSB MSB Singleton Twin Triplet SVD CS Vacuum Forceps
     Breech, into(ALERT)
873
874
875
876
877
878  **# CS rate
879  use allcountriesclean2Jan24.dta, clear
880
881  **# Dates
882  *Creating a stata readable date
883      gen date = dofc(q1date)
884      format date %td
885  *Converting date into stata weeks of the year
886      gen weeks = wofd(date)
887      format weeks %tw
888
889      gen months = mofd(date)
890      format months %tm
891
892      gen qtr3 = qofd((date))
893      format qtr3 %tq
894
895  **# WOMAN LEVEL
896  **# Number of records/Deliveries
897      gen NRecords = 1
898
899  **# Bookmark #15
900          label define country 1 " Benin" 2 "Malawi" 3 "Tanzania" 4 "Uganda"
901          label values count country
902  **# Number of records by hospital by months
903
904  *Cleaning and keeping only 30 months from July 2021 to December 2023
```

```
905
906
907   drop if months==. | hospn==29 | months==m(2020m6) | !inrange(month,7,36)
908   duplicates tag hospn month, gen(dups) // Checking for multiple months
909   drop dups
910
911   egen mean_CS = mean(CS), by(months)
912
913   collapse (sum) CS NRecords, by( months hospn)
914
915   * Calculate the proportion CS as a percentage of NRecords
916   gen CS_percentage = (CS / NRecords) * 100
917
918   * Calculate lower and upper bounds for the 95% confidence interval
919   gen lower_CI = CS_percentage - 1.96 * sqrt((CS_percentage/100) * (1 - (CS_percentage/100)) /
      NRecords)
920   gen upper_CI = CS_percentage + 1.96 * sqrt((CS_percentage/100) * (1 - (CS_percentage/100)) /
      NRecords)
921
922   graph twoway (mspline CS months) if months>733 & months<764, by(hospn)
923    graph twoway (mspline CS_percentage months) if months>733 & months<764, by(hospn)
924
925   **# Maternal Morbidity rate
926   use allcountriesclean2Jan24.dta, clear
927
928   **# Dates
929   *Creating a stata readable date
930       gen date = dofc(q1date)
931       format date %td
932   *Converting date into stata weeks of the year
933       gen weeks = wofd(date)
934       format weeks %tw
935
936       gen months = mofd(date)
937       format months %tm
938
939       gen qtr3 = qofd((date))
940       format qtr3 %tq
941
942   **# WOMAN LEVEL
943   **# Number of records/Deliveries
944       gen NRecords = 1
945
946   **# Bookmark #15
947           label define country 1 " Benin" 2 "Malawi" 3 "Tanzania" 4 "Uganda"
948           label values count country
949   **# Number of records by hospital by months
950
951   *Cleaning and keeping only 30 months from July 2021 to December 2023
952
953
954   drop if months==. | hospn==29 | months==m(2020m6) | !inrange(month,7,36)
955   duplicates tag hospn month, gen(dups) // Checking for multiple months
956   drop dups
957
958   egen mean_MM = mean(matmorb), by(months)
959
960   collapse (sum) matmorb NRecords, by( months hospn)
961
962   * Calculate the proportion CS as a percentage of NRecords
963   gen MM_percentage = (matmorb / NRecords) * 100
964
965   * Calculate lower and upper bounds for the 95% confidence interval
966   gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
      NRecords)
967   gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
```

```
NRecords)

graph twoway (mspline matmorb months) if months>733 & months<764, by(hospn)
 graph twoway (mspline MM_percentage months) if months>733 & months<764, by(hospn)

 // outcome 1 - fsb Fresh stillbirths //
 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear
 egen mean_MM = mean(fsb), by(months)

collapse (sum) fsb NRecords, by( hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (fsb / NRecords) * 1000

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)

*graph twoway (mspline fsb months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)


// outcome 2 - eperi early perinatal mortality //
 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear
 egen mean_MM = mean(eperi), by(months)

collapse (sum) eperi NRecords, by(months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (eperi / NRecords) * 1000

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)

*graph twoway (mspline fsb months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)

// outcome 3 - lowapg low apgar score (<7) //
 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear
 egen mean_MM = mean(lowapg), by(months)

collapse (sum) lowapg NRecords, by(months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (lowapg / NRecords) * 1000

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)

*graph twoway (mspline fsb months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)

// outcome 4 - Neonatal seizures seizures ///
 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear
 egen mean_MM = mean(seizure), by(months)

collapse (sum) seizure NRecords, by(months hosp)
```

```
1027  * Calculate the proportion CS as a percentage of NRecords
1028  gen MM_percentage = (seizures / NRecords) * 1000
1029
1030  * Calculate lower and upper bounds for the 95% confidence interval
1031  gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
      NRecords)
1032  gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
      NRecords)
1033
1034  *graph twoway (mspline fsb months), by(hosp)
1035   graph twoway (mspline MM_percentage months), by(hosp)
1036
1037  // outcome 5 - CS Caesarean section ///
1038   use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
      paper\Child_level.dta", clear
1039   egen mean_MM = mean(CS), by(months)
1040
1041  collapse (sum) CS NRecords, by( months hosp)
1042
1043  * Calculate the proportion CS as a percentage of NRecords
1044  gen MM_percentage = (CS / NRecords) * 100
1045
1046  * Calculate lower and upper bounds for the 95% confidence interval
1047  gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
      NRecords)
1048  gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
      NRecords)
1049  graph twoway (mspline CS months), by(hosp)
1050   graph twoway (mspline MM_percentage months), by(hosp)
1051
1052  // outcome XX - matmorb Severe Maternal morbidity //Maternal
1053   use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
      paper\Mother_level.dta", clear
1054   egen mean_MM = mean(matmorb), by(months)
1055
1056  collapse (sum) matmorb NRecords, by( months hosp)
1057
1058  * Calculate the proportion CS as a percentage of NRecords
1059  gen MM_percentage = (matmorb / NRecords) * 1000
1060
1061  * Calculate lower and upper bounds for the 95% confidence interval
1062  gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
      NRecords)
1063  gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
      NRecords)
1064  *graph twoway (mspline matmorb months), by(hosp)
1065   graph twoway (mspline MM_percentage months), by(hosp)
1066
1067
1068  // outcome XX - RESPONSIVENESS //Maternal EXIT /// Responsiveness_FS_finalscore
      Mistreatment_FS_finalscore immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
1069  use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
      plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1070  drop if months<m(2021m1)
1071  gen NRecords = 1
1072
1073   egen mean_MM = mean(Responsiveness_FS_finalscore), by(months hosp)
1074
1075  *graph twoway (mspline matmorb months), by(hosp)
1076   graph twoway (mspline mean_MM months), by(hosp)
1077
1078  // outcome XX - MISTREATMENT //Maternal EXIT /// Responsiveness_FS_finalscore
      Mistreatment_FS_finalscore immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
1079  use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
      plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1080  drop if months<m(2021m1)
```

```
gen NRecords = 1

 egen mean_MM = mean(Mistreatment_FS_finalscore), by(months hosp)

*graph twoway (mspline matmorb months), by(hosp)
 graph twoway (mspline mean_MM months), by(hosp)




// - Fetal heart check on admission rate (per 100) change over time by hospital
 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Mother_level.dta", clear
 egen mean_MM = mean(q16fet_p), by(months)

collapse (sum) q16fet_p NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (q16fet_p / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
graph twoway (mspline q16fet_p months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)



///* Fetal monitoring done and documented in 1st stage of labour q18_0fhmeas_p

 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Mother_level.dta", clear
 egen mean_MM = mean(q18_0fhmeas_p), by(months)

collapse (sum) q18_0fhmeas_p NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (q18_0fhmeas_p / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
*graph twoway (mspline matmorb months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)


/// Fetal monitoring done in 2nd stage  q21secfet_p

  use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Mother_level.dta", clear
 egen mean_MM = mean(q21secfet_p), by(months)

collapse (sum) q21secfet_p NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (q21secfet_p / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
```

```
*graph twoway (mspline matmorb months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)

 //Resuscitation for babies with APGAR < 7 resapg2
 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear

 egen mean_MM = mean(resapg2), by(months)

collapse (sum) resapg2 NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (resapg2 / NRecords) * 1000

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) / NRecords)
*graph twoway (mspline resapg2 months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)

 /// COMPANION PRESENT DURING LABOUR - eregistry  q39comp1_p

  use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Mother_level.dta", clear
 egen mean_MM = mean(q39comp1_p), by(months)

collapse (sum) q39comp1_p NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (q39comp1_p / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
*graph twoway (mspline matmorb months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)

  /// COMPANION PRESENT DURING birth - eregistry  q39comp2_p

  use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Mother_level.dta", clear
 egen mean_MM = mean(q39comp2_p), by(months)

collapse (sum) q39comp2_p NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (q39comp2_p / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
*graph twoway (mspline matmorb months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)



/// COMPANION PRESENT DURING LABOUR Responsiveness_FS_finalscore Mistreatment_FS_finalscore immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
```

```
drop if months<m(2021m1)
gen NRecords = 1

 egen mean_MM = mean(s7q1_comp_cat), by(months)

collapse (sum) s7q1_comp_cat NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (s7q1_comp_cat / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
*graph twoway (mspline resapg2 months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)

/// COMPANION PRESENT DURING BIRTHS Responsiveness_FS_finalscore Mistreatment_FS_finalscore immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
drop if months<m(2021m1)
gen NRecords = 1

 egen mean_MM = mean(s7q2_stay_cat), by(months)

collapse (sum) s7q2_stay_cat NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (s7q2_stay_cat / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
*graph twoway (mspline resapg2 months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)



///EARLY AMBULATION Responsiveness_FS_finalscore Mistreatment_FS_finalscore immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
drop if months<m(2021m1)
gen NRecords = 1

 egen mean_MM = mean(early_ambulat), by(months)

collapse (sum) early_ambulat NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (early_ambulat / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
*graph twoway (mspline resapg2 months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)
```

```
///BREASTFEEDING WITHIN 1 HOUR immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
drop if months<m(2021m1)
gen NRecords = 1

 egen mean_MM = mean(immediate_feed), by(months)

collapse (sum) immediate_feed NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (immediate_feed / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
*graph twoway (mspline resapg2 months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)



// outcome 7 - fetdist fetal distress
 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear
 egen mean_MM = mean(fetdist), by(months)

collapse (sum) fetdist NRecords, by( months hosp)

* Calculate the proportion CS as a percentage of NRecords
gen MM_percentage = (fetdist / NRecords) * 100

* Calculate lower and upper bounds for the 95% confidence interval
gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) / NRecords)
graph twoway (mspline fetdist months), by(hosp)
 graph twoway (mspline MM_percentage months), by(hosp)




*use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
    gen date = dofc(s1q2_doi)
    format date %td
*Converting date into stata weeks of the year
    gen weeks = wofd(date)
    format weeks %tw

    gen months = mofd(date)
    format months %tm

    gen qtr3 = qofd((date))
    format qtr3 %tq

**# Number of records by hospital by months

*Cleaning and keeping only 30 months from July 2021 to December 2023


//drop if months==. | months<m(2021m3)
```

```
duplicates tag hospnam month, gen(dups) // Checking for multiple months
drop dups

**Anonymised hospital names

gen hosp = "Benin-Hospital-1" if hospnam==1
replace hosp = "Benin-Hospital-2" if hospnam==2
replace hosp = "Benin-Hospital-3" if hospnam==3
replace hosp = "Benin-Hospital-4" if hospnam==4
replace hosp = "Malawi-Hospital-1" if hospnam==5
replace hosp = "Malawi-Hospital-2" if hospnam==6
replace hosp = "Malawi-Hospital-3" if hospnam==7
replace hosp = "Malawi-Hospital-4" if hospnam==8
replace hosp = "Tanzania-Hospital-1" if hospnam==9
replace hosp = "Tanzania-Hospital-2" if hospnam==10
replace hosp = "Tanzania-Hospital-3" if hospnam==11
replace hosp = "Tanzania-Hospital-4" if hospnam==12
replace hosp = "Uganda-Hospital-1" if hospnam==13
replace hosp = "Uganda-Hospital-2" if hospnam==14
replace hosp = "Uganda-Hospital-3" if hospnam==15
replace hosp = "Uganda-Hospital-4" if hospnam==16

/*
gen hp =.
replace hp = 1 if hospn==11
replace hp = 2 if hospn==12
replace hp = 3 if hospn==13
replace hp = 4 if hospn==14
replace hp = 5 if hospn==21
replace hp = 6 if hospn==22
replace hp = 7 if hospn==23
replace hp = 8 if hospn==24
replace hp = 9 if hospn==31
replace hp = 10 if hospn==32
replace hp = 11 if hospn==33
replace hp = 12 if hospn==34
replace hp = 13 if hospn==41
replace hp = 14 if hospn==42
replace hp = 15 if hospn==43
replace hp = 16 if hospn==44
*/

**# Randomisation
gen group = 1 if hospnam==1 | hospnam==5 | hospnam==9 | hospnam==13
replace group = 2 if hospnam==2 | hospnam==6 | hospnam==10 | hospnam==14
replace group = 3 if hospnam==3 | hospnam==7 | hospnam==11 | hospnam==15
replace group = 4 if hospnam==4 | hospnam==8 | hospnam==12 | hospnam==16


**# Intervention
gen hosp1_intervention = round==2 //jan2022
gen hosp2_intervention = round==3 //jul2022
gen hosp3_intervention = round==4 //jan2023
gen hosp4_intervention = round==5 //jul2023

gen intervention2 = 0
replace intervention2 = 1 if hosp1_intervention==1
replace intervention2 = 2 if hosp1_intervention==1 & hosp2_intervention==1
replace intervention2 = 3 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1
replace intervention2 = 4 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1
& hosp4_intervention==1

label define intervention2 0 "No intervention" 1 "Hosp 1" 2 "Hosp 1,2" 3 "Hosp 1,2,3" 4 "Hosp
1,2,3,4"
label values intervention2 intervention2
tab intervention2 round
```

```
1371
1372
1373    **# Treatment variable
1374    //ren time2 time
1375    generate byte has_been_treated1 = 0
1376    replace has_been_treated1 = 1 if round ==2 & group ==1 ///
1377        | round ==3 & inlist(group, 1,2) | round ==4 & inlist(group,1,2,3) | round ==5
1378
1379    generate byte has_been_treated2 = 0
1380    replace has_been_treated2 = 1 if round ==2 & group ==1 ///
1381        | round ==3 & inlist(group, 1,2) | round ==4 & inlist(group,1,2,3) | round ==5
1382
1383
1384    . table hospn time, statistic(mean has_been_treated1) nototal
1385    . table hospn time3, statistic(mean has_been_treated2) nototal
1386
1387    ren has_been_treated2 treat
1388
1389    // outcome 8 - Responsiveness_FS_finalscore Responsiveness //Maternal
1390    hist Responsiveness_FS_finalscore, normal
1391    tabstat Responsiveness_FS_finalscore, statistic(mean sd p50 p25 p75 n) by(country)
1392    tabstat Responsiveness_FS_finalscore, statistic(mean sd p50 p25 p75 n) by(treat)
1393
1394    // outcome 9 - Mistreatment_FS_finalscore Mistreatment //Maternal
1395    tabstat Mistreatment_FS_finalscore, statistic(mean sd)
1396    hist Mistreatment_FS_finalscore, normal
1397    tabstat Mistreatment_FS_finalscore, statistic(mean sd p50 p25 p75 n) by(country)
1398    tabstat Mistreatment_FS_finalscore, statistic(mean sd p50 p25 p75 n) by(treat)
1399
1400    ***Overall score   overall_FS_finalscore
1401    hist overall_FS_finalscore
1402    tabstat overall_FS_finalscore, statistic(mean sd p50 p25 p75 n) by(country)
1403    tabstat overall_FS_finalscore, statistic(mean sd p50 p25 p75 n) by(treat)
1404
1405    drop
1406    merge 1:1 alert_id using "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
        plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta",keepusing(s7q1_comp_cat s7q2_stay_cat
        early_ambulat immediate_feed)
1407
1408    // outcome 10 - immediate_feed Breastfeeding
1409    ta immediate_feed
1410     ta immediate_feed country, col mi
1411    ta immediate_feed treat, col mi
1412
1413    // outcome - Companion
1414    **Ind 7a: Was a companion present during labour
1415    ta s7q1_comp_cat, nol
1416    recode s7q1_comp_cat 2=.
1417
1418    ta s7q1_comp_cat country, col mi
1419    ta s7q1_comp_cat treat, col mi
1420    ** 7b: Companion during birth
1421    ta s7q2_stay_cat, nol
1422    recode s7q2_stay_cat 2=.
1423
1424    ta s7q2_stay_cat country, col mi
1425    ta s7q2_stay_cat treat, col mi
1426
1427
1428    ***Early Ambulation - Exit
1429     ta s6q3_walk
1430     recode s6q3_walk (0=0 "No") (1/3 = 1 "Yes") (4=.), gen(early_ambulat) lab(early_ambulat)
1431
1432     ta early_ambulat country, col mi
1433    ta early_ambulat treat, col mi
1434
```

```
1435
1436
1437    *REGRESSION
1438    cd "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\"
1439
1440   use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
       paper\Child_level.dta", clear
1441    use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
       paper\Mother_level.dta", clear
1442    **# regression
1443   // outcome 1 - fsb Fresh stillbirths
1444   // outcome 2 - eperi early perinatal mortality
1445   // outcome 3 - lowapg low apgar score (<7)
1446   // outcome 4 - seizures seizures
1447   // outcome 5 - CS Caesarean section
1448   // outcome 6 - matmorb Severe Maternal morbidity //Maternal
1449   // outcome 7 - fetdist fetal distress
1450   // outcome 8 - Responsiveness //Maternal - Responsiveness_FS_finalscore -  - Exit interview
1451   // outcome 9 - Mistreatment //Maternal - Mistreatment_FS_finalscore -  - Exit interview
1452   // outcome X - fetal heart check on admission
1453   // outcome X - fetal monitoring done and documentated in 1st stage of labour
1454   // outcome x - fetal monitoring done in 2nd staGE
1455   // outcome x - resapg2 Resuscitation for babies with APGAR <7
1456   // outcome 11a - q39comp1_p companion labour1
1457   // outcome 12a - q39comp2_p companion birth1
1458   // outcome 11b - companion labour2 - s7q1_comp_cat  - Exit interview
1459   // outcome 12b - companion birth2 - s7q2_stay_cat  - Exit interview
1460   // outcome 13 - early ambulation early_ambulat  - Exit interview
1461   // outcome 10 - q36breast_p2 Breastfeeding  - Exit interview
1462   // outcome X - q36breast_p2 immediate_feed for exit  - Exit interview
1463
1464
1465   ///PER PROTOCOL ANALYSIS
1466   **# FRESH STILLBIRTHS
1467   // outcome 1 - fsb Fresh stillbirths
1468
1469   tempname memhold
1470
1471   **# Bookmark #2
1472   postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome5_PerProtocol.dta", replace
       //outcome1_new
1473   forval j=11/44 {
1474   capture noisily melogit CS i.has_been_treated3 i.perprotocol i.group if hospn==`j' || group: , or
1475   //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
       group:, cov(ex)
1476       *set trace on
1477                   matrix p  = e(p)
1478                   local pval = p[1,1]
1479                   matrix b = e(b)
1480                   local beta = b[1,2]
1481                   matrix v = e(V)
1482                   local see = sqrt(v[2,2])
1483                   post `memhold' (`j') (`beta') (`see') (`pval')
1484                   }
1485   postclose `memhold'
1486   estat icc
1487
1488   tabstat fsb, stat(mean) by(hosp)
1489   tabstat eperi, stat(mean) by(hosp)
1490   tabstat lowapg, stat(mean) by(hosp)
1491   tabstat CS, stat(mean) by(hosp)
1492
1493
1494
1495
1496
```

```
1497
1498
1499  ///ITT ANALYSIS
1500
1501  gen time2 = time3
1502
1503  **# FRESH STILLBIRTHS
1504  // outcome 1 - fsb Fresh stillbirths
1505
1506  tempname memhold
1507
1508  **# Bookmark #2
1509  postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome1_SENSITIVITY.dta", replace
      //outcome1_new
1510  forval j=11/44 {
1511  capture noisily melogit fsb i.treat i.time3 i.group if hospn==`j' & hospn!=33 || group: , or
1512  //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
      group:, cov(ex)
1513      *set trace on
1514                  matrix p  = e(p)
1515                  local pval = p[1,1]
1516                  matrix b = e(b)
1517                  local beta = b[1,2]
1518                  matrix v = e(V)
1519                  local see = sqrt(v[2,2])
1520                  post `memhold' (`j') (`beta') (`see') (`pval')
1521                  }
1522  postclose `memhold'
1523  estat icc
1524
1525  tabstat fsb if, stat(mean) by(hosp)
1526
1527
1528  tempname memhold
1529
1530  **# Bookmark #2
1531  postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome5a_SENSITIVITY2.dta", replace
      //outcome1_new
1532  forval j=11/44 {
1533  capture noisily melogit CS i.treat i.time3 i.group if hospn==`j' & hospn!=33 || group: , or
1534  //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
      group:, cov(ex)
1535      *set trace on
1536                  matrix p  = e(p)
1537                  local pval = p[1,1]
1538                  matrix b = e(b)
1539                  local beta = b[1,2]
1540                  matrix v = e(V)
1541                  local see = sqrt(v[2,2])
1542                  post `memhold' (`j') (`beta') (`see') (`pval')
1543                  }
1544  postclose `memhold'
1545  estat icc
1546
1547
1548  tempname memhold
1549  **# Bookmark #2
1550  postfile `memhold' hosp treat_beta treat_se pvalue using "outcome5a.dta", replace
1551  forval j=11/44 {
1552  capture noisily xtlogit CS i.period i.treat if hosp==`j', pa i(id2) corr(exchangeable) vce(robust)
      or
1553      *set trace on
1554                  matrix p  = e(p)
1555                  local pval = p[1,1]
1556                  matrix b = e(b)
1557                  local beta = b[1,2]
```

```
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

**# Bookmark #2
postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome5a_SENSITIVITY.dta", replace
forval j=11/44 {
capture noisily melogit CS i.treat i.time3 i.group if hospn==`j' & hospn!=23 || group: , or
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc


// outcome 2 - eperi early perinatal mortality
tempname memhold

**# Bookmark #2
postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome2_newMAY.dta", replace
forval j=11/44 {
capture noisily melogit eperi i.treat i.time3 i.group if hospn==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

tabstat eperi, stat(mean) by(hosp)

// outcome 3 - lowapg low apgar score (<7)
tempname memhold

**# Bookmark #2
postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome3_new22.dta", replace
forval j=11/44 {
capture noisily melogit lowapg i.treat i.time3 i.group if hospn==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
```

```
estat icc

tabstat lowapg, stat(mean) by(hosp)


// outcome 4 - seizures seizures
tempname memhold

**# Bookmark #2
postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome4_new.dta", replace
forval j=11/44 {
capture noisily melogit seizures i.treat i.time3 i.group if hospn==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

tabstat seizures, stat(mean) by(hosp)

// outcome 5 - CS Caesarean section
tabstat CS, stat(mean) by(hosp)


// outcome 6 - fetdist fetal distress
tabstat fetdist, stat(mean) by(hosp)




// outcome 10 - matmorb Severe Maternal morbidity //Maternal
use Mother_level, clear

tempname memhold

**# Bookmark #2
postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome10_new.dta", replace
forval j=11/44 {
capture noisily melogit matmorb i.treat i.time3 i.group if hospn==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

tabstat matmorb, stat(mean) by(hosp)



// outcome 8 - Responsiveness //Maternal exit interviews - Responsiveness_FS_finalscore
```

```
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear

tempname memhold

**# Bookmark #2
postfile `memhold' hospnam treat_beta treat_se pvalue using "outcomeX_responsive_NEW.dta", replace
forval j=1/16 {
//capture noisily melogit s7q2_stay_cat i.treat i.round i.group if hospn==`j' || group: , or
capture noisily mixed Responsiveness_FS_finalscore i.treat i.round i.group if hospnam==`j' || group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

tabstat Responsiveness_FS_finalscore, stat(mean) by(hosp)
// outcome 9 - Mistreatment //Maternal exit interviews
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear

tempname memhold

**# Bookmark #2
postfile `memhold' hospnam treat_beta treat_se pvalue using "outcomeX_mistreatment_NEW.dta", replace
forval j=1/16 {
//capture noisily melogit s7q2_stay_cat i.treat i.round i.group if hospn==`j' || group: , or
capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' || group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

tabstat Mistreatment_FS_finalscore, stat(mean) by(hosp)

// outcome X - fetal heart check on admission - q16fet_p
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Mother_level.dta", clear

recode hospn 11=1 12=2 13=3 14=4 21=5 22=6 23=7 24=8 31=9 32=10 33=11 34=12 41=13 42=14 43=15 44=16, gen(hh)

tempname memhold

**# Bookmark #2
postfile `memhold' hh treat_beta treat_se pvalue using "outcomex_fetalheart_admiss.dta", replace
forval j=1/16 {
capture noisily melogit q16fet_p i.treat i.time3 i.group if hh==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' || group:, cov(ex)
```

```
1744        *set trace on
1745                    matrix p  = e(p)
1746                    local pval = p[1,1]
1747                    matrix b = e(b)
1748                    local beta = b[1,2]
1749                    matrix v = e(V)
1750                    local see = sqrt(v[2,2])
1751                    post `memhold' (`j') (`beta') (`see') (`pval')
1752                    }
1753    postclose `memhold'
1754    estat icc
1755
1756    tabstat q16fet_p, stat(mean) by(hosp)
1757
1758
1759    XXXX
1760    tempname memhold
1761
1762    **# Bookmark #2
1763    postfile `memhold' hospn treat_beta treat_se pvalue using "outcomex_fetalheart_check_NEW.dta",
        replace
1764    forval j=11/44 {
1765    capture noisily melogit q16fet_p i.treat i.time3 i.group if hospn==`j' || group: , or
1766    //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
        group:, cov(ex)
1767        *set trace on
1768                    matrix p  = e(p)
1769                    local pval = p[1,1]
1770                    matrix b = e(b)
1771                    local beta = b[1,2]
1772                    matrix v = e(V)
1773                    local see = sqrt(v[2,2])
1774                    post `memhold' (`j') (`beta') (`see') (`pval')
1775                    }
1776    postclose `memhold'
1777    estat icc
1778
1779    tabstat q16fet_p, stat(mean) by(hosp)
1780
1781
1782    XXXX
1783
1784    // outcome X - fetal monitoring done and documentated in 1st stage of labour - q18_0fhmeas_p
1785    use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
        paper\Mother_level.dta", clear
1786
1787    recode hospn 11=1 12=2 13=3 14=4 21=5 22=6 23=7 24=8 31=9 32=10 33=11 34=12 41=13 42=14 43=15 44=16
        , gen(hh)
1788
1789    tempname memhold
1790
1791    **# Bookmark #2
1792    postfile `memhold' hh treat_beta treat_se pvalue using "outcomex_fetmon_1ststage.dta", replace
1793    forval j=1/16 {
1794    capture noisily melogit q18_0fhmeas_p i.treat i.time3 i.group if hh==`j' || group: , or
1795    //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
        group:, cov(ex)
1796        *set trace on
1797                    matrix p  = e(p)
1798                    local pval = p[1,1]
1799                    matrix b = e(b)
1800                    local beta = b[1,2]
1801                    matrix v = e(V)
1802                    local see = sqrt(v[2,2])
1803                    post `memhold' (`j') (`beta') (`see') (`pval')
1804                    }
```

```
postclose `memhold'
estat icc

tabstat q18_0fhmeas_p, stat(mean) by(hosp)


// outcome x - fetal monitoring done in 2nd staGE
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Mother_level.dta", clear

recode hospn 11=1 12=2 13=3 14=4 21=5 22=6 23=7 24=8 31=9 32=10 33=11 34=12 41=13 42=14 43=15 44=16 , gen(hh)

tempname memhold

**# Bookmark #2
postfile `memhold' hh treat_beta treat_se pvalue using "outcomex_fetmon_2ndstage3.dta", replace
forval j=1/16 {
capture noisily melogit q21secfet i.treat i.time3 i.group if hh==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' || group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

tabstat q21secfet, stat(mean) by(hosp)




// outcome x - Resuscitation for babies with APGAR <7 - resapg2
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear

recode hospn 11=1 12=2 13=3 14=4 21=5 22=6 23=7 24=8 31=9 32=10 33=11 34=12 41=13 42=14 43=15 44=16 , gen(hh)

tempname memhold

**# Bookmark #2
postfile `memhold' hh treat_beta treat_se pvalue using "outcomex_resusitation.dta", replace
forval j=1/16 {
capture noisily melogit resapg2 i.treat i.time3 i.group if hh==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' || group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat icc

tabstat resapg2, stat(mean) by(hosp)
```

```
1865
1866
1867  // outcome 11a - q39comp1_p companion labour1
1868  tempname memhold
1869
1870  **# Bookmark #2
1871  postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome11a_new.dta", replace
1872  forval j=11/44 {
1873  capture noisily melogit q39comp1_p i.treat i.time3 i.group if hospn==`j' || group: , or
1874  //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
      group:, cov(ex)
1875      *set trace on
1876                  matrix p  = e(p)
1877                  local pval = p[1,1]
1878                  matrix b = e(b)
1879                  local beta = b[1,2]
1880                  matrix v = e(V)
1881                  local see = sqrt(v[2,2])
1882                  post `memhold' (`j') (`beta') (`see') (`pval')
1883                  }
1884  postclose `memhold'
1885  estat icc
1886
1887  tabstat q39comp1_p, stat(mean) by(hosp)
1888
1889
1890  // outcome 12a - q39comp2_p companion birth1
1891  tempname memhold
1892
1893  **# Bookmark #2
1894  postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome12a_new.dta", replace
1895  forval j=11/44 {
1896  capture noisily melogit q39comp2_p i.treat i.time3 i.group if hospn==`j' || group: , or
1897  //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
      group:, cov(ex)
1898      *set trace on
1899                  matrix p  = e(p)
1900                  local pval = p[1,1]
1901                  matrix b = e(b)
1902                  local beta = b[1,2]
1903                  matrix v = e(V)
1904                  local see = sqrt(v[2,2])
1905                  post `memhold' (`j') (`beta') (`see') (`pval')
1906                  }
1907  postclose `memhold'
1908  estat icc
1909
1910  tabstat q39comp2_p, stat(mean) by(hosp)
1911  // outcome 11b - companion labour2 - Exit interviews
1912  use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
      plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1913
1914  tempname memhold
1915
1916  **# Bookmark #2
1917  postfile `memhold' hospnam treat_beta treat_se pvalue using "outcomeX_companion_1st_New.dta",
      replace
1918  forval j=1/16 {
1919  capture noisily melogit s7q1_comp_cat i.treat i.round i.group if hospn==`j' & !inlist(hospnam,4) ||
       group: , or
1920  //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
      group:, cov(ex)
1921      *set trace on
1922                  matrix p  = e(p)
1923                  local pval = p[1,1]
1924                  matrix b = e(b)
```

```
1925                    local beta = b[1,2]
1926                    matrix v = e(V)
1927                    local see = sqrt(v[2,2])
1928                    post `memhold' (`j') (`beta') (`see') (`pval')
1929                    }
1930    postclose `memhold'
1931    estat icc
1932    table hosp, statistic(percent s7q1_comp_cat)
1933
1934
1935    // outcome 12b - companion birth2 - Exit Interviews
1936    use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
        plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1937
1938    tempname memhold
1939
1940    **# Bookmark #2
1941    postfile `memhold' hospnam treat_beta treat_se pvalue using "outcomeX_companion_2nd_New.dta",
        replace
1942    forval j=1/16 {
1943    capture noisily melogit s7q2_stay_cat i.treat i.round i.group if hospn==`j'& !inlist(hospnam,4) ||
        group: , or
1944    //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
        group:, cov(ex)
1945        *set trace on
1946                    matrix p  = e(p)
1947                    local pval = p[1,1]
1948                    matrix b = e(b)
1949                    local beta = b[1,2]
1950                    matrix v = e(V)
1951                    local see = sqrt(v[2,2])
1952                    post `memhold' (`j') (`beta') (`see') (`pval')
1953                    }
1954    postclose `memhold'
1955    estat icc
1956
1957    tabstat s7q2_stay_cat, stat(mean) by(hosp)
1958    table hosp, statistic(percent s7q2_stay_cat)
1959    // outcome 13 - early ambulation
1960    use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
        plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1961
1962    tempname memhold
1963
1964    **# Bookmark #2
1965    postfile `memhold' hospnam treat_beta treat_se pvalue using "outcomeX_early_ambulat_NEW.dta",
        replace
1966    forval j=1/16 {
1967    capture noisily melogit early_ambulat i.treat i.round i.group if hospn==`j' || group: , or
1968    //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
        group:, cov(ex)
1969        *set trace on
1970                    matrix p  = e(p)
1971                    local pval = p[1,1]
1972                    matrix b = e(b)
1973                    local beta = b[1,2]
1974                    matrix v = e(V)
1975                    local see = sqrt(v[2,2])
1976                    post `memhold' (`j') (`beta') (`see') (`pval')
1977                    }
1978    postclose `memhold'
1979    estat icc
1980
1981    tabstat early_ambulat, stat(mean) by(hosp)
1982    table hosp, statistic(percent early_ambulat)
1983
```

```
// outcome 7 - q36breast_p2 Breastfeeding
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results paper\Child_level.dta", clear

recode hospn 11=1 12=2 13=3 14=4 21=5 22=6 23=7 24=8 31=9 32=10 33=11 34=12 41=13 42=14 43=15 44=16 , gen(hh)

tempname memhold

**# Bookmark #2
postfile `memhold' hh treat_beta treat_se pvalue using "outcome7_new2_CS_birth.dta", replace
forval j=1/16 {
capture noisily melogit q36breast_p2 i.treat i.time3 i.group if hh==`j' & CS==1 || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' || group:, cov(ex)
    *set trace on
                matrix p  = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat ic

tabstat q36breast_p2, stat(mean) by(hosp)

// outcome x - Breastfeeding rate - EXIT INTERVIEWS immediate_feed
use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear

tempname memhold

**# Bookmark #2
postfile `memhold' hosp treat_beta pvalue using "outcomeX_immediatfeed_NEW.dta", replace
forval j=1/16{
capture noisily melogit immediate_feed i.treat i.round i.group if hospn==`j' || group: , or
//capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
    *set trace on
                matrix p = e(p)
                local pval = p[1,1]
                matrix b = e(b)
                local beta = b[1,2]
                matrix v = e(V)
                local see = sqrt(v[2,2])
                post `memhold' (`j') (`beta') (`see') (`pval')
                }
postclose `memhold'
estat ic

table hosp, stat(percent immediate_feed)
tabstat immediate_feed, stat(mean) by(hosp)


 use "C:\Users\eidejwai\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\2023_09_04_DATA\outcome4.dta", clear

label define hospn 11 "1.1 DeZone Comé-Grand Popo" 12 "1.2 Centre Dépt Zou-Collines" 13 "1.3 Centre National Hubert Maga" 14 "1.4 Policlinique Bon Samaritan" 21 "2.1 Mzinga" 22 "2.2 Ntcheu" 23 "2.3 Mitundu" 24 "2.4 St Gabriels" 31 "3.1 Nanda" 32 "3.2 Mkoma" 33 "3.3 Nachingwea" 34 "3.4 Newala" 41 "4.1 Iringa Regional" 42 "4.2 Kalulu" 43 "4.3 Missiga" 44 "4.4 Bugando General"
lab val hospn hospn
label var CS_rate "CS Rate"
label var hospn "Hospital"
```

```
2042  label var pvalue "P-value"
2043  label var var13 "P-value"
2044
2045  replace pvalue = round(pvalue,0.0001)
2046
2047  format %9.4f pvalue
2048
2049  **# Forest Plot
2050  metan treat_beta treat_se, eform fixedi ///
2051      lcols(hospn CS_rate) astext (60) favours (Other modes of delivery # CS mode of delivery) rcols(
      var13)   textsize(120) boxsca(80) xsize(8) ysize(6) ///
2052      t1(Difference between CS rate by hospital) ///
2053      caption("Adjusted for time")
2054
```