

```

name: <unnamed>
log: \\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Table1.log
log type: text
opened on: 23 Mar 2021, 11:49:29

```

```

. ** Table 1: Baseline characteristics
. import excel "\\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Source Data.xlsx",
sheet("Table 1") firstrow
(24 vars, 132 obs)

```

```

. destring Laboratoryconfirm, replace
LaboratoryconfirmedCongenital: all characters numeric; replaced as byte
(3 missing values generated)

```

```

. tab Laboratoryconfirm

```

Laboratory confirmed Congenital ZIKA infection	Freq.	Percent	Cum.
0	111	86.05	86.05
1	18	13.95	100.00
Total	129	100.00	

```

. * Maternal age:
. codebook Maternalage if Laboratoryconfirm==1

```

```

-----
Maternalageatbirthyears                                Maternal age
at birth (years)
-----

```

```

type: numeric (byte)

```

```

range: [18,38]          units: 1
unique values: 11      missing .: 0/18

```

```

mean: 25.8889
std. dev: 6.25807

```

```

percentiles:    10%    25%    50%    75%    90%
                19     20     25     30     38

```

```

. codebook Maternalage if Laboratoryconfirm==0

```

Maternalageatbirthyears
at birth (years)

Maternal age

type: numeric (byte)

range: [18,43] units: 1
unique values: 21 missing :: 0/111

mean: 26.5045
std. dev: 6.06161

percentiles: 10% 25% 50% 75% 90%
 19 23 26 29 37

. ranksum Maternalage, by(Laboratoryconfirm)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

Laboratory~1 | obs rank sum expected

-----+-----
0 | 111 7295 7215
1 | 18 1090 1170

-----+-----
combined | 129 8385 8385

unadjusted variance 21645.00
adjustment for ties -150.83

adjusted variance 21494.17

Ho: Matern~s(Labora~l==0) = Matern~s(Labora~l==1)

z = 0.546

Prob > |z| = 0.5853

Exact Prob = 0.5895

. stddiff Maternalage, by(Laboratoryconfirm)

-----+-----
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |
| Mean or N SD or (%) | Mean or N SD or (%) | Std Diff

-----+-----
Maternalag~s | 26.5 6.0616 | 25.89 6.2581 | 0.09993

. * Maternal socio-economic status

. tab Socioeconomics if Laboratoryconfirm==1, freq

Socio-econo |

mic status | Freq. Percent Cum.

-----+-----
. | 3 16.67 16.67
H | 1 5.56 22.22
L | 6 33.33 55.56
M | 8 44.44 100.00

```
-----+-----
Total |      18   100.00
```

```
. tab Socioeconomics if Laboratoryconfirm==0, freq
```

```
Socio-econo |
mic status |   Freq.   Percent   Cum.
-----+-----
. |      19   17.12   17.12
H |       8    7.21   24.32
L |      38   34.23   58.56
M |      46   41.44  100.00
-----+-----
Total |     111  100.00
```

```
. gen se_low=0
```

```
. replace se_low=1 if Socioeconomics=="L"
(45 real changes made)
```

```
. tab se_low Laboratoryconfirm, chi2
```

```
      | Laboratory confirmed
      | Congenital ZIKA
      | infection
se_low |      0      1 | Total
-----+-----
0 |      73     12 |     85
1 |      38      6 |     44
-----+-----
Total |     111     18 |    129
```

Pearson chi2(1) = 0.0056 Pr = 0.940

```
. stddiff se_low, by(Laboratoryconfirm)
```

```
-----+-----
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |
| Mean or N   SD or (%) | Mean or N   SD or (%) | Std Diff
-----+-----+-----+-----+-----
se low |   .3423   .47665 | .3333   .48507 | 0.01873
-----+-----+-----+-----+-----
```

```
. gen se_mod=0
```

```
. replace se_mod=1 if Socioeconomics=="M"
(56 real changes made)
```

```
. tab se_mod Laboratoryconfirm, chi2
```

```
      | Laboratory confirmed
      | Congenital ZIKA
      | infection
se_mod |      0      1 | Total
-----+-----
0 |      65     10 |     75
1 |      46      8 |     54
```

```
-----+-----+-----
Total | 111 18 | 129
```

Pearson chi2(1) = 0.0574 Pr = 0.811

```
. stddiff se_mod, by(Laboratoryconfirm)
```

```
-----+-----+-----
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |
| Mean or N SD or (%) | Mean or N SD or (%) | Std Diff
-----+-----+-----
se mod | .4144 .49485 | .4444 .51131 | -0.05968
-----+-----+-----
```

```
. gen se_hi=0
```

```
. replace se_hi=1 if Socioeconomics=="H"
(9 real changes made)
```

```
. tab se_hi Laboratoryconfirm, exact
```

```

| Laboratory confirmed
| Congenital ZIKA
| infection
se_hi | 0 1 | Total
-----+-----+-----
0 | 103 17 | 120
1 | 8 1 | 9
-----+-----+-----
Total | 111 18 | 129
```

```
Fisher's exact = 1.000
1-sided Fisher's exact = 0.634
```

```
. stddiff se_hi, by(Laboratoryconfirm)
```

```
-----+-----+-----
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |
| Mean or N SD or (%) | Mean or N SD or (%) | Std Diff
-----+-----+-----
se hi | .07207 .25978 | .05556 .2357 | 0.06659
-----+-----+-----
```

```
. gen se_unk=0
```

```
. replace se_unk=1 if Socioeconomics=="."
(22 real changes made)
```

```
. tab se_unk Laboratoryconfirm, chi2
```

```

| Laboratory confirmed
| Congenital ZIKA
| infection
se_unk | 0 1 | Total
-----+-----+-----
0 | 92 15 | 107
1 | 19 3 | 22
```

```
-----+-----+-----
Total |    111    18 |    129
```

Pearson chi2(1) = 0.0022 Pr = 0.962

```
. stddiff se_unk, by(Laboratoryconfirm)
```

```
-----+-----+-----
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |
| Mean or N   SD or (%) | Mean or N   SD or (%) | Std Diff
-----+-----+-----
se unk |   .1712    .37837 |   .1667    .38348 |   0.01182
-----+-----+-----
```

```
. * Maternal Exposures:
```

```
. tab Alcohol if Laboratoryconfirm==1, freq
```

```
Alcohol |   Freq.   Percent   Cum.
-----+-----+-----
0 |      17   94.44   94.44
1 |       1    5.56  100.00
-----+-----+-----
Total |      18  100.00
```

```
. tab Alcohol if Laboratoryconfirm==0, freq
```

```
Alcohol |   Freq.   Percent   Cum.
-----+-----+-----
0 |      99   89.19   89.19
1 |      12   10.81  100.00
-----+-----+-----
Total |     111  100.00
```

```
. tab Alcohol Laboratoryconfirm, exact
```

```
   | Laboratory confirmed
   | Congenital ZIKA
   | infection
Alcohol |    0    1 | Total
-----+-----+-----
0 |    99   17 |   116
1 |    12    1 |    13
-----+-----+-----
Total |   111   18 |   129
```

Fisher's exact = 0.692

1-sided Fisher's exact = 0.429

```
. stddiff Alcohol, by(Laboratoryconfirm)
```

```
-----+-----+-----
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |
| Mean or N   SD or (%) | Mean or N   SD or (%) | Std Diff
-----+-----+-----
Alcohol |   .1081    .31193 |   .05556    .2357 |   0.19010
-----+-----+-----
```

. tab Drug if Laboratoryconfirm==1, freq

Drug	Freq.	Percent	Cum.
0	18	100.00	100.00
Total	18	100.00	

. tab Drug if Laboratoryconfirm==0, freq

Drug	Freq.	Percent	Cum.
0	110	99.10	99.10
1	1	0.90	100.00
Total	111	100.00	

. tab Drug Laboratoryconfirm, exact

Drug	Laboratory confirmed Congenital ZIKA infection		Total
	0	1	
0	110	18	128
1	1	0	1
Total	111	18	129

Fisher's exact = 1.000
1-sided Fisher's exact = 0.860

. stddiff Drug, by(Laboratoryconfirm)

Drug	LaboratoryconfirmedCon~0		LaboratoryconfirmedCon~1		Std Diff
	Mean or N	SD or (%)	Mean or N	SD or (%)	
0	.009009	.094916	0	0	0.13423

. tab Smoking if Laboratoryconfirm==1, freq

Smoking	Freq.	Percent	Cum.
0	17	94.44	94.44
1	1	5.56	100.00
Total	18	100.00	

. tab Smoking if Laboratoryconfirm==0, freq

Smoking	Freq.	Percent	Cum.
0	105	95.45	95.45

1	5	4.55	100.00

Total	110	100.00	

. tab Smoking Laboratoryconfirm, exact

Laboratory confirmed Congenital ZIKA infection			
Smoking	0	1	Total

0	105	17	122
1	5	1	6

Total	110	18	128

Fisher's exact = 1.000
1-sided Fisher's exact = 0.605

. stddiff Smoking, by(Laboratoryconfirm)

LaboratoryconfirmedCon~0		LaboratoryconfirmedCon~1			
Mean or N	SD or (%)	Mean or N	SD or (%)	Std Diff	

Smoking	.04545	.20925	.05556	.2357	-0.04532

. tab Leadpois if Laboratoryconfirm==1, freq

Lead poisoning	Freq.	Percent	Cum.

0	17	94.44	94.44
1	1	5.56	100.00

Total	18	100.00	

. tab Leadpois if Laboratoryconfirm==0, freq

Lead poisoning	Freq.	Percent	Cum.

0	105	94.59	94.59
1	6	5.41	100.00

Total	111	100.00	

. tab Leadpois Laboratoryconfirm, exact

Laboratory confirmed Congenital ZIKA infection			
Lead poisoning	0	1	Total

0	105	17	122

1	6	1	7

Total	111	18	129

Fisher's exact = 1.000
 1-sided Fisher's exact = 0.660

. stddiff Leadpois, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1	
	Mean or N	SD or (%)	Mean or N SD or (%) Std Diff

Leadpoison~g	.05405	.22715	.05556 .2357 -0.00649

. * Maternal Comorbidities:

. tab Anymat if Laboratoryconfirm==1, freq

Any			
maternal			
comorbiditi			
es	Freq.	Percent	Cum.

0	15	83.33	83.33
1	3	16.67	100.00

Total	18	100.00	

. tab Anymat if Laboratoryconfirm==0, freq

Any			
maternal			
comorbiditi			
es	Freq.	Percent	Cum.

0	96	86.49	86.49
1	15	13.51	100.00

Total	111	100.00	

. tab Anymat Laboratoryconfirm, exact

Any	Laboratory confirmed		
maternal	Congenital ZIKA		
comorbidit	infection		
ies	0	1	Total

0	96	15	111
1	15	3	18

Total	111	18	129

Fisher's exact = 0.717
 1-sided Fisher's exact = 0.477

. stddiff Anymat, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1			
	Mean or N	SD or (%)	Mean or N	SD or (%)	Std Diff
Anymaterna~s	.1351	.34342	.1667	.38348	-0.08662

. tab Diabetes if Laboratoryconfirm==1, freq

Diabetes (previous or gestational)	Freq.	Percent	Cum.
0	17	94.44	94.44
1	1	5.56	100.00
Total	18	100.00	

. tab Diabetes if Laboratoryconfirm==0, freq

Diabetes (previous or gestational)	Freq.	Percent	Cum.
0	104	93.69	93.69
1	7	6.31	100.00
Total	111	100.00	

. tab Diabetes Laboratoryconfirm, exact

Diabetes (previous or gestational)	Laboratory confirmed Congenital ZIKA infection	Total
0	1	
0	104	17 121
1	7	1 8
Total	111	18 129

Fisher's exact = 1.000
1-sided Fisher's exact = 0.691

. stddiff Diabetes, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1			
	Mean or N	SD or (%)	Mean or N	SD or (%)	Std Diff

```
-----+-----+-----+-----+
Diabetespr~a | .06306   .24418 | .05556   .2357 | 0.03128
-----+-----+-----+-----+
```

```
. tab Vascular if Laboratoryconfirm==1, freq
```

Vascular pathologies	Freq.	Percent	Cum.
0	17	94.44	94.44
1	1	5.56	100.00
Total	18	100.00	

```
. tab Vascular if Laboratoryconfirm==0, freq
```

Vascular pathologies	Freq.	Percent	Cum.
0	106	95.50	95.50
1	5	4.50	100.00
Total	111	100.00	

```
. tab Vascular Laboratoryconfirm, exact
```

Vascular pathologies	Laboratory confirmed Congenital ZIKA infection		Total
	0	1	
0	106	17	123
1	5	1	6
Total	111	18	129

```
Fisher's exact = 1.000
1-sided Fisher's exact = 0.602
```

```
. stddiff Vascular, by(Laboratoryconfirm)
```

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1	
	Mean or N	SD or (%)	Std Diff
Vascularpa~s	.04505	.20834	-.04725

```
. tab Severe anemia if Laboratoryconfirm==1, freq
```

Severe anemia	Freq.	Percent	Cum.
0	17	94.44	94.44
1	1	5.56	100.00

```
-----+-----
Total |      18   100.00
```

```
. tab Severeanemia if Laboratoryconfirm==0, freq
```

```
Severe |
anemia |   Freq.  Percent  Cum.
-----+-----
0 |    106   95.50   95.50
1 |     5    4.50  100.00
-----+-----
Total |    111  100.00
```

```
. tab Severeanemia Laboratoryconfirm, exact
```

```
      | Laboratory confirmed
      | Congenital ZIKA
Severe | infection
anemia |    0      1 | Total
-----+-----+-----
0 |    106    17 |   123
1 |     5     1 |     6
-----+-----+-----
Total |    111    18 |   129
```

```
Fisher's exact =          1.000
1-sided Fisher's exact =      0.602
```

```
. stddiff Severeanemia, by(Laboratoryconfirm)
```

```
-----+-----+-----+-----+-----
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |
| Mean or N   SD or (%) | Mean or N   SD or (%) | Std Diff
-----+-----+-----+-----+-----
Severeanemia | .04505   .20834 | .05556   .2357 | -0.04725
-----+-----+-----+-----+-----
```

```
. tab Coinf if Laboratoryconfirm==1, freq
```

```
Co-infectio |
ns |   Freq.  Percent  Cum.
-----+-----
0 |    17   94.44   94.44
1 |     1   5.56  100.00
-----+-----
Total |    18  100.00
```

```
. tab Coinf if Laboratoryconfirm==0, freq
```

```
Co-infectio |
ns |   Freq.  Percent  Cum.
-----+-----
0 |   109   98.20   98.20
1 |     2   1.80  100.00
-----+-----
Total |   111  100.00
```

```
. tab Coinf Laboratoryconfirm, exact
```

		Laboratory confirmed Congenital ZIKA infection		Total
Co-infections	0	1		
0	109	17		126
1	2	1		3
Total	111	18		129

```
Fisher's exact = 0.365
1-sided Fisher's exact = 0.365
```

```
. stddiff Coinf, by(Laboratoryconfirm)
```

	LaboratoryconfirmedCon~0	SD or (%)	LaboratoryconfirmedCon~1	SD or (%)	Std Diff
Coinfections	.01802	.13362	.05556	.2357	-0.19593

```
. * Maternal ZIKV infection:
```

```
. tab SymptomaticM if Laboratoryconfirm==1, freq
```

Symptomatic Maternal Zika infection		Freq.	Percent	Cum.
0	14	77.78	77.78	
1	4	22.22	100.00	
Total	18	100.00		

```
. tab SymptomaticM if Laboratoryconfirm==0, freq
```

Symptomatic Maternal Zika infection		Freq.	Percent	Cum.
0	89	80.18	80.18	
1	22	19.82	100.00	
Total	111	100.00		

```
. tab SymptomaticM Laboratoryconfirm, chi2
```

Symptomatic Maternal Zika infection		Laboratory confirmed Congenital ZIKA infection		Total
	0	1		
0				
1				

0	89	14	103
1	22	4	26
-----+-----+-----			
Total	111	18	129

Pearson chi2(1) = 0.0555 Pr = 0.814

. stddiff SymptomaticM, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1		
	Mean or N	SD or (%)	Mean or N	SD or (%) Std Diff
-----+-----+-----				
Symptomatic~t	.1982	.40045	.2222	.42779 -0.05798

. tab Trimester if Laboratoryconfirm==1, freq

Trimester			
of Maternal			
Zika			
infection	Freq.	Percent	Cum.
-----+-----			
.	2	11.11	11.11
1	7	38.89	50.00
2	7	38.89	88.89
3	2	11.11	100.00
-----+-----			
Total	18	100.00	

. tab Trimester if Laboratoryconfirm==0, freq

Trimester			
of Maternal			
Zika			
infection	Freq.	Percent	Cum.
-----+-----			
.	22	19.82	19.82
1	27	24.32	44.14
2	37	33.33	77.48
3	25	22.52	100.00
-----+-----			
Total	111	100.00	

. gen t1=0

. replace t1=1 if Trimester=="1"
(34 real changes made)

. tab t1 Laboratoryconfirm, chi2

	Laboratory confirmed		
	Congenital ZIKA		
	infection		
t1	0	1	Total
-----+-----			

0	84	11	95
1	27	7	34

Total	111	18	129

Pearson chi2(1) = 1.6927 Pr = 0.193

. stddiff t1, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1		
	Mean or N	SD or (%)	Mean or N	SD or (%) Std Diff
t1	.2432	.43099	.3889	.50163 -0.31145

. gen t2=0

. replace t2=1 if Trimester=="2"
(45 real changes made)

. tab t2 Laboratoryconfirm, chi2

	Laboratory confirmed Congenital ZIKA infection		
t2	0	1	Total
0	74	11	85
1	37	7	44

Total	111	18	129

Pearson chi2(1) = 0.2127 Pr = 0.645

. stddiff t2, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1		
	Mean or N	SD or (%)	Mean or N	SD or (%) Std Diff
t2	.3333	.47354	.3889	.50163 -0.11389

. gen t3=0

. replace t3=1 if Trimester=="3"
(29 real changes made)

. tab t3 Laboratoryconfirm, exact

	Laboratory confirmed Congenital ZIKA infection		
t3	0	1	Total
0	86	16	102

1	25	2	27
-----+-----+-----			
Total	111	18	129

Fisher's exact = 0.360
 1-sided Fisher's exact = 0.220

. stddiff t3, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1	
	Mean or N	SD or (%)	Mean or N SD or (%) Std Diff
-----+-----+-----			
t3	.2252	.41963	.1111 .32338 0.30462

. gen t_unk=0

. replace t_unk=1 if Trimester=="."
 (24 real changes made)

. tab t_unk Laboratoryconfirm, exact

	Laboratory confirmed Congenital ZIKA infection		
t_unk	0	1	Total
-----+-----+-----			
0	89	16	105
1	22	2	24
-----+-----+-----			
Total	111	18	129

Fisher's exact = 0.523
 1-sided Fisher's exact = 0.304

. stddiff t_unk, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1	
	Mean or N	SD or (%)	Mean or N SD or (%) Std Diff
-----+-----+-----			
t_unk	.1982	.40045	.1111 .32338 0.23928

. * Dichorionic twins

. tab Dichorionictwins if Laboratoryconfirm==1, freq

Dichorionic	twins	Freq.	Percent	Cum.
-----+-----				
0	16	88.89	88.89	
1	2	11.11	100.00	
-----+-----				
Total	18	100.00		

. tab Dichorionictwins if Laboratoryconfirm==0, freq

Dichorionic twins	Freq.	Percent	Cum.
0	105	94.59	94.59
1	6	5.41	100.00
Total	111	100.00	

. tab Dichorionictwins Laboratoryconfirm, exact

Dichorionic twins	Laboratory confirmed infection		Total
	0	1	
0	105	16	121
1	6	2	8
Total	111	18	129

Fisher's exact = 0.309
1-sided Fisher's exact = 0.309

. stddiff Dichorionictwins, by(Laboratoryconfirm)

Dichorionictwins	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1	Std Diff
	Mean or N	SD or (%)	Mean or N
Dichorionictwins	.05405	.22715	.1111
			.32338
			-0.20418

* Gender

. tab Fetusgender if Laboratoryconfirm==1, freq

Fetus gender	Freq.	Percent	Cum.
F	10	55.56	55.56
M	8	44.44	100.00
Total	18	100.00	

. tab Fetusgender if Laboratoryconfirm==0, freq

Fetus gender	Freq.	Percent	Cum.
F	63	56.76	56.76
M	48	43.24	100.00
Total	111	100.00	

. gen male=0

. replace male=1 if Fetusgender=="M"
 (58 real changes made)

. tab male Laboratoryconfirm, chi2

	Laboratory confirmed Congenital ZIKA infection		Total
male	0	1	
0	63	10	73
1	48	8	56
Total	111	18	129

Pearson chi2(1) = 0.0091 Pr = 0.924

. stddiff male, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0		LaboratoryconfirmedCon~1		Std Diff
	Mean or N	SD or (%)	Mean or N	SD or (%)	
male	.4324	.49766	.4444	.51131	-0.02381

. * Birth
 . sum Term if Laboratoryconfirm==1, d

Term at birth (weeksâ€™ gestation)

Percentiles	Smallest		
1%	32	32	
5%	32	37	
10%	37	37	Obs 18
25%	38	37	Sum of Wgt. 18
50%	39		Mean 38.44444
	Largest		Std. Dev. 1.94701
75%	39	40	
90%	40	40	Variance 3.79085
95%	41	40	Skewness -2.029757
99%	41	41	Kurtosis 7.79679

. sum Term if Laboratoryconfirm==0, d

Term at birth (weeksâ€™ gestation)

Percentiles	Smallest		
1%	36	36	
5%	36	36	
10%	37	36	Obs 111
25%	38	36	Sum of Wgt. 111
50%	39		Mean 38.73874
	Largest		Std. Dev. 1.298333

```

75%      40      41
90%      40      41   Variance   1.685667
95%      41      41   Skewness  -.2073347
99%      41      41   Kurtosis  2.455612

```

```
. ranksum Term, by(Laboratoryconfirm)
```

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

```

Laboratory~1 |   obs   rank sum   expected
-----+-----
      0 |   111    7239    7215
      1 |    18    1146    1170
-----+-----
combined |   129    8385    8385

```

```

unadjusted variance  21645.00
adjustment for ties  -1142.03
-----
adjusted variance    20502.97

```

```

Ho: Termat~n(Labora~l==0) = Termat~n(Labora~l==1)
      z = 0.168
      Prob > |z| = 0.8669
      Exact Prob = 0.8661

```

```
. stddiff Term, by(Laboratoryconfirm)
```

```

-----+-----+-----+-----+-----+
| LaboratoryconfirmedCon~0 | LaboratoryconfirmedCon~1 |
| Mean or N   SD or (%) | Mean or N   SD or (%) | Std Diff
-----+-----+-----+-----+-----+
Termatbirt~n | 38.74   1.2983 | 38.44   1.947 | 0.17785
-----+-----+-----+-----+

```

```
. gen prema=0
```

```
. replace prema=1 if Term<37
(7 real changes made)
```

```
. tab prema Laboratoryconfirm, exact
```

```

| Laboratory confirmed
| Congenital ZIKA
| infection
prema |    0    1 | Total
-----+-----+-----
      0 |   105   17 |   122
      1 |    6    1 |    7
-----+-----+-----
Total |   111   18 |   129

```

```

Fisher's exact =          1.000
1-sided Fisher's exact =      0.660

```

```
. stddiff prema,by(Laboratoryconfirm)
```

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1			
	Mean or N	SD or (%)	Mean or N	SD or (%)	Std Diff
prema	.05405	.22715	.05556	.2357	-0.00649

. tab Mode if Laboratoryconfirm==1, freq

Mode of delivery	Freq.	Percent	Cum.
CS	5	27.78	27.78
N	13	72.22	100.00
Total	18	100.00	

. tab Mode if Laboratoryconfirm==0, freq

Mode of delivery	Freq.	Percent	Cum.
CS	14	12.61	12.61
N	97	87.39	100.00
Total	111	100.00	

. gen cs=0

. replace cs=1 if Mode=="CS"
(19 real changes made)

. tab cs Laboratoryconfirm, chi2

	Laboratory confirmed Congenital ZIKA infection		Total
cs	0	1	
0	97	13	110
1	14	5	19
Total	111	18	129

Pearson chi2(1) = 2.8362 Pr = 0.092

. stddiff cs, by(Laboratoryconfirm)

	LaboratoryconfirmedCon~0	LaboratoryconfirmedCon~1			
	Mean or N	SD or (%)	Mean or N	SD or (%)	Std Diff
cs	.1261	.3335	.2778	.46089	-0.37699

```
. gen apgar6=0
```

```
. replace apgar6=1 if Apgar<6  
(15 real changes made)
```

```
. tab apgar6 if Laboratoryconfirm==1, freq
```

apgar6	Freq.	Percent	Cum.
0	16	88.89	88.89
1	2	11.11	100.00
Total	18	100.00	

```
. tab apgar6 if Laboratoryconfirm==0, freq
```

apgar6	Freq.	Percent	Cum.
0	98	88.29	88.29
1	13	11.71	100.00
Total	111	100.00	

```
. tab apgar6 Laboratoryconfirm, exact
```

	Laboratory confirmed Congenital ZIKA infection		
apgar6	0	1	Total
0	98	16	114
1	13	2	15
Total	111	18	129

```
Fisher's exact = 1.000  
1-sided Fisher's exact = 0.651
```

```
. stddiff apgar6, by(Laboratoryconfirm)
```

	LaboratoryconfirmedCon~0 LaboratoryconfirmedCon~1		
	Mean or N	SD or (%)	Mean or N SD or (%) Std Diff
apgar6	.1171	.32302	.1111 .32338 0.01858

```
. tab Lactate if Laboratoryconfirm==1, freq
```

Lactates>4.	Freq.	Percent	Cum.
0	16	88.89	88.89
1	2	11.11	100.00
Total	18	100.00	

```
. tab Lactate if Laboratoryconfirm==0, freq
```

```
Lactates>4. |
```

5	Freq.	Percent	Cum.
0	95	85.59	85.59
1	16	14.41	100.00

Total	111	100.00	

```
. tab Lactate Laboratoryconfirm, exact
```

```
      | Laboratory confirmed  
      | Congenital ZIKA  
Lactates>4 | infection
```

.5	0	1	Total
0	95	16	111
1	16	2	18

Total	111	18	129

```
Fisher's exact = 1.000  
1-sided Fisher's exact = 0.523
```

```
. stddiff Lactate, by(Laboratoryconfirm)
```

```
-----  
|LaboratoryconfirmedCon~0 |LaboratoryconfirmedCon~1 |  
| Mean or N   SD or (%) | Mean or N   SD or (%) | Std Diff  
-----+-----+-----  
Lactates45 | .1441   .35283 | .1111   .32338 | 0.09761  
-----
```

```
. log close
```

```
name: <unnamed>
```

```
log: \\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Table1.log
```

```
log type: text
```

```
closed on: 23 Mar 2021, 11:49:30  
-----  
-----
```

```

-----
name: <unnamed>
log: \\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Table2.log
log type: text
opened on: 23 Mar 2021, 15:02:33

. import excel "\\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Source Data.xlsx",
sheet("Table 2") firstrow
(26 vars, 132 obs)

.
. destring CongZIKA, replace
CongZIKA: all characters numeric; replaced as byte
(3 missing values generated)

. destring Adverseoutcomesupto2y, replace
Adverseoutcomesupto2y: all characters numeric; replaced as byte
(21 missing values generated)

. destring Neurologicimpairments, replace
Neurologicimpairments: all characters numeric; replaced as byte
(21 missing values generated)

. destring Delayinmotoracquisitions, replace
Delayinmotoracquisitions: all characters numeric; replaced as byte
(21 missing values generated)

. destring Neurosensoryalterations, replace
Neurosensoryalterations: all characters numeric; replaced as byte
(21 missing values generated)

. destring Neurodevelopment2SDat3y, replace
Neurodevelopment2SDat3y: all characters numeric; replaced as byte
(70 missing values generated)

. destring Motordomain2SD, replace
Motordomain2SD: all characters numeric; replaced as byte
(70 missing values generated)

. destring Congitivedomain2SD, replace
Congitivedomain2SD: all characters numeric; replaced as byte
(70 missing values generated)

. destring Socioaffectivedomain2SD, replace
Socioaffectivedomain2SD: all characters numeric; replaced as byte
(70 missing values generated)

. destring Lowsocioeconomicstatus, replace
Lowsocioeconomicstatus: all characters numeric; replaced as byte
(22 missing values generated)

.
. ** Adverse outcomes at 2months of life:
. tab Adverseoutcomesupto2m if CongZIKA==1, freq

Adverse |

```

outcomes up to 2m	Freq.	Percent	Cum.
0	10	55.56	55.56
1	8	44.44	100.00
Total	18	100.00	

. tab Adverseoutcomesupto2m if CongZIKA==0, freq

Adverse outcomes up to 2m	Freq.	Percent	Cum.
0	107	96.40	96.40
1	4	3.60	100.00
Total	111	100.00	

. * Crude Analysis
. glm Adverseoutcomesupto2m CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 127
 Scale parameter = 1
Deviance = 59.17059599 (1/df) Deviance = .4659102
Pearson = 129 (1/df) Pearson = 1.015748

Variance function: V(u) = u*(1-u) [Bernoulli]
Link function : g(u) = ln(u) [Log]

 AIC = .4896945
Log likelihood = -29.58529799 BIC = -558.0256

	OIM	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]
CongZIKA	12.33333	6.87173	4.51	0.000	4.13827	36.75718
_cons	.036036	.0176904	-6.77	0.000	.0137681	.0943189

Note: _cons estimates baseline risk.

. est store CRUDE

. * Adjusted on maternal infection in the 1st trimester
. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 126
 Scale parameter = 1
Deviance = 49.46063976 (1/df) Deviance = .3925448
Pearson = 139.3390301 (1/df) Pearson = 1.105865

Variance function: V(u) = u*(1-u) [Bernoulli]

Link function : $g(u) = \ln(u)$ [Log]

AIC = .4299274
Log likelihood = -24.73031988 BIC = -562.8757

	OIM					
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	10.07381	5.427441	4.29	0.000	3.50424	28.95966
Maternalinfectioninthe1sttr	4.170967	2.163393	2.75	0.006	1.509164	11.52755
_cons	.0202444	.0116293	-6.79	0.000	.0065666	.0624127

Note: _cons estimates baseline risk.

. est store A

. lrtest CRUDE /* p=0.0018 => Difference between crude and adjusted RR */

Likelihood-ratio test LR chi2(1) = 9.71
(Assumption: CRUDE nested in A) Prob > chi2 = 0.0018

. * Effect modifiers?

. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Maternalage, fam(bin) link(log) nolog eform
convergence not achieved

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 125
Scale parameter = 1
Deviance = 49.3541955 (1/df) Deviance = .3948336
Pearson = 125.3919825 (1/df) Pearson = 1.003136

Variance function: $V(u) = u*(1-u)$ [Bernoulli]
Link function : $g(u) = \ln(u)$ [Log]

AIC = .4446062
Log likelihood = -24.67709775 BIC = -558.1224

	OIM					
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	9.294551	4.916121	4.22	0.000	3.296147	26.20899
Maternalinfectioninthe1sttr	4.250735	2.243583	2.74	0.006	1.510744	11.96017
Maternalageatbirthyears	.9689544	.0610639	-0.50	0.617	.8563677	1.096343
_cons	.0481705	.0792893	-1.84	0.065	.0019129	1.213028

Note: _cons estimates baseline risk.

Warning: parameter estimates produce inadmissible mean estimates in one or more observations.

Warning: convergence not achieved

. lrtest A

Likelihood-ratio test LR chi2(1) = 0.11
(Assumption: A nested in .) Prob > chi2 = 0.7442

. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Low, fam(bin) link(log) nolog eform
convergence not achieved

Generalized linear models Number of obs = 107
Optimization : ML Residual df = 103
 Scale parameter = 1
Deviance = 44.29026976 (1/df) Deviance = .4300026
Pearson = 198.6377814 (1/df) Pearson = 1.928522
Variance function: V(u) = u*(1-u) [Bernoulli]
Link function : g(u) = ln(u) [Log]
 AIC = .4886941
Log likelihood = -22.14513488 BIC = -437.0111

	OIM					
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	12.04362	7.95825	3.77	0.000	3.29834	43.9763
Maternalinfectioninthe1sttr	5.840566	4.057034	2.54	0.011	1.496872	22.789
Lowsocioeconomicstatus	1.553995	1.280183	0.54	0.593	.3091925	7.810347
_cons	.0121336	.011509	-4.65	0.000	.0018906	.0778704

Note: _cons estimates baseline risk.
Warning: parameter estimates produce inadmissible mean estimates in one or more observations.
Warning: convergence not achieved

. lrtest A
observations differ: 107 vs. 129
r(498);
end of do-file
r(498);
.do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Alcohol, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 125
 Scale parameter = 1
Deviance = 49.34920795 (1/df) Deviance = .3947937
Pearson = 143.6365806 (1/df) Pearson = 1.149093
Variance function: V(u) = u*(1-u) [Bernoulli]
Link function : g(u) = ln(u) [Log]
 AIC = .4445675
Log likelihood = -24.67460398 BIC = -558.1273

	OIM					
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	

```

CongZIKA | 10.398 5.671159 4.29 0.000 3.57024 30.28325
Maternalinfectioninthe1sttr | 4.311947 2.276365 2.77 0.006 1.532169 12.13501
Alcohol | 1.415908 1.389202 0.35 0.723 .2069612 9.686825
_cons | .0189497 .0117243 -6.41 0.000 .0056358 .0637156

```

Note: _cons estimates baseline risk.

. lrtest A

```

Likelihood-ratio test          LR chi2(1) =    0.11
(Assumption: A nested in .)    Prob > chi2 =   0.7385

```

. end of do-file

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Smoking, fam(bin) link(log) nolog eform

```

Generalized linear models      Number of obs =   128
Optimization   : ML           Residual df   =   124
                               Scale parameter =    1
Deviance       = 48.12350859    (1/df) Deviance = .3880928
Pearson        = 161.0006352    (1/df) Pearson  = 1.298392

```

```

Variance function: V(u) = u*(1-u)    [Bernoulli]
Link function   : g(u) = ln(u)        [Log]

```

```

                               AIC      = .4384649
Log likelihood = -24.06175429          BIC      = -553.5282

```

```

-----+-----
|           OIM
Adverseoutcomesupto2m | Risk Ratio  Std. Err.   z  P>|z|  [95% Conf. Interval]
-----+-----
CongZIKA | 12.59692  7.730123  4.13  0.000  3.783756  41.93781
Maternalinfectioninthe1sttr | 3.982913  2.037706  2.70  0.007  1.461221  10.8564
Smoking | 4.146219  4.336732  1.36  0.174  .5337515  32.20812
_cons | .016896  .0107137 -6.44  0.000  .0048757  .0585501

```

Note: _cons estimates baseline risk.

. lrtest A
observations differ: 128 vs. 129
r(498);

. end of do-file

r(498);

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

```

. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Leadp, fam(bin) link(log) nolog eform
note: Leadpoisoning != 0 predicts failure perfectly
Leadpoisoning dropped and 7 obs not used

```

Generalized linear models Number of obs = 122
 Optimization : ML Residual df = 126
 Scale parameter = 1
 Deviance = 49.49622339 (1/df) Deviance = .3928272
 Pearson = 131.2625822 (1/df) Pearson = 1.041767

Variance function: V(u) = u*(1-u) [Bernoulli]
 Link function : g(u) = ln(u) [Log]

 AIC = .42423
 Log likelihood = -24.36283646 BIC = -562.8401

```
-----+-----
```

	OIM					
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	10.13224	5.458601	4.30	0.000	3.524788	29.12583
Maternalinfectioninthe1sttr	3.820946	1.968834	2.60	0.009	1.391775	10.48994
Leadpoisoning	1 (omitted)					
_cons	.0219793	.0125777	-6.67	0.000	.00716	.0674706

```
-----+-----
```

Note: _cons estimates baseline risk.

```
. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);

end of do-file

r(498);

.do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

.glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Anymaternalco, fam(bin) link(log) nolog
eform
note: Anymaternalcomorbidities != 0 predicts failure perfectly
Anymaternalcomorbidities dropped and 18 obs not used
```

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 126
 Scale parameter = 1
 Deviance = 49.77844925 (1/df) Deviance = .3950671
 Pearson = 114.0857765 (1/df) Pearson = .9054427

Variance function: V(u) = u*(1-u) [Bernoulli]
 Link function : g(u) = ln(u) [Log]

 AIC = .4082759
 Log likelihood = -23.3337971 BIC = -562.5579

```
-----+-----
```

	OIM					
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	9.591073	5.279054	4.11	0.000	3.261029	28.20849
Maternalinfectioninthe1sttr	3.351702	1.754452	2.31	0.021	1.201443	9.350347

```
-----+-----
```

```

Anymaternalcomorbidities |      1 (omitted)
      _cons | .0266267   .01488  -6.49  0.000   .008905  .0796159

```

Note: _cons estimates baseline risk.

```

. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);

```

end of do-file

```
r(498);
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Infantgender, fam(bin) link(log) nolog eform
convergence not achieved
```

```

Generalized linear models          Number of obs =    129
Optimization   : ML                Residual df   =    125
                                Scale parameter =     1
Deviance       = 50.13978181        (1/df) Deviance = .4011183
Pearson        = 213.6708675        (1/df) Pearson  = 1.709367

```

```

Variance function: V(u) = u*(1-u)    [Bernoulli]
Link function   : g(u) = ln(u)       [Log]

```

```

                                AIC      = .450696
Log likelihood = -25.06989091          BIC      = -557.3368

```

```

-----+-----
                |      OIM
Adverseoutcomesupto2m | Risk Ratio  Std. Err.   z  P>|z|  [95% Conf. Interval]
-----+-----
CongZIKA | 16.11583  11.18632   4.00  0.000   4.134438  62.81866
Maternalinfectioninthe1sttr | 5.927055  4.261905   2.47  0.013   1.448019  24.26071
Infantgender | 1.79128  1.395039   0.75  0.454   .3892715  8.242795
      _cons | .0090272  .0100989  -4.21  0.000   .0010076  .0808742

```

Note: _cons estimates baseline risk.

Warning: parameter estimates produce inadmissible mean estimates in one or more observations.

Warning: convergence not achieved

```
. lrtest A
```

```

Likelihood-ratio test          LR chi2(1) =  -0.68
(Assumption: A nested in .)    Prob > chi2 =  1.0000

```

end of do-file

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Twins, fam(bin) link(log) nolog eform
note: Twins != 0 predicts failure perfectly
Twins dropped and 8 obs not used
```

Generalized linear models Number of obs = 121
 Optimization : ML Residual df = 126
 Scale parameter = 1
 Deviance = 49.57789331 (1/df) Deviance = .3934753
 Pearson = 127.8620699 (1/df) Pearson = 1.014778

Variance function: V(u) = u*(1-u) [Bernoulli]
 Link function : g(u) = ln(u) [Log]

 AIC = .4201519
 Log likelihood = -24.09979754 BIC = -562.7585

```
-----+-----
```

	OIM					[95% Conf. Interval]	
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z			
CongZIKA	10.47541	5.685295	4.33	0.000	3.615764	30.34881	
Maternalinfectioninthe1str	3.546996	1.830741	2.45	0.014	1.289801	9.754357	
Twins	1 (omitted)						
_cons	.0229467	.0130249	-6.65	0.000	.0075434	.0698033	

```
-----+-----
```

Note: _cons estimates baseline risk.

```
. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);

end of do-file

r(498);

.do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

.glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1str Modeofdelivery, fam(bin) link(log) nolog
eform
convergence not achieved
```

Generalized linear models Number of obs = 129
 Optimization : ML Residual df = 127
 Scale parameter = 1
 Deviance = 104.6869905 (1/df) Deviance = .824307
 Pearson = 100000049.2 (1/df) Pearson = 787402

Variance function: V(u) = u*(1-u) [Bernoulli]
 Link function : g(u) = ln(u) [Log]

 AIC = .8425348
 Log likelihood = -52.34349525 BIC = -512.5092

```
-----+-----
```

	OIM					[95% Conf. Interval]	
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z			
CongZIKA	3.810155	
Maternalinfectioninthe1str	2.028606	
Modeofdelivery	.3800644	.2491885	-1.48	0.140	.1051401	1.373871	

```
-----+-----
```

_cons | .1437552 1.44e-09 -1.9e+08 0.000 .1437552 .1437552

Note: _cons estimates baseline risk.

Warning: parameter estimates produce inadmissible mean estimates in one or more observations.

Warning: convergence not achieved

. lrtest A

Likelihood-ratio test LR chi2(1) = 55.23
(Assumption: . nested in A) Prob > chi2 = 0.0000

.
end of do-file

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. glm Adverseoutcomesupto2m CongZIKA Maternalinfectioninthe1sttr Prematurity, fam(bin) link(log) nolog eform
convergence not achieved

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 125
 Scale parameter = 1
Deviance = 51.14091788 (1/df) Deviance = .4091273
Pearson = 185.997202 (1/df) Pearson = 1.487978

Variance function: V(u) = u*(1-u) [Bernoulli]
Link function : g(u) = ln(u) [Log]

 AIC = .4584567
Log likelihood = -25.57045894 BIC = -556.3356

	OIM						
Adverseoutcomesupto2m	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]		
CongZIKA	11.95889	7.362507	4.03	0.000	3.578058	39.97001	
Maternalinfectioninthe1sttr	4.878225	2.911104	2.66	0.008	1.514619	15.7116	
Prematurity37wg	9.984096	11.48523	2.00	0.045	1.047435	95.16785	
_cons	.0143084	.0097692	-6.22	0.000	.0037534	.0545454	

Note: _cons estimates baseline risk.

Warning: parameter estimates produce inadmissible mean estimates in one or more observations.

Warning: convergence not achieved

. lrtest A

Likelihood-ratio test LR chi2(1) = -1.68
(Assumption: A nested in .) Prob > chi2 = 1.0000

.
end of do-file

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. tab Neontaldemise CongZIKA, exact

Neontal demise	CongZIKA		Total
	0	1	
0	111	17	128
1	0	1	1
Total	111	18	129

Fisher's exact = 0.140
 1-sided Fisher's exact = 0.140

. glm Structuralbrain CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
 Optimization : ML Residual df = 127
 Scale parameter = 1
 Deviance = 50.49819596 (1/df) Deviance = .3976236
 Pearson = 129 (1/df) Pearson = 1.015748

Variance function: $V(u) = u*(1-u)$ [Bernoulli]
 Link function : $g(u) = \ln(u)$ [Log]

 AIC = .4224666
 Log likelihood = -25.24909798 BIC = -566.698

	OIM					
Structuralbrainanomalies	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	12.33333	8.138462	3.81	0.000	3.383713	44.9539
_cons	.027027	.0153918	-6.34	0.000	.008852	.0825188

Note: _cons estimates baseline risk.

. glm Structuralbrain CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
 Optimization : ML Residual df = 126
 Scale parameter = 1
 Deviance = 43.76757084 (1/df) Deviance = .3473617
 Pearson = 167.458276 (1/df) Pearson = 1.329034

Variance function: $V(u) = u*(1-u)$ [Bernoulli]
 Link function : $g(u) = \ln(u)$ [Log]

 AIC = .3857951
 Log likelihood = -21.88378542 BIC = -568.5688

	OIM					
Structuralbrainanomalies	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	10.49826	6.71045	3.68	0.000	2.999385	36.74534
Maternalinfectioninthe1sttr	4.454848	2.779989	2.39	0.017	1.311148	15.1361
_cons	.014491	.0098654	-6.22	0.000	.003816	.055029

Note: _cons estimates baseline risk.

. glm Neurologicalsymptoms CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 127
 Scale parameter = 1
Deviance = 32.68034508 (1/df) Deviance = .2573256
Pearson = 128.9999999 (1/df) Pearson = 1.015748

Variance function: V(u) = u*(1-u) [Bernoulli]
Link function : g(u) = ln(u) [Log]

 AIC = .2843438
Log likelihood = -16.34017254 BIC = -584.5158

	OIM					
Neurologicalsymptoms	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	30.83333	32.85502	3.22	0.001	3.819506	248.9051
_cons	.009009	.0089683	-4.73	0.000	.0012803	.0633922

Note: _cons estimates baseline risk.

. glm Neurologicalsymptoms CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 126
 Scale parameter = 1
Deviance = 25.5258302 (1/df) Deviance = .202586
Pearson = 57.99262822 (1/df) Pearson = .460259

Variance function: V(u) = u*(1-u) [Bernoulli]
Link function : g(u) = ln(u) [Log]

 AIC = .2443863
Log likelihood = -12.7629151 BIC = -586.8105

	OIM					
Neurologicalsymptoms	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	21.4455	22.58241	2.91	0.004	2.722759	168.913
Maternalinfectioninthe1sttr	8.609643	8.936448	2.07	0.038	1.125832	65.84103
_cons	.0031805	.0039773	-4.60	0.000	.0002742	.036893

Note: _cons estimates baseline risk.

** Structural brain anomalies as effect-modifier?

. glm Neurologicalsymptoms CongZIKA Maternalinfectioninthe1sttr Structuralbrain, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 129
Optimization : ML Residual df = 125
 Scale parameter = 1

Deviance = 25.52492504 (1/df) Deviance = .2041994
 Pearson = 58.15185761 (1/df) Pearson = .4652149

Variance function: $V(u) = u*(1-u)$ [Bernoulli]
 Link function : $g(u) = \ln(u)$ [Log]

AIC = .2598831
 Log likelihood = -12.76246252 BIC = -581.9516

	OIM					
Neurologicalsymptoms	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	21.23418	23.46672	2.76	0.006	2.434106	185.2386
Maternalinfectioninthe1sttr	8.534267	9.216956	1.99	0.047	1.027717	70.86939
Structuralbrainanomalies	1.019548	.6584403	0.03	0.976	.287533	3.615157
_cons	.0031989	.0040463	-4.54	0.000	.0002681	.038166

Note: _cons estimates baseline risk.

. tab Neurologicalsymptoms CongZIKA if Structuralbrain==1, exact

Neurologic al symptoms	CongZIKA		Total
	0	1	
0	3	3	6
1	0	3	3
Total	3	6	9

Fisher's exact = 0.464
 1-sided Fisher's exact = 0.238

. glm Neurologicalsymptoms CongZIKA if Structuralbrain==0, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 120
 Optimization : ML Residual df = 118
 Scale parameter = 1
 Deviance = 22.1684435 (1/df) Deviance = .1878682
 Pearson = 120 (1/df) Pearson = 1.016949

Variance function: $V(u) = u*(1-u)$ [Bernoulli]
 Link function : $g(u) = \ln(u)$ [Log]

AIC = .2180704
 Log likelihood = -11.08422175 BIC = -542.7556

	OIM					
Neurologicalsymptoms	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	18	21.35416	2.44	0.015	1.759772	184.1148
_cons	.0092593	.0092163	-4.70	0.000	.0013162	.065137

Note: _cons estimates baseline risk.

```
. glm Neurologicalsymptoms CongZIKA Maternalinfectioninthe1str if Structuralbrain==0, fam(bin) link(log) nolog eform
```

```
Generalized linear models      Number of obs =    120
Optimization   : ML           Residual df   =    117
                               Scale parameter =     1
Deviance       = 18.57082858   (1/df) Deviance = .158725
Pearson        = 51.83984929   (1/df) Pearson  = .4430756

Variance function: V(u) = u*(1-u)      [Bernoulli]
Link function   : g(u) = ln(u)         [Log]

                               AIC       = .2047569
Log likelihood  = -9.28541429          BIC       = -541.5657
```

```
-----+-----
```

	OIM					
Neurologicalsymptoms	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	20.49089	22.96574	2.69	0.007	2.277994	184.3185
Maternalinfectioninthe1str	7.737567	8.565827	1.85	0.065	.8836632	67.75199
_cons	.0035561	.0045	-4.46	0.000	.0002977	.0424727

```
-----+-----
```

Note: _cons estimates baseline risk.

```
. end of do-file
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. ** Stratified on Maternal infection in the 1st trimester
. cs Adverseoutcomesupto2m CongZIKA, by(Maternalinfectioninthe1str)
```

```
Maternal infecti |    RR    [95% Conf. Interval]  M-H Weight
```

```
-----+-----
```

0	7.636364	1.192969 48.88143	.2315789
1	11.57143	2.947891 45.42161	.4117647
-----+-----			
Crude	12.33333	4.13827 36.75718	
M-H combined	10.15496	3.382333 30.48876	

```
-----+-----
```

```
Test of homogeneity (M-H)  chi2(1) = 0.126 Pr>chi2 = 0.7231
```

```
. end of do-file
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. ** Adverse outcomes at 2years of life:
. glm Adverseoutcomesupto2y CongZIKA, fam(bin) link(log) nolog eform
```

```
Generalized linear models      Number of obs =    111
Optimization   : ML           Residual df   =    109
                               Scale parameter =     1
Deviance       = 59.47439346   (1/df) Deviance = .5456366
```

Pearson = 111 (1/df) Pearson = 1.018349

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
Link function : $g(u) = \ln(u)$ [Log]

AIC = .5718414
Log likelihood = -29.73719673 BIC = -453.8644

	OIM					
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	7.68	4.132834	3.79	0.000	2.674882	22.05047
_cons	.0520833	.0226777	-6.79	0.000	.0221858	.1222706

Note: _cons estimates baseline risk.

. est store CRUDE

* Adjusted on maternal infection in the 1st trimester
. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
Optimization : ML Residual df = 108
Scale parameter = 1
Deviance = 58.28203098 (1/df) Deviance = .5396484
Pearson = 107.3983993 (1/df) Pearson = .9944296

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
Link function : $g(u) = \ln(u)$ [Log]

AIC = .5791174
Log likelihood = -29.14101549 BIC = -450.3472

	OIM					
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	6.667957	3.729054	3.39	0.001	2.228222	19.95387
Maternalinfectioninthe1sttr	1.78164	.9387635	1.10	0.273	.6343274	5.004104
_cons	.0449262	.0209486	-6.65	0.000	.0180133	.1120485

Note: _cons estimates baseline risk.

. est store A

. lrtest CRUDE

Likelihood-ratio test LR chi2(1) = 1.19
(Assumption: CRUDE nested in A) Prob > chi2 = 0.2749

* Effect modifiers?
. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Maternalage, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111

```

Optimization   : ML                      Residual df   =   107
Scale parameter =   1
Deviance       = 58.28068961             (1/df) Deviance = .5446793
Pearson        = 107.819364              (1/df) Pearson = 1.007658

Variance function: V(u) = u*(1-u/1)      [Binomial]
Link function   : g(u) = ln(u)           [Log]

AIC = .5971233
Log likelihood = -29.14034481            BIC = -445.639

```

```

-----
|               OIM
Adverseoutcomesupto2y | Risk Ratio Std. Err.   z   P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA | 6.682789 3.758764  3.38 0.001  2.219196 20.12425
Maternalinfectioninthe1sttr | 1.785488 .9472611  1.09 0.275  .6311988 5.050656
Maternalageatbirthyears | .9982092 .0489371 -0.04 0.971  .9067583 1.098883
_cons | .0470907 .0643476 -2.24 0.025  .0032345 .6855956
-----

```

Note: _cons estimates baseline risk.

. lrtest A

```

Likelihood-ratio test          LR chi2(1) =   0.00
(Assumption: A nested in .)    Prob > chi2 =  0.9708

```

. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Low, fam(bin) link(log) nolog eform

```

Generalized linear models      Number of obs =   93
Optimization   : ML           Residual df   =   89
Scale parameter =   1
Deviance       = 53.6510958    (1/df) Deviance = .6028213
Pearson        = 87.58781243   (1/df) Pearson = .9841327

Variance function: V(u) = u*(1-u/1)      [Binomial]
Link function   : g(u) = ln(u)           [Log]

AIC = .662915
Log likelihood = -26.8255479            BIC = -349.7503

```

```

-----
|               OIM
Adverseoutcomesupto2y | Risk Ratio Std. Err.   z   P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA | 6.628856 3.712668  3.38 0.001  2.211568 19.86904
Maternalinfectioninthe1sttr | 1.36452 .696087  0.61 0.542  .5020575 3.708567
Lowsocioeconomicstatus | 1.716076 .8379849  1.11 0.269  .6589952 4.468797
_cons | .0449557 .0232193 -6.01 0.000  .0163359 .1237158
-----

```

Note: _cons estimates baseline risk.

. lrtest A

```

observations differ: 93 vs. 111
r(498);

```

end of do-file

r(498);

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Alcohol, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 107
 Scale parameter = 1
 Deviance = 58.2782245 (1/df) Deviance = .5446563
 Pearson = 107.3874291 (1/df) Pearson = 1.003621

Variance function: V(u) = u*(1-u/1) [Binomial]
 Link function : g(u) = ln(u) [Log]

 AIC = .5971011
 Log likelihood = -29.13911225 BIC = -445.6415

	OIM						
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]		
CongZIKA	6.652203	3.733947	3.38	0.001	2.214001	19.98726	
Maternalinfectioninthe1sttr	1.772124	.9465195	1.07	0.284	.6220911	5.048174	
Alcohol	.9425184	.9145275	-0.06	0.951	.1407237	6.31266	
_cons	.0453355	.0221073	-6.34	0.000	.0174325	.1179009	

Note: _cons estimates baseline risk.

. lrtest A

Likelihood-ratio test LR chi2(1) = 0.00
 (Assumption: A nested in .) Prob > chi2 = 0.9508

. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Smoking, fam(bin) link(log) nolog eform
 note: Smoking != 0 predicts failure perfectly
 Smoking dropped and 4 obs not used

Generalized linear models Number of obs = 106
 Optimization : ML Residual df = 107
 Scale parameter = 1
 Deviance = 58.23854677 (1/df) Deviance = .5442855
 Pearson = 102.9291785 (1/df) Pearson = .9619549

Variance function: V(u) = u*(1-u/1) [Binomial]
 Link function : g(u) = ln(u) [Log]

 AIC = .573422
 Log likelihood = -28.53821188 BIC = -444.7129

	OIM						
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]		
CongZIKA	6.847706	3.851057	3.42	0.001	2.274264	20.61813	
Maternalinfectioninthe1sttr	1.641937	.8656024	0.94	0.347	.5842746	4.614196	

```
Smoking |      1 (omitted)
_cons | .0481465 .0222375 -6.57 0.000 .0194724 .1190447
```

Note: _cons estimates baseline risk.

```
. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);
```

end of do-file

```
r(498);
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Leadp, fam(bin) link(log) nolog eform
convergence not achieved
```

```
Generalized linear models          Number of obs =    111
Optimization   : ML                Residual df   =    109
                               Scale parameter =     1
Deviance       = 108.2702414        (1/df) Deviance = .993305
Pearson        = 100000057.9        (1/df) Pearson  = 917431.7
```

```
Variance function: V(u) = u*(1-u/1)    [Binomial]
Link function   : g(u) = ln(u)         [Log]
```

```
Log likelihood = -54.13512068        AIC      = 1.011444
                                           BIC      = -405.0686
```

```
-----+-----
```

	OIM					
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	3.46651
Maternalinfectioninthe1sttr	.7715198	.2863655	-0.70	0.485	.37274	1.596938
Leadpoisoning	2.432884
_cons	.165099	1.65e+09	-1.8e+08	0.000	.165099	.165099

```
-----+-----
```

Note: _cons estimates baseline risk.

Warning: parameter estimates produce inadmissible mean estimates in one or more observations.

Warning: convergence not achieved

```
.
end of do-file
```

```
. Tab Adverseoutcomesupto2y CongZIKA if Leadp==1
command Tab is unrecognized
r(199);
```

```
. tab Adverseoutcomesupto2y CongZIKA if Leadp==1
```

```
-----+-----
```

Adverse outcomes up to 2y	CongZIKA		Total
	0	1	

```
-----+-----
```

0	4	1	5
1	1	0	1

Total	5	1	6

. tab Adverseoutcomesupto2y CongZIKA if Leadp==0

Adverse	CongZIKA		
outcomes	0	1	Total
up to 2y	-----		
0	87	8	95
1	4	6	10

Total	91	14	105

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Anymaternalco, fam(bin) link(log) nolog eform

note: Anymaternalcomorbidities != 0 predicts failure perfectly
Anymaternalcomorbidities dropped and 16 obs not used

Generalized linear models Number of obs = 95
Optimization : ML Residual df = 108
 Scale parameter = 1
Deviance = 59.03125837 (1/df) Deviance = .5465857
Pearson = 94.72467703 (1/df) Pearson = .8770803

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .5414375
Log likelihood = -27.0497829 BIC = -449.598

	OIM						
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]		
CongZIKA	7.374224	4.233645	3.48	0.001	2.393479	22.71972	
Maternalinfectioninthe1sttr	1.343991	.7123262	0.56	0.577	.4756121	3.79787	
Anymaternalcomorbidities	1 (omitted)						
_cons	.056681	.0255512	-6.37	0.000	.0234274	.1371358	

Note: _cons estimates baseline risk.

. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);

end of do-file

r(498);

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

```
. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Infantgender, fam(bin) link(log) nolog eform
```

```
Generalized linear models          Number of obs =    111
Optimization   : ML                 Residual df   =    107
                                   Scale parameter =     1
Deviance       = 57.75156168         (1/df) Deviance = .5397342
Pearson        = 108.0139714         (1/df) Pearson  = 1.009476
```

```
Variance function: V(u) = u*(1-u/1)      [Binomial]
Link function   : g(u) = ln(u)           [Log]
```

```
Log likelihood = -28.87578084          AIC      = .5923564
                                           BIC      = -446.1682
```

```
-----+-----
              |      OIM
Adverseoutcomesupto2y | Risk Ratio Std. Err.   z   P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA | 6.499541  3.62741  3.35  0.001  2.176832  19.4062
Maternalinfectioninthe1sttr | 1.836386 .9526067  1.17  0.241  .6643724  5.075937
Infantgender | .6968215 .3475328 -0.72  0.469  .2621762  1.852038
   _cons | .0538296 .0280132 -5.61  0.000  .0194111  .1492765
-----+-----
```

Note: _cons estimates baseline risk.

```
. lrtest A
```

```
Likelihood-ratio test          LR chi2(1) =    0.53
(Assumption: A nested in .)     Prob > chi2 =  0.4664
```

```
. end of do-file
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Twins, fam(bin) link(log) nolog eform
note: Twins != 0 predicts failure perfectly
     Twins dropped and 5 obs not used
```

```
Generalized linear models          Number of obs =    106
Optimization   : ML                 Residual df   =    108
                                   Scale parameter =     1
Deviance       = 58.29501464         (1/df) Deviance = .5397687
Pearson        = 103.3580007         (1/df) Pearson  = .9570185
```

```
Variance function: V(u) = u*(1-u/1)      [Binomial]
Link function   : g(u) = ln(u)           [Log]
```

```
Log likelihood = -28.90493481          AIC      = .5748637
                                           BIC      = -450.3342
```

```
-----+-----
              |      OIM
Adverseoutcomesupto2y | Risk Ratio Std. Err.   z   P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA | 6.417676  3.56332  3.35  0.001  2.161527  19.05438
-----+-----
```



```
Maternalinfectioninthe1sttr | 1.743244 .912558 1.06 0.288 .6248401 4.863483
Twins | 1 (omitted)
_cons | .0473565 .0221332 -6.53 0.000 .0189474 .1183609
```

Note: _cons estimates baseline risk.

```
. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);
```

end of do-file

```
r(498);
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Modeofdelivery, fam(bin) link(log) nolog eform
```

```
Generalized linear models          Number of obs =    111
Optimization   : ML                Residual df   =    107
                               Scale parameter =     1
Deviance       = 57.99576103        (1/df) Deviance = .5420165
Pearson        = 105.1992692        (1/df) Pearson  = .9831707
```

```
Variance function: V(u) = u*(1-u/1)      [Binomial]
Link function   : g(u) = ln(u)           [Log]
```

```
Log likelihood = -28.99788052          AIC      = .5945564
                                           BIC      = -445.924
```

```
-----
|              OIM
Adverseoutcomesupto2y | Risk Ratio  Std. Err.   z   P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA | 6.639172  3.681354   3.41  0.001   2.239398  19.68324
Maternalinfectioninthe1sttr | 1.912284  1.010029   1.23  0.220   .6791498  5.384424
Modeofdelivery | .6487064  .5848379  -0.48  0.631   .1108286  3.797034
_cons | .0457759  .0214718  -6.57  0.000   .0182545  .1147899
-----
```

Note: _cons estimates baseline risk.

```
. lrtest A
```

```
Likelihood-ratio test          LR chi2(1) =    0.29
(Assumption: A nested in .)    Prob > chi2 =    0.5926
```

end of do-file

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr Prematurity, fam(bin) link(log) nolog eform
```

```
Generalized linear models          Number of obs =    111
Optimization   : ML                Residual df   =    107
                               Scale parameter =     1
```

Deviance = 56.88109024 (1/df) Deviance = .531599
 Pearson = 104.0412757 (1/df) Pearson = .9723484

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

Log likelihood = -28.44054512 AIC = .5845143
 BIC = -447.0386

	OIM					
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	7.666233	4.622367	3.38	0.001	2.35152	24.99282
Maternalinfectioninthe1sttr	1.923627	1.057265	1.19	0.234	.6550628	5.648833
Prematurity37wg	4.495911	4.734269	1.43	0.153	.5708058	35.41172
_cons	.0370707	.0194581	-6.28	0.000	.0132508	.1037096

Note: _cons estimates baseline risk.

. lrtest A

Likelihood-ratio test LR chi2(1) = 1.40
 (Assumption: A nested in .) Prob > chi2 = 0.2366

end of do-file

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. * Sub-analysis

. tab Adverseoutcomesupto2y CongZIKA if Structural==1

Adverse	CongZIKA		
outcomes	0	1	Total
up to 2y			
0	1	1	2
1	2	4	6
Total	3	5	8

. glm Adverseoutcomesupto2y CongZIKA if Structural==1, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 8
 Optimization : ML Residual df = 6
 Scale parameter = 1
 Deviance = 8.823109245 (1/df) Deviance = 1.470518
 Pearson = 8 (1/df) Pearson = 1.333333

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

Log likelihood = -4.411554623 AIC = 1.602889
 BIC = -3.65354

	OIM					
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	1.2	.5585696	0.39	0.695	.4819128	2.988092
_cons	.6666667	.2721655	-0.99	0.321	.2995071	1.483919

Note: _cons estimates baseline risk.

. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr if Structural==1, fam(bin) link(log) nolog eform
convergence not achieved

Generalized linear models Number of obs = 8
Optimization : ML Residual df = 6
 Scale parameter = 1
Deviance = 8.823109245 (1/df) Deviance = 1.470518
Pearson = 7.988612804 (1/df) Pearson = 1.331435

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = 1.602889
Log likelihood = -4.411554623 BIC = -3.65354

	OIM					
Adverseoutcomesupto2y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	1.095445	.509902	0.20	0.845	.4399242	2.727743
Maternalinfectioninthe1sttr	1.095445
_cons	.6666667	.2721655	-0.99	0.321	.2995071	1.483919

Note: _cons estimates baseline risk.

Warning: convergence not achieved

. tab Adverseoutcomesupto2y CongZIKA if Structural==0

Adverse outcomes up to 2y	CongZIKA		Total
	0	1	
0	90	8	98
1	3	2	5
Total	93	10	103

. glm Adverseoutcomesupto2y CongZIKA if Structural==0, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 103
Optimization : ML Residual df = 101
 Scale parameter = 1
Deviance = 36.51413981 (1/df) Deviance = .3615261
Pearson = 102.9999995 (1/df) Pearson = 1.019802

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

AIC = .3933412
 Log likelihood = -18.2570699 BIC = -431.5935

```
-----+-----
          |           OIM
Adverseoutcomesupto2y | Risk Ratio Std. Err.   z P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA |      6.2  5.270294   2.15 0.032   1.171737   32.80601
  _cons |   .0322581 .0183213  -6.05 0.000   .0105971   .0981948
-----+-----
```

Note: _cons estimates baseline risk.

. glm Adverseoutcomesupto2y CongZIKA Maternalinfectioninthe1sttr if Structural==0, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 103
 Optimization : ML Residual df = 100
 Scale parameter = 1
 Deviance = 36.50351232 (1/df) Deviance = .3650351
 Pearson = 104.3085701 (1/df) Pearson = 1.043086

Variance function: V(u) = u*(1-u/1) [Binomial]
 Link function : g(u) = ln(u) [Log]

AIC = .4126555
 Log likelihood = -18.25175616 BIC = -426.9694

```
-----+-----
          |           OIM
Adverseoutcomesupto2y | Risk Ratio Std. Err.   z P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA | 6.229669 5.300758   2.15 0.032   1.175403   33.01743
Maternalinfectioninthe1sttr | .8979346 .9501202  -0.10 0.919   .1128687   7.14358
  _cons |   .0329284 .0197506  -5.69 0.000   .0101628   .1066905
-----+-----
```

Note: _cons estimates baseline risk.

. tab Neurologicimpairments CongZIKA, freq

```
Neurologic |
impairment |      CongZIKA
s |      0      1 | Total
-----+-----
0 |     92     10 |    102
1 |      4      5 |      9
-----+-----
Total |     96     15 |    111
```

. glm Neurologicimpairments CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 109
 Scale parameter = 1
 Deviance = 52.35082474 (1/df) Deviance = .4802828
 Pearson = 111 (1/df) Pearson = 1.018349

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

AIC = .5076651
 Log likelihood = -26.17541237 BIC = -460.988

	OIM					
Neurologicimpairments	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	8	4.885352	3.41	0.001	2.417061	26.47844
_cons	.0416667	.0203947	-6.49	0.000	.0159643	.1087498

Note: _cons estimates baseline risk.

. glm Neurologicimpairments CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 108
 Scale parameter = 1
 Deviance = 51.25680245 (1/df) Deviance = .4746
 Pearson = 114.8890414 (1/df) Pearson = 1.063787

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

AIC = .515827
 Log likelihood = -25.62840122 BIC = -457.3725

	OIM					
Neurologicimpairments	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	7.129378	4.438435	3.16	0.002	2.104414	24.15305
Maternalinfectioninthe1sttr	1.875192	1.10714	1.06	0.287	.5895002	5.964958
_cons	.0351488	.0185808	-6.33	0.000	.012472	.0990567

Note: _cons estimates baseline risk.

. tab Delayinmotoracquisitions CongZIKA, freq

Delay in motor acquisitio	CongZIKA		
	0	1	Total
0	95	13	108
1	1	2	3
Total	96	15	111

. glm Delayinmotoracquisitions CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 109
 Scale parameter = 1

Deviance = 22.89847737 (1/df) Deviance = .2100778
 Pearson = 111 (1/df) Pearson = 1.018349

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

Log likelihood = -11.44923869 AIC = .2423286
 BIC = -490.4403

	OIM					
Delayinmotoracquisitions	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	12.8	15.26862	2.14	0.033	1.235507	132.6096
_cons	.0104167	.0103623	-4.59	0.000	.0014824	.0731957

Note: _cons estimates baseline risk.

. glm Delayinmotoracquisitions CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 108
 Scale parameter = 1
 Deviance = 21.50365408 (1/df) Deviance = .1991079
 Pearson = 60.33332903 (1/df) Pearson = .5586419

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

Log likelihood = -10.75182704 AIC = .2477807
 BIC = -487.1256

	OIM					
Delayinmotoracquisitions	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	9.000001	11.03903	1.79	0.073	.8131929	99.60738
Maternalinfectioninthe1sttr	3.923077	4.78711	1.12	0.263	.3588837	42.88447
_cons	.0065359	.0076315	-4.31	0.000	.0006629	.0644446

Note: _cons estimates baseline risk.

. tab Neurosensoryalterations CongZIKA, freq

Neurosenso	CongZIKA		Total
ry	0	1	
alteration			
s	0	1	Total
0	95	12	107
1	1	3	4
Total	96	15	111

. glm Neurosensoryalterations CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 109
 Scale parameter = 1
 Deviance = 26.13031606 (1/df) Deviance = .2397277
 Pearson = 110.9999985 (1/df) Pearson = 1.018349

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

 AIC = .2714443
 Log likelihood = -13.06515803 BIC = -487.2085

```

-----
                                                 OIM
Neurosensoryalterations | Risk Ratio  Std. Err.   z  P>|z|  [95% Conf. Interval]
-----+-----
      CongZIKA |    19.2  21.51985   2.64  0.008   2.134287  172.7228
      _cons |   .0104167  .0103623  -4.59  0.000   .0014824  .0731957
-----

```

Note: _cons estimates baseline risk.

. glm Neurosensoryalterations CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 111
 Optimization : ML Residual df = 108
 Scale parameter = 1
 Deviance = 25.66113713 (1/df) Deviance = .2376031
 Pearson = 185.4801619 (1/df) Pearson = 1.717409

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]

 AIC = .2852355
 Log likelihood = -12.83056856 BIC = -482.9681

```

-----
                                                 OIM
Neurosensoryalterations | Risk Ratio  Std. Err.   z  P>|z|  [95% Conf. Interval]
-----+-----
      CongZIKA |  22.47253  25.37779   2.76  0.006   2.45701  205.5404
Maternalinfectioninthe1sttr | .4965815  .5383341  -0.65  0.518   .0593226  4.156819
      _cons |   .0115768  .0115947  -4.45  0.000   .0016258  .082434
-----

```

Note: _cons estimates baseline risk.

. cs Adverseoutcomesupto2y CongZIKA, by(Maternalinfectioninthe1sttr)

```

-----
Maternal infecti |    RR    [95% Conf. Interval]  M-H Weight
-----+-----
      0 |  8.444444  1.993798  35.76523   .3176471
      1 |        5  1.072846  23.30251   .4615385
-----+-----
      Crude |    7.68  2.674882  22.05047
      M-H combined |  6.404181  2.23786  18.32712
-----

```

Test of homogeneity (M-H) $\chi^2(1) = 0.240$ Pr> $\chi^2 = 0.6239$

.
end of do-file

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. ** Adverse outcomes at 3years of life:
. tab Neurodevelopment2SDat3y CongZIKA

Neurodevelopment	CongZIKA		Total
<-2SD at	0	1	
3y			
0	44	4	48
1	7	7	14
Total	51	11	62

. glm Neurodevelopment2SDat3y CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 60
 Scale parameter = 1
Deviance = 55.21538369 (1/df) Deviance = .9202564
Pearson = 61.99999999 (1/df) Pearson = 1.033333

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
Link function : $g(u) = \ln(u)$ [Log]

 AIC = .9550868
Log likelihood = -27.60769185 BIC = -192.4127

	OIM		Std. Err.	z	P> z	[95% Conf. Interval]
Neurodevelopment2SDat3y	Risk Ratio					
CongZIKA	4.636364	1.940623	3.66	0.000	2.041238	10.5308
_cons	.1372549	.0481859	-5.66	0.000	.0689759	.2731229

Note: _cons estimates baseline risk.

. est store CRUDE

. * Adjusted on maternal infection in the 1st trimester
. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 59
 Scale parameter = 1
Deviance = 54.33232261 (1/df) Deviance = .9208868
Pearson = 61.13050756 (1/df) Pearson = 1.03611

Variance function: $V(u) = u*(1-u/1)$ [Binomial]
Link function : $g(u) = \ln(u)$ [Log]

AIC = .973102
 Log likelihood = -27.16616131 BIC = -189.1686

```

-----
|           OIM
Neurodevelopment2SDat3y | Risk Ratio  Std. Err.   z  P>|z|  [95% Conf. Interval]
-----+-----
CongZIKA | 4.432214  1.867274   3.53 0.000   1.940943  10.12112
Maternalinfectioninthe1str | 1.431828  .5386402   0.95 0.340   .6849787  2.992987
  _cons | .1222047  .0461757  -5.56 0.000   .0582716  .2562823
-----

```

Note: _cons estimates baseline risk.

. est store A

. lrtest CRUDE

Likelihood-ratio test LR chi2(1) = 0.88
 (Assumption: CRUDE nested in A) Prob > chi2 = 0.3474

. * Effect modifiers?

. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1str Maternalage, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
 Optimization : ML Residual df = 58
 Scale parameter = 1
 Deviance = 54.30076072 (1/df) Deviance = .93622
 Pearson = 60.23498069 (1/df) Pearson = 1.038534

Variance function: V(u) = u*(1-u/1) [Binomial]
 Link function : g(u) = ln(u) [Log]

AIC = 1.004851
 Log likelihood = -27.15038036 BIC = -185.073

```

-----
|           OIM
Neurodevelopment2SDat3y | Risk Ratio  Std. Err.   z  P>|z|  [95% Conf. Interval]
-----+-----
CongZIKA | 4.362711  1.877119   3.42 0.001   1.877219  10.13907
Maternalinfectioninthe1str | 1.467104  .593885   0.95 0.344   .6635809  3.243606
  Maternalageatbirthyears | 1.005938  .0337233   0.18 0.860   .9419665  1.074255
  _cons | .1033932  .1065144  -2.20 0.028   .0137276  .7787333
-----

```

Note: _cons estimates baseline risk.

. lrtest A

Likelihood-ratio test LR chi2(1) = 0.03
 (Assumption: A nested in .) Prob > chi2 = 0.8590

. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1str Low, fam(bin) link(log) nolog eform
 convergence not achieved

Generalized linear models Number of obs = 60

Optimization : ML Residual df = 56
 Scale parameter = 1
 Deviance = 52.70108623 (1/df) Deviance = .9410908
 Pearson = 61.34982158 (1/df) Pearson = 1.095533
 Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]
 AIC = 1.011685
 Log likelihood = -26.35054311 BIC = -176.5822

	OIM					
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	4.959629	2.066594	3.84	0.000	2.191633	11.22356
Maternalinfectioninthe1str	1.892683	.8958861	1.35	0.178	.74846	4.78616
Lowsocioeconomicstatus	1.879118	.8997054	1.32	0.188	.7352012	4.802882
_cons	.0784325	.0461682	-4.32	0.000	.0247427	.2486247

Note: _cons estimates baseline risk.
 Warning: parameter estimates produce inadmissible mean estimates in one or more observations.
 Warning: convergence not achieved

. lrtest A
 observations differ: 60 vs. 62
 r(498);

end of do-file

r(498);

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1str Alcohol, fam(bin) link(log) nolog eform
 convergence not achieved

Generalized linear models Number of obs = 62
 Optimization : ML Residual df = 60
 Scale parameter = 1
 Deviance = 97.87058364 (1/df) Deviance = 1.631176
 Pearson = 100000055.6 (1/df) Pearson = 1666668
 Variance function: $V(u) = u*(1-u/1)$ [Binomial]
 Link function : $g(u) = \ln(u)$ [Log]
 AIC = 1.643074
 Log likelihood = -48.93529182 BIC = -149.7575

	OIM					
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	2.139565
Maternalinfectioninthe1str	1.265906
Alcohol	.1674685	.1603071	-1.87	0.062	.0256526	1.09329

_cons | .3858783 3.86e-09 -9.5e+07 0.000 .3858783 .3858783

Note: _cons estimates baseline risk.

Warning: parameter estimates produce inadmissible mean estimates in one or more observations.

Warning: convergence not achieved

end of do-file

. tab Neurodevelopment2SDat3y CongZIKA if Alcohol==1

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	11	1	12
1	1	0	1
Total	12	1	13

. tab Neurodevelopment2SDat3y CongZIKA if Alcohol==0

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	33	3	36
1	6	7	13
Total	39	10	49

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1str Smoking, fam(bin) link(log) nolog eform
note: Smoking != 0 predicts failure perfectly
Smoking dropped and 2 obs not used

Generalized linear models Number of obs = 59
Optimization : ML Residual df = 58
 Scale parameter = 1
Deviance = 54.08660189 (1/df) Deviance = .9325276
Pearson = 58.53110455 (1/df) Pearson = 1.009157

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .9736936
Log likelihood = -26.69765599 BIC = -184.3441

		OIM			
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]

```

CongZIKA | 4.16078 1.748102 3.39 0.001 1.826218 9.479752
Maternalinfectioninthe1str | 1.437647 .540676 0.97 0.334 .6879061 3.004523
Smoking | 1 (omitted)
_cons | .1298248 .0487985 -5.43 0.000 .0621453 .2712106

```

Note: _cons estimates baseline risk.

```

. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);

```

end of do-file

```
r(498);
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1str Leadp, fam(bin) link(log) nolog eform
convergence not achieved
```

```

Generalized linear models          Number of obs =    62
Optimization   : ML                Residual df   =    60
                                Scale parameter =     1
Deviance       = 100.2234335        (1/df) Deviance = 1.670391
Pearson        = 100000046.9        (1/df) Pearson  = 1666667

```

```

Variance function: V(u) = u*(1-u/1)      [Binomial]
Link function   : g(u) = ln(u)           [Log]

```

```

                                AIC      = 1.681023
Log likelihood = -50.11171674          BIC      = -147.4046

```

```

-----
|           OIM
Neurodevelopment2SDat3y | Risk Ratio Std. Err.   z   P>|z|   [95% Conf. Interval]
-----+-----
CongZIKA | 2.495347      .      .      .      .
Maternalinfectioninthe1str | 1.42363      .      .      .      .
Leadpoisoning | 1.066297 .870057  0.08  0.937  .2154423  5.277468
_cons | .3128134 3.13e-09 -1.2e+08 0.000 .3128134 .3128134

```

Note: _cons estimates baseline risk.

Warning: parameter estimates produce inadmissible mean estimates in one or more observations.

Warning: convergence not achieved

```
. lrtest A
```

```

Likelihood-ratio test          LR chi2(1) = 45.89
(Assumption: . nested in A)    Prob > chi2 = 0.0000

```

end of do-file

```
. tab Neurodevelopment2SDat3y CongZIKA if Leadp==0
```

```
Neurodevel |
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	42	4	46
1	6	7	13
Total	48	11	59

```
. tab Neurodevelopment2SDat3y CongZIKA if Leadp==1
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	2	2	
1	1	1	
Total	3	3	

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1sttr Anymaternalco, fam(bin) link(log) nolog eform
```

```
note: Anymaternalcomorbidities != 0 predicts failure perfectly  
Anymaternalcomorbidities dropped and 11 obs not used
```

```
--Break--  
r(1);
```

```
end of do-file
```

```
--Break--  
r(1);
```

```
. tab Neurodevelopment2SDat3y CongZIKA if Anymaternal==1  
Anymaternal not found  
r(111);
```

```
. tab Neurodevelopment2SDat3y CongZIKA if Anymaternal==1
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	8	3	11
Total	8	3	11

```
. tab Neurodevelopment2SDat3y CongZIKA if Anymaternal==0
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0			
1			
Total	0	1	1

0	36	1	37
1	7	7	14
Total	43	8	51

. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"

. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1str Infantgender, fam(bin) link(log) nolog eform
convergence not achieved

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 60
 Scale parameter = 1
Deviance = 90.4375652 (1/df) Deviance = 1.507293
Pearson = 100000047.9 (1/df) Pearson = 1666667

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = 1.523187
Log likelihood = -45.2187826 BIC = -157.1905

	OIM					
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	2.135364	
Maternalinfectioninthe1str	1.352287	
Infantgender	.3170819	.1175789	-3.10	0.002	.1532967	.6558587
_cons	.4065965	4.07e-09	-9.0e+07	0.000	.4065965	.4065965

Note: _cons estimates baseline risk.
Warning: parameter estimates produce inadmissible mean estimates in one or more observations.
Warning: convergence not achieved

. lrtest A

Likelihood-ratio test LR chi2(1) = 36.11
(Assumption: . nested in A) Prob > chi2 = 0.0000

. end of do-file

. tab Neurodevelopment2SDat3y Infantgender, chi2

Neurodevel			
opment			
<-2SD at	Infant gender		
3y	0	1	Total
0	16	32	48
1	8	6	14
Total	24	38	62

Pearson chi2(1) = 2.5898 Pr = 0.108

. glm Neurodevelopment2SDat3y CongZIKA Infantgender, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 59
 Scale parameter = 1
Deviance = 52.950206 (1/df) Deviance = .8974611
Pearson = 63.68186783 (1/df) Pearson = 1.079354

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .9508098
Log likelihood = -26.475103 BIC = -190.5507

	OIM					
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	4.286504	1.776361	3.51	0.000	1.902648	9.657126
Infantgender	.5602415	.2291838	-1.42	0.157	.2512843	1.249065
_cons	.1906202	.0758524	-4.17	0.000	.0873887	.4157981

Note: _cons estimates baseline risk.

. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);

. glm Neurodevelopment2SDat3y CongZIKA Twins, fam(bin) link(log) nolog eform
note: Twins != 0 predicts failure perfectly
Twins dropped and 3 obs not used

Generalized linear models Number of obs = 59
Optimization : ML Residual df = 60
 Scale parameter = 1
Deviance = 55.24601818 (1/df) Deviance = .920767
Pearson = 59.51219511 (1/df) Pearson = .9918699

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .9403265
Log likelihood = -27.15012226 BIC = -192.382

	OIM					
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	4.363636	1.82007	3.53	0.000	1.926695	9.882894
Twins	1 (omitted)					
_cons	.1458333	.0509424	-5.51	0.000	.0735387	.2891996

Note: _cons estimates baseline risk.

```
. lrtest A
observations differ: 62 vs. 59
r(498);
```

```
. glm Neurodevelopment2SDat3y CongZIKA Modeofdelivery, fam(bin) link(log) nolog eform
--Break--
r(1);
```

```
. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);
```

```
. tab Neurodevelopment2SDat3y CongZIKA Modeofdelivery
too many variables specified
r(103);
```

```
. tab Neurodevelopment2SDat3y CongZIKA if Modeofdeliver==1
```

Neurodevelopment	CongZIKA		Total
<-2SD at	0	1	
3y			
0	6	0	6
1	1	1	2
Total	7	1	8

```
. tab Neurodevelopment2SDat3y CongZIKA if Modeofdeliver==0
```

Neurodevelopment	CongZIKA		Total
<-2SD at	0	1	
3y			
0	38	4	42
1	6	6	12
Total	44	10	54

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1sttr Prematurity, fam(bin) link(log) nolog
eform
--Break--
r(1);
```

```
end of do-file
```

```
--Break--
r(1);
```

```
. glm Neurodevelopment2SDat3y CongZIKA Prematurity, fam(bin) link(log) nolog eform
```

```
Generalized linear models          Number of obs =      62
```


Optimization : ML Residual df = 59
 Scale parameter = 1
 Deviance = 54.40961952 (1/df) Deviance = .9221969
 Pearson = 61.99999999 (1/df) Pearson = 1.050847
 Variance function: V(u) = u*(1-u/1) [Binomial]
 Link function : g(u) = ln(u) [Log]
 AIC = .9743487
 Log likelihood = -27.20480976 BIC = -189.0913

```
-----
```

	OIM		Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	5.090909	2.264061	3.66	0.000	2.129334	12.17158	
Prematurity37wg	2.666667	2.403701	1.09	0.277	.4557283	15.60384	
_cons	.125	.0477352	-5.45	0.000	.059136	.2642214	

```
-----
```

Note: _cons estimates baseline risk.

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. lrtest A
df(unrestricted) = df(restricted) = 3
r(498);
```

end of do-file

```
r(498);
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD3ed0_000000.tmp"
```

```
. * Sub-analysis
. tab Neurodevelopment2SDat3y CongZIKA if Structural==1, exact
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	2	0	2
1	0	4	4
Total	2	4	6

Fisher's exact = 0.067
 1-sided Fisher's exact = 0.067

```
. tab Neurodevelopment2SDat3y CongZIKA if Structural==0
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	42	4	46

1	7	3	10
-----+-----+-----			
Total	49	7	56

. glm Neurodevelopment2SDat3y CongZIKA if Structural==0, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 56
Optimization : ML Residual df = 54
 Scale parameter = 1
Deviance = 49.75211266 (1/df) Deviance = .9213354
Pearson = 56 (1/df) Pearson = 1.037037

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .9598592
Log likelihood = -24.87605633 BIC = -167.6169

	OIM					
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	3	1.678191	1.96	0.050	1.002216	8.980096
_cons	.1428571	.0499896	-5.56	0.000	.0719521	.2836354

Note: _cons estimates baseline risk.

. glm Neurodevelopment2SDat3y CongZIKA Maternalinfectioninthe1sttr if Structural==0, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 56
Optimization : ML Residual df = 53
 Scale parameter = 1
Deviance = 49.68726937 (1/df) Deviance = .9374956
Pearson = 55.37021041 (1/df) Pearson = 1.044721

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .9944155
Log likelihood = -24.84363469 BIC = -163.6564

	OIM					
Neurodevelopment2SDat3y	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	2.996958	1.673399	1.97	0.049	1.003226	8.952877
Maternalinfectioninthe1sttr	1.164735	.6840908	0.26	0.795	.3683713	3.682718
_cons	.1368373	.0537176	-5.07	0.000	.0633946	.2953634

Note: _cons estimates baseline risk.

. tab Motordomain CongZIKA, freq

Motor	
domain	CongZIKA

<-2SD	0	1	Total
0	50	9	59
1	1	2	3
Total	51	11	62

. glm Motordomain CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 60
 Scale parameter = 1
Deviance = 20.27497888 (1/df) Deviance = .3379163
Pearson = 61.99998564 (1/df) Pearson = 1.033333

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .3915319
Log likelihood = -10.13748944 BIC = -227.3531

	OIM					
Motordomain2SD	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	9.272729	10.93035	1.89	0.059	.9201159	93.44855
_cons	.0196078	.0194147	-3.97	0.000	.0028159	.1365353

Note: _cons estimates baseline risk.

. glm Motordomain CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 59
 Scale parameter = 1
Deviance = 18.30323253 (1/df) Deviance = .3102243
Pearson = 112.0075866 (1/df) Pearson = 1.898434

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]

 AIC = .3919876
Log likelihood = -9.151616264 BIC = -225.1977

	OIM					
Motordomain2SD	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	9.344466	10.71218	1.95	0.051	.9880204	88.37778
Maternalinfectioninthe1sttr	4.573782	5.188736	1.34	0.180	.4950261	42.25935
_cons	.0093458	.0116673	-3.74	0.000	.000809	.1079583

Note: _cons estimates baseline risk.

. tab Congitive CongZIKA, freq

Congitive domain <-2SD	CongZIKA		Total
	0	1	
0	48	5	53
1	3	6	9
Total	51	11	62

. glm Congitive CongZIKA, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 60
 Scale parameter = 1
Deviance = 37.97744701 (1/df) Deviance = .6329575
Pearson = 61.99999999 (1/df) Pearson = 1.033333
Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]
 AIC = .6770556
Log likelihood = -18.9887235 BIC = -209.6506

	OIM					
Congivedomain2SD	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	9.272727	5.786977	3.57	0.000	2.728882	31.50868
_cons	.0588235	.0329478	-5.06	0.000	.0196238	.1763272

Note: _cons estimates baseline risk.

. glm Congitive CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform

Generalized linear models Number of obs = 62
Optimization : ML Residual df = 59
 Scale parameter = 1
Deviance = 35.61810621 (1/df) Deviance = .6036967
Pearson = 55.36963588 (1/df) Pearson = .9384684
Variance function: V(u) = u*(1-u/1) [Binomial]
Link function : g(u) = ln(u) [Log]
 AIC = .6712598
Log likelihood = -17.8090531 BIC = -207.8828

	OIM					
Congivedomain2SD	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	8.286445	5.18194	3.38	0.001	2.432586	28.22724
Maternalinfectioninthe1sttr	2.114485	1.074745	1.47	0.141	.7808331	5.725995
_cons	.0447738	.0271193	-5.13	0.000	.0136602	.146755

Note: _cons estimates baseline risk.

.

```
. tab Socioaffectivedomain2SD CongZIKA, freq
```

Socio-af- ctive domain	CongZIKA		Total
<-2SD	0	1	
0	45	7	52
1	6	4	10
Total	51	11	62

```
. glm Socioaffectivedomain2SD CongZIKA, fam(bin) link(log) nolog eform
```

```
Generalized linear models          Number of obs =    62
Optimization   : ML                Residual df   =    60
                                   Scale parameter =     1
Deviance       = 51.36607585        (1/df) Deviance = .8561013
Pearson        =    62              (1/df) Pearson = 1.033333

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function   : g(u) = ln(u)      [Log]

                                   AIC      = .8930012
Log likelihood = -25.68303793        BIC      = -196.262
```

```
-----+-----
```

	OIM					
Socioaffectivedomain2SD	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	3.090909	1.710225	2.04	0.041	1.044984	9.142455
_cons	.1176471	.0451156	-5.58	0.000	.055483	.2494606

```
-----+-----
```

Note: _cons estimates baseline risk.

```
. glm Socioaffectivedomain2SD CongZIKA Maternalinfectioninthe1sttr, fam(bin) link(log) nolog eform
```

```
Generalized linear models          Number of obs =    62
Optimization   : ML                Residual df   =    59
                                   Scale parameter =     1
Deviance       = 48.7697619        (1/df) Deviance = .8266061
Pearson        = 67.94200592        (1/df) Pearson = 1.151559

Variance function: V(u) = u*(1-u/1) [Binomial]
Link function   : g(u) = ln(u)      [Log]

                                   AIC      = .8833833
Log likelihood = -24.38488095        BIC      = -194.7312
```

```
-----+-----
```

	OIM					
Socioaffectivedomain2SD	Risk Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
CongZIKA	3.28655	1.698334	2.30	0.021	1.193656	9.049011
Maternalinfectioninthe1sttr	2.424121	1.27574	1.68	0.092	.8641584	6.800101
_cons	.0810377	.0388727	-5.24	0.000	.0316502	.2074902

```
-----+-----
```

Note: _cons estimates baseline risk.

```
. tab Neurodevelopment2SDat3y CongZIKA if Maternalinfectioninthe1sttr==1
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	12	1	13
1	3	3	6
Total	15	4	19

```
. tab Neurodevelopment2SDat3y CongZIKA if Maternalinfectioninthe1sttr==0
```

Neurodevelopment <-2SD at 3y	CongZIKA		Total
	0	1	
0	32	3	35
1	4	4	8
Total	36	7	43

```
. cs Neurodevelopment2SDat3y CongZIKA, by(Maternalinfectioninthe1sttr)
```

Maternal infecti	RR	[95% Conf. Interval]	M-H Weight
0	5.142857	1.669925 15.83842	.6511628
1	3.75	1.176125 11.95663	.6315789
Crude	4.636364	2.041238 10.5308	
M-H combined	4.457061	1.989707 9.984078	

Test of homogeneity (M-H) $\chi^2(1) = 0.147$ $Pr > \chi^2 = 0.7010$

.

```
. log close
```

name: <unnamed>

log: \\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Table2.log

log type: text

closed on: 23 Mar 2021, 17:55:04

```
-----  
-----  
name: <unnamed>  
log: \\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Tables3-4.log  
log type: text  
opened on: 24 Mar 2021, 20:51:56  
  
. import excel "\\HOME\lpomar\Mes Documents\Zika_enfants-Guyane\Nature\R1\Dataset\Source Data.xlsx",  
sheet("Tables 3 & 4") firstrow  
(44 vars, 140 obs)  
  
.   
. destring CongZIKA HCatbirthcm HCat1mcm HCat2mcm HCat1ycm HCat2ycm HCat3ycm Birthweightg  
Weightat1mkg Weightat2mKg Weightat1ykg Weightat2yKg Weightat3yKg Structuralbrainanomal  
> ies Corticaldevelopmentanomaly Corpuscallosumanomaly Calcificationsorcysticlesions Posteriorfossaanomaly  
Ventriculomegaly Microphtalmy AbnormalOAE Neurologicalsymptomsat2m Ar  
> throgyriposis Hypertonia Dysphagiaswallowingdisorders Seizures Neurologicimpairmentsat2y Cerebralpalsyat2y  
Severedystoniaortremors Seizuresat2y Delayinmotoracquisitions Ageats  
> ittingpositionm Ageatwalkingm Neurosensoryalterations Impairedresponsetovisualstim  
Impairedresponsetoauditoryst Neurodevelopment2SDat3y Motordomain2SD Congitivedomain2SD Soci  
> ooaffectivedomain2SD, replace  
CongZIKA: all characters numeric; replaced as byte  
(11 missing values generated)  
HCatbirthcm already numeric; no replace  
HCat1mcm: all characters numeric; replaced as double  
(12 missing values generated)  
HCat2mcm: all characters numeric; replaced as byte  
(12 missing values generated)  
HCat1ycm: all characters numeric; replaced as double  
(28 missing values generated)  
HCat2ycm: all characters numeric; replaced as double  
(30 missing values generated)  
HCat3ycm: all characters numeric; replaced as double  
(78 missing values generated)  
Birthweightg already numeric; no replace  
Weightat1mkg: all characters numeric; replaced as double  
(6 missing values generated)  
Weightat2mKg: all characters numeric; replaced as double  
(7 missing values generated)  
Weightat1ykg: all characters numeric; replaced as double  
(22 missing values generated)  
Weightat2yKg: all characters numeric; replaced as double  
(25 missing values generated)  
Weightat3yKg: all characters numeric; replaced as double  
(72 missing values generated)  
Structuralbrainanomalies: all characters numeric; replaced as byte  
(11 missing values generated)  
Corticaldevelopmentanomaly: all characters numeric; replaced as byte  
(11 missing values generated)  
Corpuscallosumanomaly: all characters numeric; replaced as byte  
(11 missing values generated)  
Calcificationsorcysticlesions: all characters numeric; replaced as byte  
(11 missing values generated)  
Posteriorfossaanomaly: all characters numeric; replaced as byte  
(11 missing values generated)  
Ventriculomegaly: all characters numeric; replaced as byte  
(11 missing values generated)
```

Microphthalmia: all characters numeric; replaced as byte
 (11 missing values generated)
 AbnormalOAE: all characters numeric; replaced as byte
 (85 missing values generated)
 Neurologicalsymptomsat2m: all characters numeric; replaced as byte
 (11 missing values generated)
 Arthrogryposis: all characters numeric; replaced as byte
 (11 missing values generated)
 Hypertonia: all characters numeric; replaced as byte
 (11 missing values generated)
 Dysphagiaswallowingdisorders: all characters numeric; replaced as byte
 (11 missing values generated)
 Seizures: all characters numeric; replaced as byte
 (11 missing values generated)
 Neurologicimpairmentsat2y: all characters numeric; replaced as byte
 (29 missing values generated)
 Cerebralpalsyat2y: all characters numeric; replaced as byte
 (29 missing values generated)
 Severedystoniaortremors: all characters numeric; replaced as byte
 (29 missing values generated)
 Seizuresat2y: all characters numeric; replaced as byte
 (29 missing values generated)
 Delayinmotoracquisitions: all characters numeric; replaced as byte
 (27 missing values generated)
 Ageatsittingpositionm: all characters numeric; replaced as double
 (28 missing values generated)
 Ageatwalkingm: all characters numeric; replaced as double
 (29 missing values generated)
 Neurosensoryalterations: all characters numeric; replaced as byte
 (29 missing values generated)
 Impairedresponsetovisualstim: all characters numeric; replaced as byte
 (27 missing values generated)
 Impairedresponsetoauditoryst: all characters numeric; replaced as byte
 (27 missing values generated)
 Neurodevelopment2SDat3y: all characters numeric; replaced as byte
 (78 missing values generated)
 Motordomain2SD: all characters numeric; replaced as byte
 (78 missing values generated)
 Congitivedomain2SD: all characters numeric; replaced as byte
 (78 missing values generated)
 Socioaffectivedomain2SD: all characters numeric; replaced as byte
 (78 missing values generated)

.
 . * Neonatal demise & NICU admission:
 . tab Neonataldemise CongZIKA, exact

Neonatal demise	CongZIKA		Total
	0	1	
0	111	17	128
1	0	1	1
Total	111	18	129

Fisher's exact = 0.140
 1-sided Fisher's exact = 0.140


```
. tab NICU CongZIKA, chi2
```

NICU admission	CongZIKA		Total
	0	1	
0	97	15	112
1	14	3	17
Total	111	18	129

Pearson chi2(1) = 0.2225 Pr = 0.637

```
. * HC:  
. codebook HCatbirth if CongZIKA==1
```

```
-----  
-----  
HCatbirthcm  
birth (cm) HC at  
-----  
-----
```

type: numeric (double)

range: [27.5,35.5] units: .1
unique values: 10 missing .: 0/18

mean: 32.5556
std. dev: 1.84621

percentiles: 10% 25% 50% 75% 90%
 31 31.5 32.75 34 35

```
. codebook HCatbirth if CongZIKA==0
```

```
-----  
-----  
HCatbirthcm  
birth (cm) HC at  
-----  
-----
```

type: numeric (double)

range: [29,38] units: .1
unique values: 14 missing .: 0/111

mean: 33.3784
std. dev: 1.70056

percentiles: 10% 25% 50% 75% 90%
 31 32.5 33 34.5 35.5

```
. ranksum HCatbirth, by(CongZIKA)
```

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	111	7471	7215
1	18	914	1170
combined	129	8385	8385

unadjusted variance 21645.00

adjustment for ties -529.81

adjusted variance 21115.19

Ho: HCatbi~m(CongZIKA==0) = HCatbi~m(CongZIKA==1)

z = 1.762

Prob > |z| = 0.0781

Exact Prob = 0.0784

. codebook HCat1m if CongZIKA==1

 HCat1mcm HC at
 1m (cm)

type: numeric (double)

range: [31,39] units: 1
 unique values: 8 missing .: 1/18

tabulation: Freq. Value
 1 31
 2 33
 1 34
 1 35
 3 36
 4 37
 4 38
 1 39
 1 .

. codebook HCat1m if CongZIKA==0

 HCat1mcm HC at
 1m (cm)

type: numeric (double)

range: [33,40] units: .1
 unique values: 11 missing .: 0/111

mean: 36.536
std. dev: 1.60922

percentiles: 10% 25% 50% 75% 90%
34 36 37 38 39

. ranksum HCat1m, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	111	7226	7159.5
1	17	1030	1096.5
combined	128	8256	8256

unadjusted variance 20285.25
adjustment for ties -639.72

adjusted variance 19645.53

Ho: HCat1mcm(CongZIKA==0) = HCat1mcm(CongZIKA==1)

z = 0.474

Prob > |z| = 0.6352

Exact Prob = 0.6391

. codebook HCat1ycm if CongZIKA==1

HCat1ycm HC at 1y
(cm)

type: numeric (double)

range: [37,47] units: 1
unique values: 8 missing : 3/18

tabulation: Freq. Value
1 37
1 41
1 42
4 43
4 44
2 45
1 46
1 47
3 .

. codebook HCat1ycm if CongZIKA==0

HCat1ycm
(cm)

HC at 1y

type: numeric (double)

range: [41,50] units: .1
unique values: 11 missing .: 14/111

mean: 45.5722
std. dev: 2.19729

percentiles: 10% 25% 50% 75% 90%
 42 44 46 47 48

. ranksum HCat1ycm, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	97	5851.5	5480.5
1	15	476.5	847.5
combined	112	6328	6328

unadjusted variance 13701.25
adjustment for ties -244.67

adjusted variance 13456.58

Ho: HCat1ycm(CongZIKA==0) = HCat1ycm(CongZIKA==1)

z = 3.198

Prob > |z| = 0.0014

Exact Prob = 0.0010

. codebook HCat2ycm if CongZIKA==1

HCat2ycm
(cm)

HC at 2y

type: numeric (double)

range: [38,50] units: 1
unique values: 8 missing .: 3/18

tabulation: Freq. Value
 1 38
 1 44
 2 45
 4 46

```

1 47
3 48
2 49
1 50
3 .

```

```
. codebook HCat2ycm if CongZIKA==0
```

```
-----
-----
HCat2ycm                                     HC at 2y
(cm)
-----
-----
```

```
type: numeric (double)
```

```
range: [44,53]          units: .1
unique values: 11      missing :: 16/111
```

```
mean: 48.4053
std. dev: 2.14537
```

```
percentiles:   10%   25%   50%   75%   90%
               45    47    48    50    51
```

```
. ranksum HCat2ycm, by(CongZIKA)
```

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	95	5585	5272.5
1	15	520	832.5
combined	110	6105	6105

```
unadjusted variance 13181.25
adjustment for ties -242.39
-----
adjusted variance 12938.86
```

```
Ho: HCat2ycm(CongZIKA==0) = HCat2ycm(CongZIKA==1)
z = 2.747
Prob > |z| = 0.0060
Exact Prob = 0.0053
```

```
. codebook HCat3ycm if CongZIKA==1
```

```
-----
-----
HCat3ycm                                     HC at 3y
(cm)
-----
-----
```


Birthweightg
Birthweight (g)

type: numeric (double)

range: [1910,3310] units: 1
unique values: 17 missing .: 0/18

mean: 2791.61
std. dev: 353.75

percentiles: 10% 25% 50% 75% 90%
 2160 2675 2905 2970 3190

. codebook Birthweightg if CongZIKA==0

Birthweightg
Birthweight (g)

type: numeric (double)

range: [1930,4620] units: 1
unique values: 98 missing .: 0/111

mean: 3144.13
std. dev: 490.859

percentiles: 10% 25% 50% 75% 90%
 2455 2755 3185 3495 3665

. ranksum Birthweightg, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	111	7649.5	7215
1	18	735.5	1170
combined	129	8385	8385

unadjusted variance 21645.00
adjustment for ties -1.15

adjusted variance 21643.85

Ho: Birthw~g(CongZIKA==0) = Birthw~g(CongZIKA==1)

z = 2.953

Prob > |z| = 0.0031

Exact Prob = 0.0027

. codebook Weightat1mkg if CongZIKA==1

Weightat1mkg Weight at
1m (kg)

type: numeric (double)

range: [3,4.1] units: .1
unique values: 9 missing .: 1/18

tabulation: Freq. Value
1 3
1 3.2
1 3.4
2 3.5
3 3.7
5 3.8
2 3.9
1 4
1 4.1
1 .

. codebook Weightat1mkg if CongZIKA==0

Weightat1mkg Weight at
1m (kg)

type: numeric (double)

range: [2.4,5.4] units: .01
unique values: 28 missing .: 0/111

mean: 4.05315
std. dev: .549577

percentiles: 10% 25% 50% 75% 90%
 3.4 3.7 4.2 4.4 4.7

. ranksum Weightat1mkg, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	111	7613	7159.5
1	17	643	1096.5

-----+-----
combined | 128 8256 8256

unadjusted variance 20285.25
adjustment for ties -95.07

adjusted variance 20190.18

Ho: Weig~mkg(CongZIKA==0) = Weig~mkg(CongZIKA==1)
z = 3.192
Prob > |z| = 0.0014
Exact Prob = 0.0011

. codebook Weightat2m if CongZIKA==1

Weightat2mKg Weight at
2m (Kg)

type: numeric (double)

range: [4,6.2] units: .1
unique values: 10 missing :: 1/18

mean: 4.85294
std. dev: .458418

percentiles: 10% 25% 50% 75% 90%
4.4 4.6 4.8 5 5.3

. codebook Weightat2m if CongZIKA==0

Weightat2mKg Weight at
2m (Kg)

type: numeric (double)

range: [3.5,6.5] units: .1
unique values: 25 missing :: 1/111

mean: 5.18455
std. dev: .670641

percentiles: 10% 25% 50% 75% 90%
4.2 4.7 5.2 5.7 6

. ranksum Weightat2m, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	110	7362.5	7040
1	17	765.5	1088
combined	127	8128	8128

unadjusted variance 19946.67

adjustment for ties -58.55

adjusted variance 19888.12

Ho: Weig~mKg(CongZIKA==0) = Weig~mKg(CongZIKA==1)

z = 2.287

Prob > |z| = 0.0222

Exact Prob = 0.0214

. codebook Weightat1y if CongZIKA==1

 Weightat1ykg Weight at
 1y (kg)

type: numeric (double)

range: [6,11.3] units: .1
 unique values: 13 missing : 3/18

mean: 9.63333
 std. dev: 1.37616

percentiles: 10% 25% 50% 75% 90%
 8 8.9 10 10.7 11.2

. codebook Weightat1y if CongZIKA==0

 Weightat1ykg Weight at
 1y (kg)

type: numeric (double)

range: [6.4,13.3] units: .1
 unique values: 45 missing : 14/111

mean: 10.0299
 std. dev: 1.34507

percentiles: 10% 25% 50% 75% 90%
 8.3 8.9 10.1 10.9 11.8

```
. ranksum Weightat1y, by(CongZIKA)
```

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	97	5558	5480.5
1	15	770	847.5
combined	112	6328	6328

unadjusted variance 13701.25

adjustment for ties -12.00

adjusted variance 13689.25

Ho: Weig~ykg(CongZIKA==0) = Weig~ykg(CongZIKA==1)

z = 0.662

Prob > |z| = 0.5077

Exact Prob = 0.5128

```
. codebook Weightat2y if CongZIKA==1
```

Weightat2yKg
2y (Kg)

Weight at

type: numeric (double)

range: [9.6,13.9] units: .1
unique values: 15 missing .: 3/18

mean: 12.1333
std. dev: 1.25338

percentiles: 10% 25% 50% 75% 90%
 9.8 11.5 12.3 13.1 13.8

```
. codebook Weightat2y if CongZIKA==0
```

Weightat2yKg
2y (Kg)

Weight at

type: numeric (double)

range: [9.4,15] units: .1
unique values: 42 missing .: 17/111

mean: 12.3851

std. dev: 1.22246

percentiles:	10%	25%	50%	75%	90%
	10.8	11.6	12.4	13.2	14

. ranksum Weightat2y, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	94	5223.5	5170
1	15	771.5	825
combined	109	5995	5995

unadjusted variance 12925.00

adjustment for ties -14.61

adjusted variance 12910.39

Ho: $Wei \sim 2yKg(CongZIKA==0) = Wei \sim 2yKg(CongZIKA==1)$

z = 0.471

Prob > |z| = 0.6377

Exact Prob = 0.6425

. codebook Weightat3y if CongZIKA==1

Weightat3yKg Weight at
3y (Kg)

type: numeric (double)

range: [11.4,20]

units: .1

unique values: 11

missing :: 6/18

mean: 15.15

std. dev: 2.15259

percentiles:	10%	25%	50%	75%	90%
	13.9	14.2	14.6	16.05	17.5

. codebook Weightat3y if CongZIKA==0

Weightat3yKg Weight at
3y (Kg)

type: numeric (double)

range: [12,19.4] units: .1
 unique values: 35 missing .: 61/111

mean: 14.826
 std. dev: 1.54521

percentiles: 10% 25% 50% 75% 90%
 12.9 13.8 14.7 15.8 16.85

. ranksum Weightat3y, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	50	1547.5	1575
1	12	405.5	378
combined	62	1953	1953

unadjusted variance 3150.00
 adjustment for ties -4.20

 adjusted variance 3145.80

Ho: Wei~3yKg(CongZIKA==0) = Wei~3yKg(CongZIKA==1)
 z = -0.490
 Prob > |z| = 0.6239
 Exact Prob = 0.6313

. * Structural brain anomalies:
 . tab Structuralbrainanomalies CongZIKA, chi2

Structural brain anomalies	CongZIKA		Total
	0	1	
0	108	12	120
1	3	6	9
Total	111	18	129

Pearson chi2(1) = 22.3910 Pr = 0.000

. tab Cortical CongZIKA, exact

Cortical development anomaly	CongZIKA		Total
	0	1	
0	111	14	125
1	0	4	4
Total	111	18	129

Fisher's exact = 0.000

1-sided Fisher's exact = 0.000

. tab Corpuscall CongZIKA, exact

Corpus callosum anomaly	CongZIKA		Total
	0	1	
0	109	14	123
1	2	4	6
Total	111	18	129

Fisher's exact = 0.003

1-sided Fisher's exact = 0.003

. tab Calcifications CongZIKA, exact

Calcificat ions or cystic lesions	CongZIKA		Total
	0	1	
0	110	13	123
1	1	5	6
Total	111	18	129

Fisher's exact = 0.000

1-sided Fisher's exact = 0.000

. tab Posteriorfossa CongZIKA, exact

Posterior fossa anomaly	CongZIKA		Total
	0	1	
0	111	14	125
1	0	4	4
Total	111	18	129

Fisher's exact = 0.000

1-sided Fisher's exact = 0.000

. tab Ventriculomegaly CongZIKA, exact

Ventriculo megaly	CongZIKA		Total
	0	1	
0	110	14	124
1	1	4	5
Total	111	18	129

Fisher's exact = 0.001

1-sided Fisher's exact = 0.001

. * Ocular anomalies
 . tab Microphthalmia CongZIKA, exact

Microphthalmia	CongZIKA		Total
	0	1	
0	111	17	128
1	0	1	1
Total	111	18	129

Fisher's exact = 0.140
 1-sided Fisher's exact = 0.140

. tab Fundoscopy CongZIKA, exact

Enumerating sample-space combinations:

stage 5: enumerations = 1
 stage 4: enumerations = 2
 stage 3: enumerations = 5
 stage 2: enumerations = 7
 stage 1: enumerations = 0

Fundoscopy	CongZIKA		Total
	0	1	
.	75	9	84
0	34	6	40
Macula atrophy, cho..	1	1	2
Subretinal hemorrhage	1	1	2
Subretinal hemorrhha..	0	1	1
Total	111	18	129

Fisher's exact = 0.033

. cci 3 2 8 32

	Exposed	Unexposed	Total	Proportion Exposed
Cases	3	2	5	0.6000
Controls	8	32	40	0.2000
Total	11	34	45	0.2444
	Point estimate		[95% Conf. Interval]	
Odds ratio	6		.5561587	79.06791 (exact)
Attr. frac. ex.	.8333333		-.7980481	.9873526 (exact)
Attr. frac. pop	.5			

chi2(1) = 3.85 Pr>chi2 = 0.0497				

. cci 2 1 8 33

	Exposed	Unexposed	Total	Proportion Exposed
--	---------	-----------	-------	--------------------

Cases	2	1	3	0.6667
Controls	8	33	41	0.1951
Total	10	34	44	0.2273
	Point estimate		[95% Conf. Interval]	
Odds ratio	8.25		.3613468	500.877 (exact)
Attr. frac. ex.	.8787879		-1.767424	.9980035 (exact)
Attr. frac. pop	.5858586			

chi2(1) = 3.54 Pr>chi2 = 0.0599

. cci 1 1 9 33

	Exposed	Unexposed	Total	Exposed
Cases	1	1	2	0.5000
Controls	9	33	42	0.2143
Total	10	34	44	0.2273
	Point estimate		[95% Conf. Interval]	
Odds ratio	3.666667		.0420734	296.3017 (exact)
Attr. frac. ex.	.7272727		-22.76798	.9966251 (exact)
Attr. frac. pop	.3636364			

chi2(1) = 0.89 Pr>chi2 = 0.3462

* OAE
 . tab AbnormalOAE CongZIKA, exact

Abnormal OAE	CongZIKA		Total
	0	1	
0	42	10	52
1	1	2	3
Total	43	12	55

Fisher's exact = 0.117
 1-sided Fisher's exact = 0.117

* Severe neurological symptoms:
 . tab Neurologicalsymptomsat2m CongZIKA, exact

Neurological symptoms at 2m	CongZIKA		Total
	0	1	
0	110	13	123
1	1	5	6

Total	111	18	129
-------	-----	----	-----

Fisher's exact = 0.000
 1-sided Fisher's exact = 0.000

. tab Arthrogryposis CongZIKA, exact

Arthrogryposis	CongZIKA		Total
	0	1	
0	111	17	128
1	0	1	1
Total	111	18	129

Fisher's exact = 0.140
 1-sided Fisher's exact = 0.140

. tab Hypertonia CongZIKA, exact

Hypertonia	CongZIKA		Total
	0	1	
0	111	15	126
1	0	3	3
Total	111	18	129

Fisher's exact = 0.002
 1-sided Fisher's exact = 0.002

. tab Dysphagiaswallowingdisorders CongZIKA, exact

Dysphagia / swallowing disorders	CongZIKA		Total
	0	1	
0	111	16	127
1	0	2	2
Total	111	18	129

Fisher's exact = 0.019
 1-sided Fisher's exact = 0.019

. tab Seizures CongZIKA, exact

Seizures	CongZIKA		Total
	0	1	
0	110	17	127
1	1	1	2
Total	111	18	129

Fisher's exact = 0.261
 1-sided Fisher's exact = 0.261

. tab Calcifications CongZIKA, exact

Calcifications or lesions	CongZIKA		Total
	0	1	
0	110	13	123
1	1	5	6
Total	111	18	129

Fisher's exact = 0.000
 1-sided Fisher's exact = 0.000

. tab Posteriorfossa CongZIKA, exact

Posterior fossa anomaly	CongZIKA		Total
	0	1	
0	111	14	125
1	0	4	4
Total	111	18	129

Fisher's exact = 0.000
 1-sided Fisher's exact = 0.000

. tab Ventriculomegaly CongZIKA, exact

Ventriculomegaly	CongZIKA		Total
	0	1	
0	110	14	124
1	1	4	5
Total	111	18	129

Fisher's exact = 0.001
 1-sided Fisher's exact = 0.001

. * Neurologicimpairmentsat 2years
 . tab Neurologicimpairmentsat2y CongZIKA, chi2

Neurologic impairment s at 2y	CongZIKA		Total
	0	1	
0	92	10	102
1	4	5	9

Total | 96 15 | 111

Pearson chi2(1) = 14.8121 Pr = 0.000

. tab Cerebralpalsyat2y CongZIKA, exact

Cerebral palsy at 2y	CongZIKA		Total
	0	1	
0	96	13	109
1	0	2	2
Total	96	15	111

Fisher's exact = 0.017
1-sided Fisher's exact = 0.017

. tab Severedystoniaortremors CongZIKA, chi2

Severe dystonia or tremors at 2y	CongZIKA		Total
	0	1	
0	93	12	105
1	3	3	6
Total	96	15	111

Pearson chi2(1) = 7.2249 Pr = 0.007

. tab Seizuresat2y CongZIKA, exact

Seizures at 2y	CongZIKA		Total
	0	1	
0	94	12	106
1	2	3	5
Total	96	15	111

Fisher's exact = 0.017
1-sided Fisher's exact = 0.017

. * Motor acquisitions
. codebook Ageatsittingposition if CongZIKA==1

Ageatsittingpositionm Age at sitting
position (m)

type: numeric (double)

range: [0,24] units: .1
unique values: 9 missing .: 3/18

tabulation: Freq. Value
1 0
1 3
3 5
1 5.5
4 6
1 7
2 8
1 14
1 24
3 .

. codebook Ageatsittingposition if CongZIKA==0

```
-----
Ageatsittingpositionm                               Age at sitting
position (m)
-----
```

type: numeric (double)

range: [4,11] units: .1
unique values: 10 missing .: 14/111

mean: 6.22165
std. dev: 1.44692

percentiles:	10%	25%	50%	75%	90%
	4	5	6	7	8

. ranksum Ageatsittingposition, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	97	5508	5480.5
1	15	820	847.5
combined	112	6328	6328

unadjusted variance 13701.25
adjustment for ties -671.50

adjusted variance 13029.75

Ho: Ageats~m(CongZIKA==0) = Ageats~m(CongZIKA==1)
z = 0.241
Prob > |z| = 0.8096
Exact Prob = 0.8113

. gen delaysit=0

```
. replace delaysit=1 if (Ageatsittingposition>9 and Ageatsittingposition!=.)
9andAgeatsittingposition invalid name
r(198);
```

end of do-file

```
r(198);
```

```
. do "C:\Users\lpomar\AppData\Local\Temp\STD1d6c_000000.tmp"
```

```
. replace delaysit=1 if (Ageatsittingposition>9 & Ageatsittingposition!=.)
(3 real changes made)
```

```
. tab delaysit CongZIKA, exact
```

delaysit	CongZIKA		Total
	0	1	
0	110	16	126
1	1	2	3
Total	111	18	129

```
Fisher's exact = 0.051
1-sided Fisher's exact = 0.051
```

```
. codebook Ageatwalkingm if CongZIKA==1
```

```
-----
Ageatwalkingm                                     Age at
walking (m)
-----
```

```
type: numeric (double)
```

```
range: [0,24]          units: .1
unique values: 9       missing .: 3/18
```

```
tabulation: Freq. Value
             1 0
             2 8
             1 9
             2 10
             4 11
             2 12
             1 12.5
             1 18
             1 24
             3 .
```

```
. codebook Ageatwalkingm if CongZIKA==0
```

```
-----
-----
```

Ageatwalkingm
walking (m)

Age at

type: numeric (double)

range: [7,17] units: 1
unique values: 11 missing .: 15/111

mean: 11.4271
std. dev: 2.03001

percentiles: 10% 25% 50% 75% 90%
 9 10 11 12 14

. ranksum Ageatwalkingm, by(CongZIKA)

Two-sample Wilcoxon rank-sum (Mann-Whitney) test

CongZIKA	obs	rank sum	expected
0	96	5488.5	5376
1	15	727.5	840
combined	111	6216	6216

unadjusted variance 13440.00
adjustment for ties -426.93

adjusted variance 13013.07

Ho: Ageatw~m(CongZIKA==0) = Ageatw~m(CongZIKA==1)

z = 0.986

Prob > |z| = 0.3240

Exact Prob = 0.3289

. gen delaywalk=0

. replace delaywalk=1 if (Ageatwalking>18 & Ageatwalking! =.)
(1 real change made)

. tab delaywalk CongZIKA, exact

	CongZIKA		
delaywalk	0	1	Total
0	111	17	128
1	0	1	1
Total	111	18	129

Fisher's exact = 0.140
1-sided Fisher's exact = 0.140

. * Vision and hearing evaluation:

. tab Impairedresponsetovisualstim CongZIKA, chi2

Impaired response to visual stimuli	CongZIKA		Total
	0	1	
0	97	13	110
1	1	2	3
Total	98	15	113

Pearson chi2(1) = 7.6314 Pr = 0.006

. tab Impairedresponsetoauditorystim CongZIKA, chi2

Impaired response to auditory stimuli	CongZIKA		Total
	0	1	
0	97	13	110
1	1	2	3
Total	98	15	113

Pearson chi2(1) = 7.6314 Pr = 0.006

. * CDAS

. tab Neurodevelopment2SDat3y CongZIKA, chi2

Neurodevel opment <-2SD at 3y	CongZIKA		Total
	0	1	
0	44	4	48
1	7	7	14
Total	51	11	62

Pearson chi2(1) = 12.8936 Pr = 0.000

. tab Motordomain2SD CongZIKA, exact

Motor domain <-2SD	CongZIKA		Total
	0	1	
0	50	9	59
1	1	2	3
Total	51	11	62

Fisher's exact = 0.079

1-sided Fisher's exact = 0.079

. tab Congitivedomain2SD CongZIKA, chi2

Congitive domain <-2SD	CongZIKA		Total
	0	1	
0	48	5	53
1	3	6	9
Total	51	11	62

Pearson chi2(1) = 17.2677 Pr = 0.000

. tab Socioaffectivedomain2SD CongZIKA, chi2

Socio-affe ctive domain	CongZIKA		Total
	<-2SD	0	
0	45	7	52
1	6	4	10
Total	51	11	62

Pearson chi2(1) = 4.0475 Pr = 0.044

. log close

name: <unnamed>

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log type: text

closed on: 24 Mar 2021, 20:52:26
