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1  **** SAMPLE STATA SCRIPT FOR ANALYSIS OF FETAL ABDOMINAL CIRCUMFERENCE
2  * Supplement to "Quantitative approach to quality review of prenatal ultrasound
   examinations – fetal biometry"
3  * Lines that start with an Asterisk (*) are comments
4  * Lines that start without an Asterisk are Stata commands
5
6  cd "/Users/andrewcombs/Desktop/Analysis/Approach to QR Sample script/"
7  log using "LOG Biometry QR Sample Script", replace
8  * log is a Stata file that keeps a listing off all comments, commands, and results.
9  * cd means Change Directory, making this the default file folder for data and results
10 * You will NEED TO CUSTOMIZE the default directory to match your computer's file structure
11
12 cd "/Users/andrewcombs/Desktop/Analysis/Approach to QR Sample script/"
13 version 13
14 set more off
15
16 **** IMPORT EXCEL DATA FILE
17 import excel "EXCEL SiteName Year.xlsx", firstrow clear
18 * You will NEED TO CUSTOMIZE the name of the Excel file to match your file name
19
20 ***** DATA DICTIONARY *****
21 * The Excel file imported has the following fields (columns), named in Viewpoint:
22 * Examdate – self explanatory
23 * Examtype – examples Comp Basic, Comp Detailed, Follow up, Fetal Echo, etc
24 * ExamID – arbitrary number assigned by Viewpoint, unique to each exam
25 * Cardiacactivity – fetal heart beat (present or absent)
26 * Numberofgestationalsacsfetu – 1=singleton, 2=twin, etc.
27 * Sonographer – Viewpoint shows actual sonographer name.
28 * Readingphysician – Viewpoint shows actual physician name
29 * For confidentiality, we replaced sonographer and physician names
30 * with dummy names. For example, Sono-2 or Phys-3.
31 * You NEED TO CUSTOMIZE with actual names any place you see these dummy names.
32 * (Dummy names are used in the graph commands)
33 * AssignedEDD – "due date" based on best obstetrical estimate
34 * BPDmm – biparietal diameter in mm
35 * HCmm – head circumference in mm
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36 * ACmm - abdominal circumference in mm
37 * Femurmm - femur length in mm
38
39 *** DEFINE NEW VARIABLES and CLEAN-UP
40 generate GAd = 280 - (AssignedEDD - Examdate)
41 generate GA = GAd/7
42 * GAd is gestational age in days
43 * GA is gestational age in weeks
44
45 generate HC=HCmm/10
46 generate AC=ACmm/10
47 generate FL=Femurmm/10
48 * HC, AC, FL are measurements in centimeters
49
50 keep if (trim(Examstatus)=="Finalized" | substr(trim(Examstatus),1,8)=="Revised ")
51 keep if trim(Numberofgestationalsacsfetu) == "1"
52 keep if trim(Cardiacactivity) == "present"
53 keep if GA>=14 & GA<41
54 * These steps will drop incomplete reports, multifetal pregnancy, absent fetal heart beat
55 * and GA outside target range 14-40 weeks.
56
57
58 *** CALCULATE z-SCORE FOR AC
59 generate hadAC= -13.3 + 1.61*GA - 0.00998*GA^2
60 generate sdAC=1.34
61 generate zAC= (AC-hadAC)/sdAC
62 * hadAC is Hadlock's predicted AC for gestational age.
63 * The formula is in Hadlock et al, Radiology 1884;152:497-501, footnote to Table III
64 * sdAC is Hadlock's standard deviation of AC, same source, constant at 1.34 cm
65 * zAC is calculated z-Score.
66
67 list Examdate, ExamID, GA, AC, zAC if abs(zAC) >6
68 * lists extreme outliers (absolute value of zAC more than 6)
69 drop if abs(zAC) >6
70 * deletes extreme outliers
71
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72 *** CALCULATIONS FOR TABLE 1: z-SCORES BY SONOGRAPHER
73 oneway zAC Sonographer, tabulate scheffe
74 * oneway is the Stata command for oneway ANOVA
75 * The tabulate option generates a table similar to Table 1 in our article
76 * (columns for number of exams, mean z-score, and SD of z).
77 * At the bottom of the displayed table, the value under "Prob >F" is overall P-value.
78 * A P-value < 0.05 means that some of the sonographers have a different mean z-score
79 * than others, but does not show who are different.
80 * The scheffe option generates a multiple comparisons table, showing P-values for
81 * all possible 2-way comparisons between sonographers.
82 summarize zAC
83 * summarize shows the mean and SD of z-score for the entire practice
84 * (includes sonographers not included in Sono-1 through Sono-8)
85
86 bysort Sonographer: ttest zAC==0
87 * the t-test assesses whether mean is different than 0
88
89 * the next section generates values for the right 2 columns of Table 1
90 generate zClass=""
91 replace zClass="LGA" if zAC<.
92 replace zClass="AGA" if zAC<=1.2816
93 replace zClass="SGA" if zAC<-1.2816
94 * z-score 1.2816 is the 90th percentile
95 * z-score -1.2816 is the 10th percentile
96 tabulate Sonographer zClass, row chi
97 tabulate zClass
98
99
100 *** CALCULATIONS FOR TABLE 2: z-SCORES BY PHYSICIAN
101
102 oneway zAC Readingphysician, tabulate
103 * oneway ANOVA of AC z-score, unadjusted columns of Table 2 (mean and SD)
104
105 * adjust z-score for sonographer
106 replace Sonographer="Other " if Sonographer=="
107 bysort Sonographer: egen SonoMean=mean(zAC)

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108 generate zACadj = zAC-SonoMean
109 * SonoMean is each sonographer's mean z-score
110 * zACadj adjusts each observed z-score by subtracting sonographer mean
111 oneway zACadj Readingphysician, tabulate scheffe
112 * this ANOVA is used for the Adjusted columns of Table 2.
113 bysort Readingphysician: ttest zACadj==0
114 * the t-test is used to assess whether mean is different than 0
115
116
117 *** GENERATE LIST OF 20 EXAMS for IMAGE REVIEW
118
119 * You NEED TO CUSTOMIZE the "generate randomID" command: insert sonographer name instead of
120 "Sono-2" etc.
121 * The "runiform()" function generates a random number between 0 and 1.
122 * tGA is GA in completed weeks (truncated by removing any decimal fraction of weeks).
123 * After sort, the exams are in numerical order from smallest to largest randomID.
124 * Then we list the first 20 exams.
125
126 generate randomID=runiform() if Sonographer=="Sono-2"
127 generate tGA=trunc(GA)
128 sort randomID
129 list ExamID Examdate Examtype tGA Sonographer in 1/20, noobs
130
131 * Repeat the process for another sonographer.
132 * Again, you NEED TO CUSTOMIZE by inserting sonographer name rather than "Sono-8"
133 drop randomID
134 generate randomID=runiform() if Sonographer=="Sono-8"
135 sort randomID
136 list ExamID Examdate Examtype tGA Sonographer in 1/20, noobs
137
138 * Copy-paste these 4 commands as needed to add listings for other sonographers.
139
140
141 ***** GRAPHS *****
142
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143 *** FIGURE 2 SCATTERPLOTS AND HISTOGRAMS

144

145 * You NEED TO CUSTOMIZE these commands: insert sonographer name instead of "Sono-2" etc.

146 * For the "graph save" commands, you can insert your own title instead of "Sono-2"

147 * The /// at the end of some lines means that the command continues on the next line.

148

149 generate AC90=hadAC + 1.2816*sdAC

150 generate AC10=hadAC - 1.2816*sdAC

151 bysort GA: generate nGA=_n

152

153 twoway (scatter AC GA if(Sonographer=="Sono-2"), mcolor(blue) msymbol(smx)) ///

154 (line AC90 hadAC AC10 GA if(nGA==1), lcolor(red black green)), ///

155 ytitle(Abdominal Circumference mm) xtitle(Gestational Age weeks) ///

156 legend(position(11) ring(0) label(1 Sonographer 2) label(3 AC50))

157 graph save Graph "GRAPH zAC scatterplot tech 2.gph", replace

158

159 twoway (scatter AC GA if(Sonographer=="Sono-8"), mcolor(blue) msymbol(smx)) ///

160 (line AC90 hadAC AC10 GA if(nGA==1), lcolor(red black green)), ///

161 ytitle(Abdominal Circumference mm) xtitle(Gestational Age weeks) ///

162 legend(position(11) ring(0) label(1 Sonographer 8) label(3 AC50))

163 graph save Graph "GRAPH zAC scatterplot tech 8.gph", replace

164

165 histogram zAC if zAC^2 <16 & Sonographer=="Sono-2", xtitle("AC z-score, Sonographer-2") ///

166 addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)

167 graph save Graph "GRAPH zAC Sono-2.gph" , replace

168

169 histogram zAC if zAC^2 <16 & Sonographer=="Sono-8", xtitle("AC z-score, Sonographer-8") ///

170 addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)

171 graph save Graph "GRAPH zAC Sono-8.gph" , replace

172

173

174 ***** FIGURE 3 - COMBINING 2 NORMAL CURVES WITH DIFFERENT MEANS and SD=1

175 cd "/Users/andrewcombs/Desktop/Analysis/Approach to QR Biometry/Graphs"

176 generate Even = 0

177 replace Even=1 if ExamID/2==trunc(ExamID/2)

178 generate Nm1=.

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179  replace Nml=rnormal()-0.5 if Even==1
180  replace Nml=rnormal()+0.5 if Even==0
181  * The rnormal() function generates random number that are normally distributed.
182  * This amounts to a Montecarlo simulation of random normal sampling from the population
183  * If the ExamID is an even number, the function generates a normal distribution with z =
  -0.5
184  * If the ExamID is odd, the function generates a normal distribution with z = +0.5
185
186  histogram Nml if Nml^2 <16 & Even==1, xtitle("z-score, fetuses w risk of SGA") ///
187      addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
188  graph save Graph "GRAPH z SGA.gph" , replace
189
190  histogram Nml if Nml^2 <16 & Even==0, xtitle("z-score, fetuses w risk of LGA") ///
191      addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
192  graph save Graph "GRAPH z LGA.gph" , replace
193
194  histogram Nml if Nml^2 <16, xtitle("z-score, combined") ///
195      addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
196  graph save Graph "GRAPH z Both.gph" , replace
197
198
199  **** FIGURE 4 – HISTOGRAMS FOR SONOGRAPHER 3 and SONOGRAPHER 1
200
201  histogram zAC if zAC^2 <16 & Sonographer=="Sono-3", xtitle("AC z-score, Sonographer-3") ///
202      addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
203  graph save Graph "GRAPH zAC Sono-3.gph" , replace
204
205  histogram zAC if zAC^2 <16 & Sonographer=="Sono-1", xtitle("AC z-score, Sonographer-1") ///
206      addplot(function y=normalden(x), range(-4 4) droplines(-1.2816 0 1.2816)) legend(off)
207  graph save Graph "GRAPH zAC Sono-1.gph" , replace
208
209  **** z-SCORES FOR HC and FL
210  * Hadlock 1984, same reference as for AC, formulas in footnote to Table III.
211  * Analysis can use same scripts as for AC, replacing "AC" with "HC" or "FL" everywhere.
212
213  *** HC

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```
214 generate hadHC=-11.48+ 1.56*GA - .0002548*GA^3
215 generate sdHC=1
216 generate zHC=(HC-hadHC)/sdHC
217
218 *** FL
219 generate hadFL= -3.91 + 0.427*GA - 0.0034*GA^2
220 generate sdFL = 0.3
221 generate zFL = (FL-hadFL)/sdFL
222
223 save "DATA from Sample Script.dta", replace
224 log close
225 exit
226
227
228
229
```