

**** SAMPLE STATA SCRIPT FOR ANALYSIS OF FETAL ABDOMINAL CIRCUMFERENCE

* Supplement to "Quantitative approach to quality review of prenatal ultrasound examinations – fetal biometry"

* Lines that start with an Asterisk (*) are comments

* Lines that start without an Asterisk are Stata commands

cd "/Users/andrewcombs/Desktop/Analysis/Approach to QR Sample script/"

log using "LOG Biometry QR Sample Script", replace

* log is a Stata file that keeps a listing of all comments, commands, and results.

* cd means Change Directory, making this the default file folder for data and results

* You will NEED TO CUSTOMIZE the default directory to match your computer's file structure

cd "/Users/andrewcombs/Desktop/Analysis/Approach to QR Sample script/"

version 13

set more off

**** IMPORT EXCEL DATA FILE

import excel "EXCEL SiteName Year.xlsx", firstrow clear

* You will NEED TO CUSTOMIZE the name of the Excel file to match your file name

***** DATA DICTIONARY *****

* The Excel file imported has the following fields (columns), named in Viewpoint:

* Examdate – self explanatory

* Examtype – examples Comp Basic, Comp Detailed, Follow up, Fetal Echo, etc

* ExamID – arbitrary number assigned by Viewpoint, unique to each exam

* Cardiacactivity – fetal heart beat (present or absent)

* Numberofgestationalsacsfetu – 1=singleton, 2=twin, etc.

* Sonographer – Viewpoint shows actual sonographer name.

* Readingphysician – Viewpoint shows actual physician name

* For confidentiality, we replaced sonographer and physician names

* with dummy names. For example, Sono-2 or Phys-3.

* You NEED TO CUSTOMIZE with actual names any place you see these dummy names.

* (Dummy names are used in the graph commands)

* AssignedEDD – "due date" based on best obstetrical estimate

* BPDmm – biparietal diameter in mm

* HCmm – head circumference in mm

- * ACmm – abdominal circumference in mm
- * Femurmm – femur length in mm

*** DEFINE NEW VARIABLES and CLEAN-UP

generate GAd = 280 – (AssignedEDD – Examdate)

generate GA = GAd/7

- * GAd is gestational age in days

- * GA is gestational age in weeks

generate HC=HCmm/10

generate AC=ACmm/10

generate FL=Femurmm/10

- * HC, AC, FL are measurements in centimeters

keep if (trim(Examstatus)=="Finalized" | substr(trim(Examstatus),1,8)=="Revised ")

keep if trim(Numberofgestationalsacsfetu) == "1"

keep if trim(Cardiacactivity) == "present"

keep if GA>=14 & GA<41

- * These steps will drop incomplete reports, multifetal pregnancy, absent fetal heart beat

- * and GA outside target range 14–40 weeks.

*** CALCULATE z-SCORE FOR AC

generate hadAC= -13.3 + 1.61*GA – 0.00998*GA^2

generate sdAC=1.34

generate zAC= (AC–hadAC)/sdAC

- * hadAC is Hadlock's predicted AC for gestational age.

- * The formula is in Hadlock et al, Radiology 1884;152:497–501, footnote to Table III

- * sdAC is Hadlock's standard deviation of AC, same source, constant at 1.34 cm

- * zAC is calculated z-Score.

list Examdate, ExamID, GA, AC, zAC if abs(zAC) >6

- * lists extreme outliers (absolute value of zAC more than 6)

drop if abs(zAC) >6

- * deletes extreme outliers

*** CALCULATIONS FOR TABLE 1: z-SCORES BY SONOGRAPHER

```
oneway zAC Sonographer, tabulate scheffe
```

```
* oneway is the Stata command for oneway ANOVA
```

```
* The tabulate option generates a table similar to Table 1 in our article
```

```
* (columns for number of exams, mean z-score, and SD of z).
```

```
* At the bottom of the displayed table, the value under "Prob >F" is overall P-value.
```

```
* A P-value < 0.05 means that some of the sonographers have a different mean z-score
```

```
* than others, but does not show who are different.
```

```
* The scheffe option generates a multiple comparisons table, showing P-values for
```

```
* all possible 2-way comparisons between sonographers.
```

```
summarize zAC
```

```
* summarize shows the mean and SD of z-score for the entire practice
```

```
* (includes sonographers not included in Sono-1 through Sono-8)
```

```
bysort Sonographer: ttest zAC==0
```

```
* the t-test assesses whether mean is different than 0
```

```
* the next section generates values for the right 2 columns of Table 1
```

```
generate zClass=""
```

```
replace zClass="LGA" if zAC<.
```

```
replace zClass="AGA" if zAC<=1.2816
```

```
replace zClass="SGA" if zAC<-1.2816
```

```
* z-score 1.2816 is the 90th percentile
```

```
* z-score -1.2816 is the 10th percentile
```

```
tabulate Sonographer zClass, row chi
```

```
tabulate zClass
```

*** CALCULATIONS FOR TABLE 2: z-SCORES BY PHYSICIAN

```
oneway zAC Readingphysician, tabulate
```

```
* oneway ANOVA of AC z-score, unadjusted columns of Table 2 (mean and SD)
```

```
* adjust z-score for sonographer
```

```
replace Sonographer="Other " if Sonographer=="
```

```
bysort Sonographer: egen SonoMean=mean(zAC)
```

```

generate zACadj = zAC-SonoMean
* SonoMean is each sonographer's mean z-score
* zACadj adjusts each observed z-score by subtracting sonographer mean
oneway zACadj Readingphysician, tabulate scheffe
* this ANOVA is used for the Adjusted columns of Table 2.
bysort Readingphysician: ttest zACadj==0
* the t-test is used to assess whether mean is different than 0

```

*** GENERATE LIST OF 20 EXAMS for IMAGE REVIEW

```

* You NEED TO CUSTOMIZE the "generate randomID" command: insert sonographer name instead of
"Sono-2" etc.
* The "runiform()" function generates a random number between 0 and 1.
* tGA is GA in completed weeks (truncated by removing any decimal fraction of weeks).
* After sort, the exams are in numerical order from smallest to largest randomID.
* Then we list the first 20 exams.

```

```

generate randomID=runiform() if Sonographer=="Sono-2"
generate tGA=trunc(GA)
sort randomID
list ExamID Examdate Examtype tGA Sonographer in 1/20, noobs

```

```

* Repeat the process for another sonographer.
* Again, you NEED TO CUSTOMIZE by inserting sonographer name rather than "Sono-8"
drop randomID
generate randomID=runiform() if Sonographer=="Sono-8"
sort randomID
list ExamID Examdate Examtype tGA Sonographer in 1/20, noobs

```

```

* Copy-paste these 4 commands as needed to add listings for other sonographers.

```

***** GRAPHS *****

*** FIGURE 2 SCATTERPLOTS AND HISTOGRAMS

- * You NEED TO CUSTOMIZE these commands: insert sonographer name instead of "Sono-2" etc.
- * For the "graph save" commands, you can insert your own title instead of "Sono-2"
- * The /// at the end of some lines means that the command continues on the next line.

```
generate AC90=hadAC + 1.2816*sdAC
generate AC10=hadAC - 1.2816*sdAC
bysort GA: generate nGA=_n
```

```
twoway (scatter AC GA if(Sonographer=="Sono-2"), mcolor(blue) msymbol(smx)) ///
      (line AC90 hadAC AC10 GA if(nGA==1), lcolor(red black green)), ///
      ytitle(Abdominal Circumference mm) xtitle(Gestational Age weeks) ///
      legend(position(11) ring(0) label(1 Sonographer 2) label(3 AC50))
graph save Graph "GRAPH zAC scatterplot tech 2.gph", replace
```

```
twoway (scatter AC GA if(Sonographer=="Sono-8"), mcolor(blue) msymbol(smx)) ///
      (line AC90 hadAC AC10 GA if(nGA==1), lcolor(red black green)), ///
      ytitle(Abdominal Circumference mm) xtitle(Gestational Age weeks) ///
      legend(position(11) ring(0) label(1 Sonographer 8) label(3 AC50))
graph save Graph "GRAPH zAC scatterplot tech 8.gph", replace
```

```
histogram zAC if zAC^2 <16 & Sonographer=="Sono-2", xtitle("AC z-score, Sonographer-2") ///
      addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
graph save Graph "GRAPH zAC Sono-2.gph" , replace
```

```
histogram zAC if zAC^2 <16 & Sonographer=="Sono-8", xtitle("AC z-score, Sonographer-8") ///
      addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
graph save Graph "GRAPH zAC Sono-8.gph" , replace
```

```
**** FIGURE 3 - COMBINING 2 NORMAL CURVES WITH DIFFERENT MEANS and SD=1
cd "/Users/andrewcombs/Desktop/Analysis/Approach to QR Biometry/Graphs"
generate Even = 0
replace Even=1 if ExamID/2==trunc(ExamID/2)
generate Nm1=.
```

```

replace Nml=rnormal()-0.5 if Even==1
replace Nml=rnormal()+0.5 if Even==0
* The rnormal() function generates random number that are normally distributed.
* This amounts to a Montecarlo simulation of random normal sampling from the population
* If the ExamID is an even number, the function generates a normal distribution with z =
-0.5
* If the ExamID is odd, the function generates a normal distribution with z = +0.5

```

```

histogram Nml if Nml^2 <16 & Even==1, xtitle("z-score, fetuses w risk of SGA") ///
    addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
graph save Graph "GRAPH z SGA.gph" , replace

```

```

histogram Nml if Nml^2 <16 & Even==0, xtitle("z-score, fetuses w risk of LGA") ///
    addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
graph save Graph "GRAPH z LGA.gph" , replace

```

```

histogram Nml if Nml^2 <16, xtitle("z-score, combined") ///
    addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
graph save Graph "GRAPH z Both.gph" , replace

```

**** FIGURE 4 – HISTOGRAMS FOR SONOGRAPHER 3 and SONOGRAPHER 1

```

histogram zAC if zAC^2 <16 & Sonographer=="Sono-3", xtitle("AC z-score, Sonographer-3") ///
    addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
graph save Graph "GRAPH zAC Sono-3.gph" , replace

```

```

histogram zAC if zAC^2 <16 & Sonographer=="Sono-1", xtitle("AC z-score, Sonographer-1") ///
    addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
graph save Graph "GRAPH zAC Sono-1.gph" , replace

```

**** z-SCORES FOR HC and FL

```

* Hadlock 1984, same reference as for AC, formulas in footnote to Table III.
* Analysis can use same scripts as for AC, replacing "AC" with "HC" or "FL" everywhere.

```

```

*** HC

```

```
generate hadHC=-11.48+ 1.56*GA - .0002548*GA^3
generate sdHC=1
generate zHC=(HC-hadHC)/sdHC
```

```
*** FL
generate hadFL= -3.91 + 0.427*GA - 0.0034*GA^2
generate sdFL = 0.3
generate zFL = (FL-hadFL)/sdFL
```

```
save "DATA from Sample Script.dta", replace
log close
exit
```