

30 Supplementary material 4: Stata code

```
31 // 1st April 2020
32
33 /* Code for:
34
35 Byrne, AW, McEvoy, D, et al. 2020
36
37 Inferred duration of infectious period of SARS-CoV-2: rapid review and analysis of
38 available evidence for asymptomatic and symptomatic COVID-19 cases
39
40
41 */
42
43 * Figure 2
44
45 gen davies1_gamma = rgamma(5, 1.4)
46
47 gen davies2_gamma = rgamma(4, 1.25)
48
49 gen ma_normal = rnormal(7.2, 4.96)
50
51
52 input hu_data
53
54 12
55
56 1
57
58 1
59
60 11
61
62 3
63
64 16
65
66 6
67
68 4
69
70 6
71
72 18
73
74 8
75
76 8
77
78 11
79
80 14
81
82 14
83
84 12
85
86 13
87
88 1
89
90 17
91
92 3
93
94 11
95
96 5
```

```
97
98 6
99
100 21
101
102 end
103
104
105
106 // Fig 2 visualise
107
108 twoway (histogram hu_data, fcolor(gs14) lcolor(black)) (histogram davies1_gamma,
109 bin(180) fcolor(ltbluishgray%86) lcolor(none) lwidth(none)) (kdensity
110 davies1_gamma, lcolor(gs11) lwidth(thick)) (kdensity davies2_gamma, lcolor(gs11)
111 lwidth(thick)) (histogram davies2_gamma, bin(120) fcolor(orange_red%20)
112 lcolor(none) lwidth(none)) (histogram ma_normal, bin(100) fcolor(lime%20)
113 lwidth(none)) (kdensity ma_normal, lcolor(gs11) lwidth(thick)) if ma_n>=0,
114 yscale(line) xtitle(Days since infected) xline(6 6.5 11 3.5, lpattern(dash)
115 lcolor(black) noextend) xlabel(0(5)30) legend(off) scheme(s2color) xsize(20)
116 ysize(16) graphregion(fcolor(white)) plotregion(fcolor(white))
117
118
119
120 * Figure 3
121
122 gen rothet3_normal = rnormal(2, 0.6)
123
124 gen huangt3_normal = rnormal(3.75, 0.332)
125
126 gen het3_normal = rnormal(2.3, 0.49)
127
128 gen weit3_normal = rnormal(2.5, 0.89)
129
130 gen peakt3_normal = rnormal(0.8, 0.5)
131
132 gen daviesAt3_normal = rgamma(5, 0.48)
133
134 gen daviesBt3_normal = rgamma(4, 0.375)
135
136 twoway (histogram rothe, bin(120) fcolor(orange_red%20) lcolor(none) lwidth(none))
137 (kdensity rothe, lcolor(gs11) lwidth(thick)) (histogram he, bin(100)
138 fcolor(lime%20) lwidth(none)) (kdensity he, lcolor(gs11) lwidth(thick)) (histogram
139 wei, bin(100) fcolor(orange%20) lwidth(none)) (kdensity wei, lcolor(gs11)
140 lwidth(thick)) (histogram peak, bin(100) fcolor(purple%20) lwidth(none)) (kdensity
141 peak, lcolor(gs11) lwidth(thick)) (histogram daviesA, bin(100) fcolor(brown%20)
142 lwidth(none)) (kdensity daviesA, lcolor(gs11) lwidth(thick)) (histogram daviesB,
143 bin(100) fcolor(yellow%20) lwidth(none)) (kdensity daviesB, lcolor(gs11)
144 lwidth(thick)) if peak>=0 & wei>=0 & rothe>=0, yscale(line) xtitle(Pre-symptomatic
145 infectious period) xline(0.5 1 1.2 2.6 2.9 3.75 8.2, lpattern(dash) lcolor(black)
146 noextend) xlabel(0(1)10) legend(off) scheme(s2color) xsize(20) ysize(16)
147 graphregion(fcolor(white)) plotregion(fcolor(white)) ytitle(Density)
148
149 * Figure 4
150
151 // meta analysis & meta regression
152
153 clear
154
155
156
157 // open data =
158
159 * meta_analysis_dataset.xls
160
161
162
163 // Fit random effects meta-analytical model, and specify forest plot
164
```

```
165 metaan mean se, dl forest label(paper)
166
167 // forest plot is figure 4.
168
169 // meta regression
170
171 // binary child (y/n) variable
172
173 gen kid_cat = 1 if child==1
174
175 replace kid = 2 if adult==1 & child!=1
176
177 tab kid_cat
178
179 * binary children inclusion in sample [REML]
180
181 xi: metareg mean i.kid if se>0, wsse(se)
182
183 // monte carlo model of P-value
184
185 xi: metareg mean i.kid if se>0, wsse(se) permute(1000, joint(i.kid))
186
187
188 // binary severe (y/n) variable
189
190 encode sever, gen(sev_num) // 4 way categorical
191
192
193 gen sev_bin = 0 if sev_n<3
194
195 replace sev_bin = 1 if sev_n==3 | sev_n==4
196
197
198
199 xi: metareg mean i.sev_bin if se>0, wsse(se)
200
201 // monte carlo model of P-value
202
203 xi: metareg mean i.sev_bin if se>0, wsse(se) permute(1000, joint(i.sev_bin))
204
205
206
207 * Figure 5
208
209
210
211 // Import, open time_to_discharge_death.csv
212
213
214 // numeric indicator for study category
215
216 encode study, gen(study_)
217
218
219
220 // random effects model for time from onset to removal (discharge or death)
221
222 // 3 levels of study as RE
223
224 xi: xtreg overall_time, i(study_)
225
226 // summarise post-estimation
227
228 estat summarize
229
230 // Breusch and Pagan Lagrangian multiplier test for random effects
231
232 xttest0
```

```
233
234 // Figure 5: histogram plot with kernel density
235
236 twoway(hist overall_time if study_== 3 , bin(10) fcolor(green%20)) ( hist
237 overall_time if study_== 1, bin(10) fcolor(red%20)) ( hist overall_time if study_==
238 2, bin(10) fcolor(purple%20)) (kdensity overall_time_disc_death , lcolor(gs11)
239 lwidth(mthick)), scheme(s2gcolor) legend(off) xsize(20) ysize(16)
240 graphregion(fcolor(white)) plotregion(fcolor(white)) xline(15.13663 18.06537
241 20.99411, lpattern(dash) lcolor(black) noextend)
242
243
244
245 // GLM reporting the variation in mean duration across studies
246
247 xi: reg overall_time i.study_
248
249 // GOF test
250
251 estat hettest
252
253 // residuals plot
254
255 rvfplot
256
257 // prediction
258
259 predict pred_study
260
261 // visualise
262
263 twoway(scatter pred_study study_)
264
265
266
267 // GLM reporting the variation in mean duration across removal type [death or
268 discharge]
269
270 xi: reg overall_time i.discharge
271
272 // GOF test
273
274 estat hettest
275
276 // residuals plot
277
278 rvfplot
279
280 // prediction
281
282 predict pred_study
283
284 // visualise
285
286 twoway(scatter pred_study study_)
```