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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

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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)

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130 // collapse (sum) NRecords, by(period hospn)
131
132 egen time3 = cut(month), group(5) label //1 missing value created
133
134 *** Randomisation
135 gen group = 1 if hospn==11 | hospn==21 | hospn==31 | hospn==41
136 replace group = 2 if hospn==12 | hospn==22 | hospn==32 | hospn==42
137 replace group = 3 if hospn==13 | hospn==23 | hospn==33 | hospn==43
138 replace group = 4 if hospn==14 | hospn==24 | hospn==34 | hospn==44
139
140
141 *** Intervention
142 gen hosp1_intervention = month>=13 //jan2022
143 gen hosp2_intervention = month>=19 //jul2022
144 gen hosp3_intervention = month>=25 //jan2023
145 gen hosp4_intervention = month>=31 //jul2023
146
147 gen intervention = 0
148 replace intervention = 1 if hosp1_intervention==1
149 replace intervention = 2 if hosp1_intervention==1 & hosp2_intervention==1
150 replace intervention = 3 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1
151 replace intervention = 4 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1 &
  hosp4_intervention==1
152
153 label define intervention 0 "No intervention" 1 "Hosp 1" 2 "Hosp 1,2" 3 "Hosp 1,2,3" 4 "Hosp
  1,2,3,4"
154 label values intervention intervention
155 tab intervention
156
157
158 *** Treatment variable
159 ren time2 time
160 generate byte has_been_treated1 = 0
161 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
162
163
164 generate byte has_been_treated2 = 0
165 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
166
167
168
169 . table hospn time, statistic(mean has_been_treated1) nototal
170 . table hospn time3, statistic(mean has_been_treated2) nototal
171
172 ren has_been_treated2 treat
173
174
175 //PER PROTOCOL ANALYSIS
176 generate byte has_been_treated3 = 0
177 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
178
179
180
181 *** Table 1
182 *** Number of records by hospital by months
183 // collapse (sum) NRecords, by(hosp period)
184 // sort hosp period, stable
185 // drop months
186
187 *** Table 1 Baseline data
188 // keep alert_id hospnam q1date todaydate q2ref q2aqta q2bwhe q3age q4grav q7ces q8anc q9aga
  q10symp q11hiv q12acom q12bcom q12ccom q12dcom q12ecom q12fcom q12gcom q12hcom q12icom q12lcom
  q12mcom q12ncom q13onq q13aaind__1 q13aaind__2 q13aaind__3 q13aaind__4 q13aaind__5 q13aaind__6
  q14acervix q15aug q16fet q17pret q17adex q17cdos q25babies country count hosp hospn hosp2 year
  month week

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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") (1 = 1 "1") (2/4 = 3 "3") (4/5 = 4 "5+"), gen(parity) label(parity)
209
210 **# Previous CS
211 tab q7ces
212
213 **# ANC visits
214 tab q8anc
215 recode q8anc (min/31 ">") (4/14 "4"), gen(ancno) label(ancno)
216
217 **# TESTS AT ANC
218 label define q10syph1 1 "Positive" 2 "Negative" 3 "Not done"
219 format q10syph1 label value Xtests
220 tab q10syph1
221
222 tab q11hiv
223
224 **# Antenatal complications
225 tab1 q12acom q12bcm q12ccom q12dcom 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 q13aimd_1 q13aimd_2 q13aimd_3 q13aimd_4 q13aimd_5 q13aimd_6
233
234 **# Start of labour
235 sort alert_id
236 merge using "\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\TimeofLabour.dta", keep(using time)
237
238 drop _merge
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 \ q10syph cat \
q11hiv cat \ q12acom bin \ q12bcm bin \ q12ccom bin \ q12dcom bin \ q12ecom bin \ q12fcom bin \

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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

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table1, by(count) vars( q3age conts %5.1f \ agemum cat \ q2ref bin \ q2aqta cat \ q2bwhe cat \
q4grav conts %5.1f \ gravity 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))

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table1, by(treat) vars( q3age conts %5.1f \ agemum cat \ q2ref bin \ q2aqta cat \ q2bwhe cat \
q4grav conts %5.1f \ gravity 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))

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#####
*Prepare new variables that indicate number of missing or other property of interest
#####
**ADMISSION STANDARDS AND PROCEDURES
**INDICATOR 1 - appropriate admission standards and procedures
**Ind 1 Q1,2,3,4,8,9,10,11,12

foreach p in q1date q2ref q3age q4grav q8anc q9dob q9aga q10syp /*
  /* q11hiv q12acom q12bcom q12ccom q12dcom /*
  /* q12ecom q12fcom q12gcom q12hcom q12icom {
    gen `p'_ = !missing(`p')
    gen `p'_m = `p'_*100 //multiply by 100 to make percentages in the table
    drop `p'_
    //replace `p'_m = . //if babynr!="1"
  }

**Ind 1 Q2
gen q2aqta_m = .
replace q2aqta_m = 100 if q2ref==1 & q2aqta!=. //& babynr=="1"
replace q2aqta_m = 0 if q2ref==1 & q2aqta==. //& babynr=="1"

**Ind 1 Q5
gen q5out_m = .
replace q5out_m = 100 if q4grav>1 & q4grav!=. & q5out!=. //& babynr=="1"
replace q5out_m = 0 if q4grav>1 & q4grav!=. & q5out==. //& babynr=="1"

**Ind 1 Q6
gen q6par_m = .
replace q6par_m = 100 if q4grav>1 & q4grav!=. & q6par!=. //& babynr=="1"
replace q6par_m = 0 if q4grav>1 & q4grav!=. & q6par==. //& babynr=="1"

**Ind 1 Q7
gen q7ces_m = .
replace q7ces_m = 100 if q4grav>1 & q4grav!=. & q7ces!=. //& babynr=="1"
replace q7ces_m = 0 if q4grav>1 & q4grav!=. & q7ces==. //& babynr=="1"

**Summary of indicator 1
gen ind1_sum = (q1date_m+q2ref_m+q2aqta_m+q3age_m+q4grav_m+q5out_m+q6par_m+q7ces_m+ /*
  /* q8anc_m+q9dob_m+q9aga_m+q10syp_m+q11hiv_m+ /*
  /* q12acom_m+q12bcom_m+q12ccom_m+q12dcom_m+q12ecom_m+q12fcom_m+ /*
  /* q12gcom_m+q12hcom_m+q12icom_m)/22

**INDICATOR 2 - Fetal heart on admission
**Ind 2: fetal check at admission done

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303 gen q16fet_p = .
304 replace q16fet_p = 1 if (q16fet==1 | q16fet==2) //& babynr=="1"
305 replace q16fet_p = 0 if (q16fet==3 | q16fet==.) //& babynr=="1"
306 ta q16fet_p
307 **INDICATOR 3 - fetal monitoring done and documented in 1st stage of labour
308 gen q18_0fhmeas_p = .
309 replace q18_0fhmeas_p = 1 if q18_0fhmeas==1 //& babynr=="1"
310 replace q18_0fhmeas_p = 0 if (q18_0fhmeas==0 | q18_0fhmeas==.) //& babynr=="1"
311 ta q18_0fhmeas_p
312 **INDICATOR 4 - fetal monitoring done in 2nd stage
313 gen q21secfet_p = .
314 replace q21secfet_p = 1 if q21secfet==1 //& babynr=="1"
315 replace q21secfet_p = 0 if (q21secfet==0 | q21secfet==.) //& babynr=="1"
316
317 **EMERGENCY PREPAREDNESS
318 **Ind 5: Decision to delivery time in case of Caesarean section
319 gen del_time = minutes(q23birth-q22etimedec) // Decision to delivery time in case of Caesarean
section
320
321 ***THIS INDICATOR NEEDS CHECKING AGAIN
322 // replace del_time = . if del_time < 0 // make negative time missing
323 gen emergencycs = .
324 // replace emergencycs = 100 if (q19ddec==2 | q22ddec==3) & del_time<45 & del_time!=.
325 // replace emergencycs = 0 if (q19ddec==2 | q22ddec==3) & del_time!=. // THIS REPLACES THE ABOVE
326
327 **Ind 6: Resuscitation for babies with APGAR < 7
328 gen resapg = .
329 replace resapg = 1 if q32resc==1 & q30apg<7
330 replace resapg = 0 if q32resc!=1 & q30apg<7
331
332 **RESPONSIVENESS FOCUSED
333 **INDICATOR 7 - Companionship
334 **Ind 7a: Was a companion present during labour
335 gen q39comp1_p = 0
336 replace q39comp1_p = 1 if q39comp1==1
337
338 ** 7b: Companion during birth
339 gen q39comp2_p = 0
340 replace q39comp2_p = 1 if q39comp2==1
341
342
343 **ACTIVE MANAGEMENT OF THIRD STAGE/EARLY NEWBORN CARE
344 **Ind 8: Breastfeeding within 1 h
345 gen q36breast_p = 0
346 replace q36breast_p = 1 if q36breast==1 & q27out ==1
347
348 **QUALITY IMPROVEMENT
349 **Ind 9: Fresh stillbirth with a positive heartbeat at admission
350 gen freshheart = .
351 replace freshheart = 1 if q16fet==1 & q27out==2
352 replace freshheart = 0 if q16fet!=1 & q27out==2
353
354 *SEVERE MATERNAL OUTCOMES
355 **Definition from protocol paper
356 gen sevmatout=.
357 recode sevmatout .=1 if q42kperint==1 //hysterectomy
358 recode sevmatout .=1 if q42jperint==1 //laparotomy for ruptured uterus
359 recode sevmatout .=1 if q42iperint==1 //blood transfusion
360 recode sevmatout .=1 if q49==3 // 3 referred to ICU or higher level facility
361 recode sevmatout .=0
362 tab sevmat
363
364 label variable ind1_sum "Appropriate admission standards and procedures"
365 label variable q16fet_p "Fetal heart check at admission done"
366 label variable q18_0fhmeas_p "Fetal monitoring done and documented in 1st stage of labour"
367 label variable q21secfet_p "Fetal monitoring done in 2nd stage "

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368 label variable resapg "Resuscitation for babies with APGAR < 7"
369 label variable q39comp1_p "Companion present during labour"
370 label variable q39comp2_p "Companion present during birth"
371 label variable q36breast_p "Breastfeeding within 1 hour"
372 label variable freshheart "Fresh stillbirth with a positive heartbeat at admission"
373 label variable sevmat"Severe maternal outcomes"
374 label variable emergencycs "Decision to delivery time in case of Caesarean section"
375
376 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))
377
378 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))
379 x
380 ***# MAIN STUDY OUTCOMES
381
382 *MATERNAL MORBIDITY - hysterectomy, laparotomy, blood transfusion, adm to intensive care, referral
to higher facility
383
384 gen matmorb=.
385 lab var matmorb "Severe Maternal morbidity"
386 recode matmorb .=1 if (q42j==1|q42k==1|q42iperint==1|q49==3) //|q49==4)
387 recode matmorb .=0
388 lab def matmorb 1 "severe maternal morbidity" 0 "none"
389 lab val matmorb matmorb
390
391
392 table1, by(count) vars(matmorb bin ) format(%9.1fc) missing onecol saving(Results_Table1.xlsx,
sheet("Table3", replace))
393
394 table1, by(treat) vars(matmorb bin) format(%9.1fc) missing onecol saving(Results_Table1.xlsx, sheet
("Table3b", replace))
395 x
396 ***# BABY LEVEL
397 // use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\UG\2023_09_04_UG.dta", clear
398
399 *Reshaping to long
400 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"
401
402
403 svyset hospn
404
405 *INTRAPARTUM SB (based on visual identification) *this should be run after reshaping? or add
numbers from baby 1, 2, 3?
406 gen ipsb=.
407 recode ipsb .=1 if q27out==2
408 recode ipsb .=0 if (q27out==1|q27out==3|q27out==.)
409
410 *gen stillbirthrate=prop(ipsb)/1000
411 *gen proplarger = (_N-_n)/_N
412
413 *denominator is live births and stillbirths BIRTHS
414 *live births from q27out
415 gen births=.
416 recode births .=1 if (q27out==1|2|3)
417 tab births
418
419 *do reshape
420
421 *1 FRESH STILLBIRTH RATE
422 gen fsb=.
423 lab var fsb "Fresh stillbirths"

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424 recode fsb .=1 if q27out==2
425 recode fsb .=0 if (q27out==1|3)
426 label define fsb 1 "fresh stillbirth" 0 "macerated or live births"
427 label val fsb fsb
428
429 // svy: tab fsb, subpop(if country1==1) percent ci format (%2.1f)
430 // svy: tab fsb, subpop(if country1==2) percent ci format (%2.1f)
431 // svy: tab fsb, subpop(if country1==3) percent ci format (%2.1f)
432 // svy: tab fsb, subpop(if country1==4) percent ci format (%2.1f)
433
434 *2. In-facility early perinatal mortality
435 *Number of fresh stillbirths (as above) and up-to discharge neonatal deaths per 1000 live and
stillbirths (composite indicator)
436 ren eperi eperi_old
437 gen eperi=.
438 lab var eperi "early perinatal mortality"
439 recode eperi .=1 if q27out==2
440 recode eperi .=1 if (q27out==1|q27out==.) & (q44status==1|q44status==.) & q45status==3
441 *recode eperi .=1 if (q27out==1|q27out==.) & q44status==2 &
(q45status==3|q45status==4|q45status==5|q45status==.)
442 recode eperi .=1 if (q27out==1|q27out==.) & q44status==2
443 recode eperi .=1 if (q27out==1|q27out==.) & (q45status==3)
444 *recode eperi .=1 if (q27out==1|q27out==.) & (q45status==3|q45status==4)
445
446 recode eperi .=0
447 tab eperi
448 tab eperi q27out, mi
449 tab eperi q44status, mi
450 tab eperi q45status, mi
451
452
453 gen eperi2=.
454 lab var eperi2 "early perinatal mortality"
455 recode eperi2 .=1 if q27out==2
456 recode eperi2 .=1 if (q27out==1|q27out==.) & (q44status==1|q44status==.) & q45status==3
457 *recode eperi2 .=1 if (q27out==1|q27out==.) & q44status==2 &
(q45status==3|q45status==4|q45status==5|q45status==.)
458 recode eperi2 .=1 if (q27out==1|q27out==.) & q44status==2
459 recode eperi2 .=1 if (q27out==1|q27out==.) //& (q45status==3|q45status==4)
460 recode eperi2 .=0
461 tab eperi2
462 tab eperi2 q27out, mi
463 tab eperi2 q44status, mi
464 tab eperi2 q45status, mi
465 *3. Fetal distress (neonates with Apgar <7 at 5 min out 1000 live births and stillbirths)
466 gen lowapgar =.
467 lab var lowapgar "low apgar score (<7)"
468 recode lowapgar .=0 if q30apg>=7
469 recode lowapgar .=1 if q30apg <7
470 tab q30apg lowapgar, m
471 label define lowapgar 1 "apgar <7" 0 "apgar ≥7"
472 lab val lowapgar lowapgar
473
474 *3. Neonatal seizures (number of neonates diagnosed with seizures per 1000 live and stillbirths)
475 gen seizures=.
476 recode seizures .=1 if (q46b==1)
477 recode seizures .=0
478 tab seizures
479 label define seizures 1 "seizures" 0 "no seizures"
480 lab val seizures seizures
481 prop seizures, percent
482 // svy: tab seizures, subpop(if country1==1) percent ci format (%2.1f)
483 // svy: tab seizures, subpop(if country1==2) percent ci format (%2.1f)
484 // svy: tab seizures, subpop(if country1==3) percent ci format (%2.1f)
485 // svy: tab seizures, subpop(if country1==4) percent ci format (%2.1f)
486

```

```

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

```

```

548 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
549 drop sex
550
551 tab sga,mi
552
553
554 *LBW
555 recode q28weight (min/2499 = 1 "<2500g") (2500/4500 = 2 "normal birthweight (2500 - 4500g)") (4501/
9000 = 3 "macrosomia (>4500)"), gen(bwt) label(bwt)
556 ta bwt, mi
557
558 **# SVN
559 **# Small and Vulnerable newborn
560 gen svn = cond((preterm==1 | sga<0 | bwt==1),1,0)
561
562 label variable svn "Small and Vulnerable Newborn"
563
564 *TABLES
565 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))
566
567 *table by Treatment arm
568
569 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))
570
571
572
573 **# Labour information and process measurement
574 **# First stage
575 *First stage labour monitoring documented
576 gen firststage = !missing(dur_stage1)
577 lab var firststage "First stage of labour monitoring documented"
578 *Duration of first stage in hours
579 sum dur_stage1
580 lab var dur_stage1 "Duration of first stage in hours"
581
582 *Fetal heart beat measured at 1st stage
583 tab q18_0fhmeas
584 lab var q18_0fhmeas "Fetal heart beat measured at 1st stage"
585
586 *Fetal heart abnormality found - 1st stage
587 recode q18anom 2=.
588 ta q18anom , nol
589 lab var q18anom "Fetal heart abnormality found - 1st stage"
590
591 *Senior midwife informed at 1st stage
592 ta q19binfo
593 lab var q19binfo "Senior midwife informed at 1st stage"
594
595 *Doctor informed at 1 stage
596 ta q19cdoc
597 lab var q19cdoc "Doctor informed at 1 stage"
598
599 *Decision made at 1st stage
600 tab q19ddec
601 lab var q19ddec "Decision made at 1st stage"
602
603 *Duration of decision at 1st stage in minutes
604 tab decbir_tim
605 lab var decbir_tim "Duration of decision at 1st stage in minutes"
606

```

```

607 ## Second stage
608 tab q20sec
609 lab var q20sec "Second stage of labour monitoring documented"
610
611
612 // (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)

613
614 *Duration of second stage in hours
615 sum dur_stage2
616 lab var dur_stage2 "Duration of second stage in hours"
617
618 *Fetal heart beat measured at first stage
619 tab q21secfet
620 lab var q21secfet "Fetal heart beat measured at first stage"
621
622 *Fetal heart anormally
623 ta q22path
624 lab var q22path "Fetal heart abnormality found - 2nd stage"
625
626 *Senior midwife informed
627 ta q22binfo
628 lab var q22binfo "Senior midwife informed a 2nd stage"
629
630 *Doctor informed
631 ta q22cdoc
632 lab var q22cdoc "Doctor informed at 2nd stage"
633
634 *Decision made
635 tab q22ddec
636 lab var q22ddec "Decision made at 2nd stage"
637
638 *Duration of decision at 1st stage in minutes
639 tab decbir_tim2
640 lab var decbir_tim2 "Duration of decision at 1st stage in minutes"
641
642 ## Length of labour in hours
643 ta lol
644 lab var lol "Length of labour in hours"
645
646 ## Time from Admission to birth in hours
647 sum adm_birth //hours
648 ta adm_birth
649 lab var adm_birth "Time from Admission to birth in hours"
650
651 ## Length of stay in facility (hours)
652 sum los, detail
653 lab var los "Length of stay in facility (hours)"
654
655 *Mode of delivery
656 tab q24mode
657 lab var q24mode "Mode of delivery"
658
659 *Indication of operative birth
660 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
661
662 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))

663
664 table1, byvars(firststage bin dur_stage1 \ q18_0timeap18anom bin q19binfo bin q19cdoc bin q19ddet
\ decbictin \ q20sec bin dur_stage2 conts \ q21secfet bin q22path bin q22binfo bin q22dct
q22ddc 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)

665 */
666
667 **Ind 6: Resuscitation for babies with APGAR < 7
668 genresapg2
669 replcesapg2fq32=1&q30apg7
670 replcesapg2fq32=1&q30apg7
671
672 **ACTIVE MANAGEMENT OF THIRD STAGE/EARLY NEWBORN CARE
673 **Ind 8: Breastfeeding within 1 h
674 genq36breast_p2
675 replq36breast_p2fq26=1&q27out =1
676
677 **QUALITY IMPROVEMENT
678 **Ind 9: Fresh stillbirth with a positive heartbeat at admission
679 genfreshheart2
680 replfreshheartfq16fet=1 & q27out=2
681 replfreshheartfq16fet!1 & q27out=2
682 labelresapg2 "Resuscitation for babies with APGAR < 7"
683 labelq36breast_p2 "Breastfeeding within 1 hour"
684 labelfreshheart2 "Fresh stillbirth with a positive heartbeat at admission"
685
686 *Mode of delivery
687 tabq24mode
688 labq24mode "Mode of delivery"
689
690
691 table1, by(count) vars(resapg2 q36breast_p2 freshheart q24mode cat ) for(%9.1fc) missing onecol saving(
Results_Table1.xlsx, sheet("Table2_pregnancy_baby"))
692
693 table1, byvars(resapg2 q36breast_p2 freshheart q24mode cat ) for(%9.1fc) missing onecol saving(
Results_Table1.xlsx, sheet("Table2b_pregnancy_baby"))
694
695
696
697
698
699
700 x
701 **# regression
702 // outcome 1 - fsb Fresh stillbirths
703 // outcome 2 - eperi early perinatal mortality
704 // outcome 3 - lowapg low apgar score (<7)
705 // outcome 4 - seizures seizures
706 // outcome 5 - CS Caesarean section
707 // outcome 6 - matmorb Severe Maternal morbidity //Maternal
708 // outcome 7 - fetdist fetal distress
709 // outcome 8 - Responsiveness //Maternal
710 // outcome 9 - Mistreatment //Maternal
711 // outcome 10 - q36breast_p2 Breastfeeding
712
713
714
715 gettime2time3

```

```

716 **# FRESH STILLBIRTHS
717 tempname memhold
718 **# Bookmark #2
719 postfile `memhold' hospn treat_beta treat_se pvalue using "outcomex.dta", replace
720 forval j=11/44 {
721 capture noisily melogit q20sec i.treat i.time2 i.group if hospn==`j' || group: , or
722     *set trace on
723         matrix p = e(p)
724         local pval = p[1,1]
725         matrix b = e(b)
726         local beta = b[1,2]
727         matrix v = e(V)
728         local see = sqrt(v[2,2])
729         post `memhold' (`j') (`beta') (`see') (`pval')
730     }
731 postclose `memhold'
732 estat icc
733
734 postfile `memhold' hosp treat_beta treat_se pvalue using "outcome5a.dta", replace
735 forval j=11/44 {
736 capture noisily xtlogit CS i.period i.treat if hosp==`j', pa i(id2) corr(exchangeable) vce(robust)
or
737     *set trace on
738         matrix p = e(p)
739         local pval = p[1,1]
740         matrix b = e(b)
741         local beta = b[1,2]
742         matrix v = e(V)
743         local see = sqrt(v[2,2])
744         post `memhold' (`j') (`beta') (`see') (`pval')
745     }
746 postclose `memhold'
747 estat icc
748
749
750 Applied
751
752 gen id = alert_id
753 replace id = substr(id, "-", "", .)
754 replace id = substr(id, "/", "", .)
755
756 alert_id
757 344-504613
758 344-5-04613
759 344-504613
760 344-5-04613
761
762 alert_id
763 111-5-00980
764 1115-00980
765 111-5-00980
766 1115-00980
767
768 gen id2 = real(id)
769 gen last5 = substr(alert_id, strlen(alert_id) - 4, 5)
770 gen last
771
772 tempname memhold
773 postfile `memhold' hospn treat_beta treat_se pvalue using "outcome5a.dta", replace
774
775 forval j=1/16 {
776     capture noisily {
777         xtgee CS i.treat if hp==`j', i(id2) family(binomial 1) link(log) ///
778             corr(exchangeable) vce(robust)
779         *set trace on
780         matrix b = e(b)

```

```

781         local beta = b[1,2]
782         matrix v = e(V)
783         local see = sqrt(v[2,2])
784         post `memhold' (`j') (`beta') (`see')
785     }
786 }
787 }
788 postclose `memhold'
789
790
791 tempname memhold
792 postfile `memhold' hospn treat_beta treat_se pvalue using "outcome5a.dta", replace
793
794 * Loop through each hospital to fit the model and store results
795 forval j=1/16 {
796     * Check if there is data for the current hospital
797     count if hp == `j'
798     if r(N) > 0 {
799         capture noisily {
800             xtgee CS i.treat if hp==`j', i(id2) family(binomial 1) link(log) ///
801                 corr(exchangeable) vce(robust)
802             if _rc == 0 {
803                 matrix b = e(b)
804                 local beta = b[1,2]
805                 matrix v = e(V)
806                 local see = sqrt(v[2,2])
807
808                 * Calculate p-value (assuming z-test)
809                 local z = `beta' / `see'
810                 local pvalue = 2 * (1 - normal(abs(`z')))
811
812                 post `memhold' (`j') (`beta') (`see') (`pvalue')
813             }
814         }
815     }
816 }
817
818 postclose `memhold'
819
820 * Display the results
821 use "outcome5a.dta", clear
822 list
823
824
825
826 . table hospn time2, statistic(sum NRecords )
827 . table hospn time2, statistic(sum fsb )
828 . table hospn time2, statistic(mean fsb )
829
830 gen type = .
831 recode type .=1 if q27out==1
832 recode type .=2 if fsb==1
833 tab type
834 tab q27out fsb
835 gen type2 = .
836 recode type2 .=1 if q27out==1
837 recode type2 .=2 if eperi==1
838 mean fsb if inrange(type,1,2), over(hospn)
839 mean eperi if inrange(type2,1,2), over(hospn)
840 mean lowapg , over(hospn)
841 mean seizures, over(hospn)
842 mean CS, over(hospn)
843 mean matmorb, over(hospn)
844 mean fetdist, over(hospn)
845 mean fetdist, over(hospn)
846 mean q36breast_p2, over(hospn)

```

```

847
848 tabstat q36breast_p2, statistic(mean) by(hospn)
849
850 use "C:\Users\eidewjai\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)
968
969 graph twoway (mspline matmorb months) if months>733 & months<764, by(hospn)
970 graph twoway (mspline MM_percentage months) if months>733 & months<764, by(hospn)
971
972 // outcome 1 - fsb Fresh stillbirths //
973 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear
974 egen mean_MM = mean(fsb), by(months)
975
976 collapse (sum) fsb NRecords, by( hosp)
977
978 * Calculate the proportion CS as a percentage of NRecords
979 gen MM_percentage = (fsb / NRecords) * 1000
980
981 * Calculate lower and upper bounds for the 95% confidence interval
982 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
983 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
984
985 *graph twoway (mspline fsb months), by(hosp)
986 graph twoway (mspline MM_percentage months), by(hosp)
987
988
989 // outcome 2 - eperi early perinatal mortality //
990 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear
991 egen mean_MM = mean(eperi), by(months)
992
993 collapse (sum) eperi NRecords, by(months)
994
995 * Calculate the proportion CS as a percentage of NRecords
996 gen MM_percentage = (eperi / NRecords) * 1000
997
998 * Calculate lower and upper bounds for the 95% confidence interval
999 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
1000 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
1001
1002 *graph twoway (mspline fsb months), by(hosp)
1003 graph twoway (mspline MM_percentage months), by(hosp)
1004
1005 // outcome 3 - lowapg low apgar score (<7) //
1006 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear
1007 egen mean_MM = mean(lowapg), by(months)
1008
1009 collapse (sum) lowapg NRecords, by(months)
1010
1011 * Calculate the proportion CS as a percentage of NRecords
1012 gen MM_percentage = (lowapg / NRecords) * 1000
1013
1014 * Calculate lower and upper bounds for the 95% confidence interval
1015 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
1016 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
1017
1018 *graph twoway (mspline fsb months), by(hosp)
1019 graph twoway (mspline MM_percentage months), by(hosp)
1020
1021 // outcome 4 - Neonatal seizures seizures ///
1022 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear
1023 egen mean_MM = mean(seizure), by(months)
1024
1025 collapse (sum) seizure NRecords, by(months)
1026

```

```

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)

```

```

1081 gen NRecords = 1
1082
1083 egen mean_MM = mean(Mistreatment_FS_finalscore), by(months hosp)
1084
1085 *graph twoway (mspline matmorrb months), by(hosp)
1086 graph twoway (mspline mean_MM months), by(hosp)
1087
1088
1089
1090
1091 // - Fetal heart check on admission rate (per 100) change over time by hospital
1092 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Mother_level.dta", clear
1093 egen mean_MM = mean(q16fet_p), by(months)
1094
1095 collapse (sum) q16fet_p NRecords, by( months hosp)
1096
1097 * Calculate the proportion CS as a percentage of NRecords
1098 gen MM_percentage = (q16fet_p / NRecords) * 100
1099
1100 * Calculate lower and upper bounds for the 95% confidence interval
1101 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1102 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1103 graph twoway (mspline q16fet_p months), by(hosp)
1104 graph twoway (mspline MM_percentage months), by(hosp)
1105
1106
1107
1108 ///* Fetal monitoring done and documented in 1st stage of labour q18_0fhmeas_p
1109
1110 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Mother_level.dta", clear
1111 egen mean_MM = mean(q18_0fhmeas_p), by(months)
1112
1113 collapse (sum) q18_0fhmeas_p NRecords, by( months hosp)
1114
1115 * Calculate the proportion CS as a percentage of NRecords
1116 gen MM_percentage = (q18_0fhmeas_p / NRecords) * 100
1117
1118 * Calculate lower and upper bounds for the 95% confidence interval
1119 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1120 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1121 *graph twoway (mspline matmorrb months), by(hosp)
1122 graph twoway (mspline MM_percentage months), by(hosp)
1123
1124
1125 /// Fetal monitoring done in 2nd stage q21secfet_p
1126
1127 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Mother_level.dta", clear
1128 egen mean_MM = mean(q21secfet_p), by(months)
1129
1130 collapse (sum) q21secfet_p NRecords, by( months hosp)
1131
1132 * Calculate the proportion CS as a percentage of NRecords
1133 gen MM_percentage = (q21secfet_p / NRecords) * 100
1134
1135 * Calculate lower and upper bounds for the 95% confidence interval
1136 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1137 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)

```

```

1138 *graph twoway (mspline matmorb months), by(hosp)
1139     graph twoway (mspline MM_percentage months), by(hosp)
1140
1141 //Resuscitation for babies with APGAR < 7 resapg2
1142 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear
1143
1144     egen mean_MM = mean(resapg2), by(months)
1145
1146 collapse (sum) resapg2 NRecords, by( months hosp)
1147
1148 * Calculate the proportion CS as a percentage of NRecords
1149 gen MM_percentage = (resapg2 / NRecords) * 1000
1150
1151 * Calculate lower and upper bounds for the 95% confidence interval
1152 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
1153 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/1000) * (1 - (MM_percentage/1000)) /
NRecords)
1154 *graph twoway (mspline resapg2 months), by(hosp)
1155     graph twoway (mspline MM_percentage months), by(hosp)
1156
1157 /// COMPANION PRESENT DURING LABOUR - eregistry q39comp1_p
1158
1159 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Mother_level.dta", clear
1160     egen mean_MM = mean(q39comp1_p), by(months)
1161
1162 collapse (sum) q39comp1_p NRecords, by( months hosp)
1163
1164 * Calculate the proportion CS as a percentage of NRecords
1165 gen MM_percentage = (q39comp1_p / NRecords) * 100
1166
1167 * Calculate lower and upper bounds for the 95% confidence interval
1168 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1169 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1170 *graph twoway (mspline matmorb months), by(hosp)
1171     graph twoway (mspline MM_percentage months), by(hosp)
1172
1173 /// COMPANION PRESENT DURING birth - eregistry q39comp2_p
1174
1175 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Mother_level.dta", clear
1176     egen mean_MM = mean(q39comp2_p), by(months)
1177
1178 collapse (sum) q39comp2_p NRecords, by( months hosp)
1179
1180 * Calculate the proportion CS as a percentage of NRecords
1181 gen MM_percentage = (q39comp2_p / NRecords) * 100
1182
1183 * Calculate lower and upper bounds for the 95% confidence interval
1184 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1185 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1186 *graph twoway (mspline matmorb months), by(hosp)
1187     graph twoway (mspline MM_percentage months), by(hosp)
1188
1189
1190
1191 /// COMPANION PRESENT DURING LABOUR Responsiveness_FS_finalscore Mistreatment_FS_finalscore
immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
1192 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear

```

```

1193 drop if months<m(2021m1)
1194 gen NRecords = 1
1195
1196 egen mean_MM = mean(s7q1_comp_cat), by(months)
1197
1198 collapse (sum) s7q1_comp_cat NRecords, by( months hosp)
1199
1200 * Calculate the proportion CS as a percentage of NRecords
1201 gen MM_percentage = (s7q1_comp_cat / NRecords) * 100
1202
1203 * Calculate lower and upper bounds for the 95% confidence interval
1204 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1205 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1206 *graph twoway (mspline resapg2 months), by(hosp)
1207 graph twoway (mspline MM_percentage months), by(hosp)
1208
1209 /// COMPANION PRESENT DURING BIRTHS Responsiveness_FS_finalscore Mistreatment_FS_finalscore
immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
1210 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1211 drop if months<m(2021m1)
1212 gen NRecords = 1
1213
1214 egen mean_MM = mean(s7q2_stay_cat), by(months)
1215
1216 collapse (sum) s7q2_stay_cat NRecords, by( months hosp)
1217
1218 * Calculate the proportion CS as a percentage of NRecords
1219 gen MM_percentage = (s7q2_stay_cat / NRecords) * 100
1220
1221 * Calculate lower and upper bounds for the 95% confidence interval
1222 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1223 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1224 *graph twoway (mspline resapg2 months), by(hosp)
1225 graph twoway (mspline MM_percentage months), by(hosp)
1226
1227
1228
1229 ///EARLY AMBULATION Responsiveness_FS_finalscore Mistreatment_FS_finalscore immediate_feed
s7q1_comp_cat s7q2_stay_cat early_ambulat
1230 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1231 drop if months<m(2021m1)
1232 gen NRecords = 1
1233
1234 egen mean_MM = mean(early_ambulat), by(months)
1235
1236 collapse (sum) early_ambulat NRecords, by( months hosp)
1237
1238 * Calculate the proportion CS as a percentage of NRecords
1239 gen MM_percentage = (early_ambulat / NRecords) * 100
1240
1241 * Calculate lower and upper bounds for the 95% confidence interval
1242 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1243 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1244 *graph twoway (mspline resapg2 months), by(hosp)
1245 graph twoway (mspline MM_percentage months), by(hosp)
1246
1247
1248

```

```

1249 ///BREASTFEEDING WITHIN 1 HOUR immediate_feed s7q1_comp_cat s7q2_stay_cat early_ambulat
1250 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1251 drop if months<m(2021m1)
1252 gen NRecords = 1
1253
1254 egen mean_MM = mean(immediate_feed), by(months)
1255
1256 collapse (sum) immediate_feed NRecords, by( months hosp)
1257
1258 * Calculate the proportion CS as a percentage of NRecords
1259 gen MM_percentage = (immediate_feed / NRecords) * 100
1260
1261 * Calculate lower and upper bounds for the 95% confidence interval
1262 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1263 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1264 *graph twoway (mspline resapg2 months), by(hosp)
1265 graph twoway (mspline MM_percentage months), by(hosp)
1266
1267
1268
1269 // outcome 7 - fetdist fetal distress
1270 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear
1271 egen mean_MM = mean(fetdist), by(months)
1272
1273 collapse (sum) fetdist NRecords, by( months hosp)
1274
1275 * Calculate the proportion CS as a percentage of NRecords
1276 gen MM_percentage = (fetdist / NRecords) * 100
1277
1278 * Calculate lower and upper bounds for the 95% confidence interval
1279 gen lower_CI = MM_percentage - 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1280 gen upper_CI = MM_percentage + 1.96 * sqrt((MM_percentage/100) * (1 - (MM_percentage/100)) /
NRecords)
1281 graph twoway (mspline fetdist months), by(hosp)
1282 graph twoway (mspline MM_percentage months), by(hosp)
1283
1284
1285
1286
1287 *use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1288 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1289 gen date = dofc(s1q2_doi)
1290 format date %td
1291 *Converting date into stata weeks of the year
1292 gen weeks = wofd(date)
1293 format weeks %tw
1294
1295 gen months = mofd(date)
1296 format months %tm
1297
1298 gen qtr3 = qofd((date))
1299 format qtr3 %tq
1300
1301 **# Number of records by hospital by months
1302
1303 *Cleaning and keeping only 30 months from July 2021 to December 2023
1304
1305
1306 //drop if months==. | months<m(2021m3)

```

```

1307 duplicates tag hospnam month, gen(dups) // Checking for multiple months
1308 drop dups
1309
1310 **Anonymised hospital names
1311
1312 gen hosp = "Benin-Hospital-1" if hospnam==1
1313 replace hosp = "Benin-Hospital-2" if hospnam==2
1314 replace hosp = "Benin-Hospital-3" if hospnam==3
1315 replace hosp = "Benin-Hospital-4" if hospnam==4
1316 replace hosp = "Malawi-Hospital-1" if hospnam==5
1317 replace hosp = "Malawi-Hospital-2" if hospnam==6
1318 replace hosp = "Malawi-Hospital-3" if hospnam==7
1319 replace hosp = "Malawi-Hospital-4" if hospnam==8
1320 replace hosp = "Tanzania-Hospital-1" if hospnam==9
1321 replace hosp = "Tanzania-Hospital-2" if hospnam==10
1322 replace hosp = "Tanzania-Hospital-3" if hospnam==11
1323 replace hosp = "Tanzania-Hospital-4" if hospnam==12
1324 replace hosp = "Uganda-Hospital-1" if hospnam==13
1325 replace hosp = "Uganda-Hospital-2" if hospnam==14
1326 replace hosp = "Uganda-Hospital-3" if hospnam==15
1327 replace hosp = "Uganda-Hospital-4" if hospnam==16
1328
1329 /*
1330 gen hp =.
1331 replace hp = 1 if hospn==11
1332 replace hp = 2 if hospn==12
1333 replace hp = 3 if hospn==13
1334 replace hp = 4 if hospn==14
1335 replace hp = 5 if hospn==21
1336 replace hp = 6 if hospn==22
1337 replace hp = 7 if hospn==23
1338 replace hp = 8 if hospn==24
1339 replace hp = 9 if hospn==31
1340 replace hp = 10 if hospn==32
1341 replace hp = 11 if hospn==33
1342 replace hp = 12 if hospn==34
1343 replace hp = 13 if hospn==41
1344 replace hp = 14 if hospn==42
1345 replace hp = 15 if hospn==43
1346 replace hp = 16 if hospn==44
1347 */
1348
1349 *** Randomisation
1350 gen group = 1 if hospnam==1 | hospnam==5 | hospnam==9 | hospnam==13
1351 replace group = 2 if hospnam==2 | hospnam==6 | hospnam==10 | hospnam==14
1352 replace group = 3 if hospnam==3 | hospnam==7 | hospnam==11 | hospnam==15
1353 replace group = 4 if hospnam==4 | hospnam==8 | hospnam==12 | hospnam==16
1354
1355 *** Intervention
1356 gen hosp1_intervention = round==2 //jan2022
1357 gen hosp2_intervention = round==3 //jul2022
1358 gen hosp3_intervention = round==4 //jan2023
1359 gen hosp4_intervention = round==5 //jul2023
1360
1361 gen intervention2 = 0
1362 replace intervention2 = 1 if hosp1_intervention==1
1363 replace intervention2 = 2 if hosp1_intervention==1 & hosp2_intervention==1
1364 replace intervention2 = 3 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1
1365 replace intervention2 = 4 if hosp1_intervention==1 & hosp2_intervention==1 & hosp3_intervention==1
1366 & hosp4_intervention==1
1367
1368 label define intervention2 0 "No intervention" 1 "Hosp 1" 2 "Hosp 1,2" 3 "Hosp 1,2,3" 4 "Hosp
1,2,3,4"
1369 label values intervention2 intervention2
1370 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
1441 paper\Child_level.dta", clear
1442 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
1443 paper\Mother_level.dta", clear
1444 ***# regression
1445 // outcome 1 - fsb Fresh stillbirths
1446 // outcome 2 - eperi early perinatal mortality
1447 // outcome 3 - lowapg low apgar score (<7)
1448 // outcome 4 - seizures seizures
1449 // outcome 5 - CS Caesarean section
1450 // outcome 6 - matmorb Severe Maternal morbidity //Maternal
1451 // outcome 7 - fetdist fetal distress
1452 // outcome 8 - Responsiveness //Maternal - Responsiveness_FS_finalscore - - Exit interview
1453 // outcome 9 - Mistreatment //Maternal - Mistreatment_FS_finalscore - - Exit interview
1454 // outcome X - fetal heart check on admission
1455 // outcome X - fetal monitoring done and documented in 1st stage of labour
1456 // outcome x - fetal monitoring done in 2nd staGE
1457 // outcome x - resapg2 Resuscitation for babies with APGAR <7
1458 // outcome 11a - q39comp1_p companion labour1
1459 // outcome 12a - q39comp2_p companion birth1
1460 // outcome 11b - companion labour2 - s7q1_comp_cat - Exit interview
1461 // outcome 12b - companion birth2 - s7q2_stay_cat - Exit interview
1462 // outcome 13 - early ambulation early_ambulat - Exit interview
1463 // outcome 10 - q36breast_p2 Breastfeeding - Exit interview
1464 // outcome X - q36breast_p2 immediate_feed for exit - Exit interview
1465
1466 ///PER PROTOCOL ANALYSIS
1467 ***# FRESH STILLBIRTHS
1468 // outcome 1 - fsb Fresh stillbirths
1469
1470 tempname memhold
1471 ***# Bookmark #2
1472 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome5_PerProtocol.dta", replace
1473 //outcome1_new
1474 forval j=11/44 {
1475 capture noisily melogit CS i.has_been_treated3 i.perprotocol i.group if hospn==`j' || group: , or
1476 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
1477 group:, cov(ex)
1478 *set trace on
1479 matrix p = e(p)
1480 local pval = p[1,1]
1481 matrix b = e(b)
1482 local beta = b[1,2]
1483 matrix v = e(V)
1484 local see = sqrt(v[2,2])
1485 post `memhold' (`j') (`beta') (`see') (`pval')
1486 }
1487 postclose `memhold'
1488 estat icc
1489
1490 tabstat fsb, stat(mean) by(hosp)
1491 tabstat eperi, stat(mean) by(hosp)
1492 tabstat lowapg, stat(mean) by(hosp)
1493 tabstat CS, stat(mean) by(hosp)
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
1510 //outcome1_new
1511 forval j=11/44 {
1512 capture noisily melogit fsb i.treat i.time3 i.group if hospn==`j' & hospn!=33 || group: , or
1513 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
1514 group:, cov(ex)
1515 *set trace on
1516 matrix p = e(p)
1517 local pval = p[1,1]
1518 matrix b = e(b)
1519 local beta = b[1,2]
1520 matrix v = e(V)
1521 local see = sqrt(v[2,2])
1522 post `memhold' (`j') (`beta') (`see') (`pval')
1523 }
1524 postclose `memhold'
1525 estat icc
1526
1527 tabstat fsb if, stat(mean) by(hosp)
1528
1529 tempname memhold
1530
1531 *** Bookmark #2
1532 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome5a_SENSITIVITY2.dta", replace
1533 //outcome1_new
1534 forval j=11/44 {
1535 capture noisily melogit CS i.treat i.time3 i.group if hospn==`j' & hospn!=33 || group: , or
1536 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
1537 group:, cov(ex)
1538 *set trace on
1539 matrix p = e(p)
1540 local pval = p[1,1]
1541 matrix b = e(b)
1542 local beta = b[1,2]
1543 matrix v = e(V)
1544 local see = sqrt(v[2,2])
1545 post `memhold' (`j') (`beta') (`see') (`pval')
1546 }
1547 postclose `memhold'
1548 estat icc
1549
1550 tempname memhold
1551 *** Bookmark #2
1552 postfile `memhold' hosp treat_beta treat_se pvalue using "outcome5a.dta", replace
1553 forval j=11/44 {
1554 capture noisily xtlogit CS i.period i.treat if hosp==`j', pa i(id2) corr(exchangeable) vce(robust)
1555 or
1556 *set trace on
1557 matrix p = e(p)
1558 local pval = p[1,1]
1559 matrix b = e(b)
1560 local beta = b[1,2]

```

```

1558         matrix v = e(V)
1559         local see = sqrt(v[2,2])
1560         post `memhold' (`j') (`beta') (`see') (`pval')
1561     }
1562 postclose `memhold'
1563 estat icc
1564
1565 *** Bookmark #2
1566 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome5a_SENSITIVITY.dta", replace
1567 forval j=11/44 {
1568 capture noisily melogit CS i.treat i.time3 i.group if hospn==`j' & hospn!=23 || group: , or
1569     *set trace on
1570         matrix p = e(p)
1571         local pval = p[1,1]
1572         matrix b = e(b)
1573         local beta = b[1,2]
1574         matrix v = e(V)
1575         local see = sqrt(v[2,2])
1576         post `memhold' (`j') (`beta') (`see') (`pval')
1577     }
1578 postclose `memhold'
1579 estat icc
1580
1581
1582 // outcome 2 - eperi early perinatal mortality
1583 tempname memhold
1584
1585 *** Bookmark #2
1586 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome2_newMAY.dta", replace
1587 forval j=11/44 {
1588 capture noisily melogit eperi i.treat i.time3 i.group if hospn==`j' || group: , or
1589 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
1590 group:, cov(ex)
1591     *set trace on
1592         matrix p = e(p)
1593         local pval = p[1,1]
1594         matrix b = e(b)
1595         local beta = b[1,2]
1596         matrix v = e(V)
1597         local see = sqrt(v[2,2])
1598         post `memhold' (`j') (`beta') (`see') (`pval')
1599     }
1600 postclose `memhold'
1601 estat icc
1602
1603
1604 tabstat eperi, stat(mean) by(hosp)
1605
1606 // outcome 3 - lowapg low apgar score (<7)
1607 tempname memhold
1608
1609 *** Bookmark #2
1610 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome3_new22.dta", replace
1611 forval j=11/44 {
1612 capture noisily melogit lowapg i.treat i.time3 i.group if hospn==`j' || group: , or
1613 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
1614 group:, cov(ex)
1615     *set trace on
1616         matrix p = e(p)
1617         local pval = p[1,1]
1618         matrix b = e(b)
1619         local beta = b[1,2]
1620         matrix v = e(V)
1621         local see = sqrt(v[2,2])
1622         post `memhold' (`j') (`beta') (`see') (`pval')
1623     }
1624 postclose `memhold'

```

```

1622 estat icc
1623
1624 tabstat lowapg, stat(mean) by(hosp)
1625
1626
1627 // outcome 4 - seizures seizures
1628 tempname memhold
1629
1630 *** Bookmark #2
1631 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome4_new.dta", replace
1632 forval j=11/44 {
1633 capture noisily melogit seizures i.treat i.time3 i.group if hospn==`j' || group: , or
1634 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
1635     *set trace on
1636         matrix p = e(p)
1637         local pval = p[1,1]
1638         matrix b = e(b)
1639         local beta = b[1,2]
1640         matrix v = e(V)
1641         local see = sqrt(v[2,2])
1642         post `memhold' (`j') (`beta') (`see') (`pval')
1643     }
1644 postclose `memhold'
1645 estat icc
1646
1647 tabstat seizures, stat(mean) by(hosp)
1648
1649 // outcome 5 - CS Caesarean section
1650 tabstat CS, stat(mean) by(hosp)
1651
1652
1653 // outcome 6 - fetdist fetal distress
1654 tabstat fetdist, stat(mean) by(hosp)
1655
1656
1657
1658
1659 // outcome 10 - matmorb Severe Maternal morbidity //Maternal
1660 use Mother_level, clear
1661
1662 tempname memhold
1663
1664 *** Bookmark #2
1665 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcome10_new.dta", replace
1666 forval j=11/44 {
1667 capture noisily melogit matmorb i.treat i.time3 i.group if hospn==`j' || group: , or
1668 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
1669     *set trace on
1670         matrix p = e(p)
1671         local pval = p[1,1]
1672         matrix b = e(b)
1673         local beta = b[1,2]
1674         matrix v = e(V)
1675         local see = sqrt(v[2,2])
1676         post `memhold' (`j') (`beta') (`see') (`pval')
1677     }
1678 postclose `memhold'
1679 estat icc
1680
1681 tabstat matmorb, stat(mean) by(hosp)
1682
1683
1684
1685 // outcome 8 - Responsiveness //Maternal exit interviews - Responsiveness_FS_finalscore

```

```

1686 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1687
1688 tempname memhold
1689
1690 *** Bookmark #2
1691 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcomeX_responsive_NEW.dta", replace
1692 forval j=1/16 {
1693 //capture noisily melogit s7q2_stay_cat i.treat i.round i.group if hospn==`j' || group: , or
1694 capture noisily mixed Responsiveness_FS_finalscore i.treat i.round i.group if hospnam==`j' || group
:, cov(ex)
1695     *set trace on
1696         matrix p = e(p)
1697         local pval = p[1,1]
1698         matrix b = e(b)
1699         local beta = b[1,2]
1700         matrix v = e(V)
1701         local see = sqrt(v[2,2])
1702         post `memhold' (`j') (`beta') (`see') (`pval')
1703     }
1704 postclose `memhold'
1705 estat icc
1706
1707 tabstat Responsiveness_FS_finalscore, stat(mean) by(hosp)
1708 // outcome 9 - Mistreatment //Maternal exit interviews
1709 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear
1710
1711 tempname memhold
1712
1713 *** Bookmark #2
1714 postfile `memhold' hospnam treat_beta treat_se pvalue using "outcomeX_mistreatment_NEW.dta",
replace
1715 forval j=1/16 {
1716 //capture noisily melogit s7q2_stay_cat i.treat i.round i.group if hospn==`j' || group: , or
1717 capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' || group:,
cov(ex)
1718     *set trace on
1719         matrix p = e(p)
1720         local pval = p[1,1]
1721         matrix b = e(b)
1722         local beta = b[1,2]
1723         matrix v = e(V)
1724         local see = sqrt(v[2,2])
1725         post `memhold' (`j') (`beta') (`see') (`pval')
1726     }
1727 postclose `memhold'
1728 estat icc
1729
1730 tabstat Mistreatment_FS_finalscore, stat(mean) by(hosp)
1731
1732 // outcome X - fetal heart check on admission - q16fet_p
1733 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Mother_level.dta", clear
1734
1735 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)
1736
1737 tempname memhold
1738
1739 *** Bookmark #2
1740 postfile `memhold' hh treat_beta treat_se pvalue using "outcomex_fetalheart_admiss.dta", replace
1741 forval j=1/16 {
1742 capture noisily melogit q16fet_p i.treat i.time3 i.group if hh==`j' || group: , or
1743 //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 documented 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     }

```

```

1805 postclose `memhold'
1806 estat icc
1807
1808 tabstat q18_0fhmeas_p, stat(mean) by(hosp)
1809
1810
1811 // outcome x - fetal monitoring done in 2nd staGE
1812 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Mother_level.dta", clear
1813
1814 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)
1815
1816 tempname memhold
1817
1818 *** Bookmark #2
1819 postfile `memhold' hh treat_beta treat_se pvalue using "outcomex_fetmon_2ndstage3.dta", replace
1820 forval j=1/16 {
1821 capture noisily melogit q21secfet i.treat i.time3 i.group if hh==`j' || group: , or
1822 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
1823 *set trace on
1824 matrix p = e(p)
1825 local pval = p[1,1]
1826 matrix b = e(b)
1827 local beta = b[1,2]
1828 matrix v = e(V)
1829 local see = sqrt(v[2,2])
1830 post `memhold' (`j') (`beta') (`see') (`pval')
1831 }
1832 postclose `memhold'
1833 estat icc
1834
1835 tabstat q21secfet, stat(mean) by(hosp)
1836
1837
1838
1839
1840 // outcome x - Resuscitation for babies with APGAR <7 - resapg2
1841 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear
1842
1843 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)
1844
1845 tempname memhold
1846
1847 *** Bookmark #2
1848 postfile `memhold' hh treat_beta treat_se pvalue using "outcomex_resusitation.dta", replace
1849 forval j=1/16 {
1850 capture noisily melogit resapg2 i.treat i.time3 i.group if hh==`j' || group: , or
1851 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
1852 *set trace on
1853 matrix p = e(p)
1854 local pval = p[1,1]
1855 matrix b = e(b)
1856 local beta = b[1,2]
1857 matrix v = e(V)
1858 local see = sqrt(v[2,2])
1859 post `memhold' (`j') (`beta') (`see') (`pval')
1860 }
1861 postclose `memhold'
1862 estat icc
1863
1864 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

```

```

1984 // outcome 7 - q36breast_p2 Breastfeeding
1985 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis plan\Main results
paper\Child_level.dta", clear

1986
1987 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)

1988
1989 tempname memhold
1990
1991 *** Bookmark #2
1992 postfile `memhold' hh treat_beta treat_se pvalue using "outcome7_new2_CS_birth.dta", replace
1993 forval j=1/16 {
1994 capture noisily melogit q36breast_p2 i.treat i.time3 i.group if hh==`j' & CS==1 || group: , or
1995 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
1996 *set trace on
1997 matrix p = e(p)
1998 local pval = p[1,1]
1999 matrix b = e(b)
2000 local beta = b[1,2]
2001 matrix v = e(V)
2002 local see = sqrt(v[2,2])
2003 post `memhold' (`j') (`beta') (`see') (`pval')
2004 }
2005 postclose `memhold'
2006 estatc
2007
2008 tabstat q36breast_p2 by(hosp)

2009
2010 // outcome x - Breastfeeding rate - EXIT INTERVIEWS immediate_feed
2011 use "C:\Users\josep\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\final-dataset-analysis_WP2.dta", clear

2012
2013 tempname memhold
2014
2015 *** Bookmark #2
2016 postfile `memhold' hospn treat_beta pval using "outcomeX_immediatfeed_NEW.dta", replace
2017 forval j=1/16{
2018 capture noisily melogit immediate_feed i.treat i.round i.group if hospn==`j' || group: , or
2019 //capture noisily mixed Mistreatment_FS_finalscore i.treat i.round i.group if hospnam==`j' ||
group:, cov(ex)
2020 *set trace on
2021 matrix p = e(p)
2022 local pval = p[1,1]
2023 matrix b = e(b)
2024 local beta = b[1,2]
2025 matrix v = e(V)
2026 local see = sqrt(v[2,2])
2027 post `memhold' (`j') (`beta') (`see') (`pval')
2028 }
2029 postclose `memhold'
2030 estatc
2031
2032 tabstat (outcome) immediate_feed
2033 tabstat (outcome) immediate_feed by(hosp)

2034
2035
2036 use "C:\Users\ejdejwai\Dropbox\DELL Latitute LAPT2126\ALERT\Analysis
plan\2023_09_04_DATA\outcome4.dta", clear

2037
2038 label define hospn 11 "1.1 DeZone 12mè1G2aGdnPpòpòt Dépt Zou-Collines" 13 "1.3 Centre National Hubert
Maga" 14 "1.4 Polyclinique Bon Samaritan" 21 "2.1 M20ih3i2 N23" 22 "2.2 Mitu" 23 "2.3 Ou3D" 24 "2.4 Rura" 31 "3.1 Lel" 32 "3.2 Mko" 33
"3.3 Na34" 34 "3.4 Ngwè" 41 "4.1 Distric" 42 "4.2 Régic" 43 "4.3 Missigang" 44 "4.4 Refe" 45 "4.5 Bugl'i General"
2039 label values hospn hospn
2040 label CS_rate "CS Rate"
2041 label 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) boxesca(80) xsize(8) ysize(6) ///
2052     t1(Difference between CS rate by hospital) ///
2053     caption("Adjusted for time")
2054
```