```
 1
 2
 3  cls
 4  import excel "db1.xlsx", sheet("Data") firstrow clear
 5
 6  *****************
 7  ***descriptive***
 8  *****************
 9  gen py_calc = 1 if pyears == .
10  replace py_calc = 0 if pyears != .
11  replace pyears = fu_years * part if pyears == .
12  gen rate_exp = c_exp*1000/(p_exp*fu_years)
13  gen rate_noexp = c_noexp*1000/(p_noexp*fu_years)
14  gsort endpoint rate_exp
15  distinct id
16  distinct pmid
17  tab endpoint
18
19  **rates graph
20  preserve
21  keep if endpoint == "DM"
22  sencode id, replace
23  twoway  (scatter id rate_exp, mcolor(red%60) msize(small) mlcolor(black) mlwidth(vthin)) (scatter id rate_noexp, mcolor(blue%60)
    msize(small) mlcolor(black) mlwidth(vthin)), xtitle("Rate (per 1000 person-years)", size(small)) /*
24  */ ylabel(1(1)20, labels labsize(vsmall) angle(horizontal) valuelabel) xlabel(0(10)120, labsize(vsmall) grid) xmtick(##5) legend(
    off) name(DM, replace) title("Diabetes Mellitus", size(small))
25  graph close _all
26  restore
27  preserve
28  keep if endpoint == "CV"
29  sencode id, replace
30  twoway  (scatter id rate_exp, mcolor(red%60) msize(small) mlcolor(black) mlwidth(vthin)) (scatter id rate_noexp, mcolor(blue%60)
    msize(small) mlcolor(black) mlwidth(vthin)), xtitle("Rate (per 1000 person-years)", size(small)) /*
31  */ ylabel(1(1)13, labels labsize(vsmall) angle(horizontal) valuelabel) xlabel(0(20)180, labsize(vsmall) grid) xmtick(##5) legend(
    off) name(CV, replace) title("Cardiovascular events", size(small))
32  graph close _all
33  restore
34  graph combine CV DM, cols(2) xsize(7)
35  graph close _all
36
37  **table descriptive
38  preserve
39  keep id pmid year country region endpoint fu_years sex age *_exp *_noexp
40  drop rate*
41  sort endpoint year
42  tostring fu_years, format(%7.1f) replace force
43  tostring age, format(%7.1f) replace force
44  rename id First_Author
45  rename year Publication_Year
46  rename region Region
47  rename endpoint Outcome
```

```
48  rename fu_years Follow_up_years
49  rename sex Sex
50  rename age Age_years
51  rename c_exp Cases_NAFLD
52  rename p_exp Participants_MAFLD
53  rename c_noexp Cases_noNAFLD
54  rename p_noexp Participants_noNAFLD
55  merge 1:1 pmid using "sex"
56  order Outcome First_Author pmid Region Publication_Year Age_years men_p
57  drop Sex _merge
58  dataout, save("Table descriptive_sept2018") excel replace dec(1)
59  sort Outcome country Publication_Year
60  restore
61
62  **************
63  ***analysis***
64  **************
65  foreach var of varlist est lb ub {
66      gen ln`var' = ln(`var')
67      }
68  gen seln = (lnub-lnlb)/3.92
69  gen z = abs(lnest/seln)
70  gen pval = exp(-0.717*z - 0.416*z^2)
71  drop z
72  saveold "Rdb1", version(13) replace
73
74  clear
75  set obs 2
76  gen id in 1 = "zCV"
77  replace id = "zDM" if id == ""
78  gen lnest = 0.3940 if id == "zCV"                       /*from R*/
79  replace lnest = 0.7739 if id == "zDM"                   /*from R*/
80  gen seln = (0.8280 + 0.0399)/3.92 if id == "zCV"        /*from R*/
81  replace seln = (0.9763 - 0.5715)/3.92 if id == "zDM"    /*from R*/
82  append using "Rdb1"
83
84  replace endpoint = "DM" if id == "zDM"
85  replace endpoint = "CV" if id == "zCV"
86  gen sort = 2 if (id == "zCV" | id == "zDM")
87  replace sort = 1 if sort == .
88  sort endpoint sort lnest
89  replace endpoint = "Cardiovascular Events" if endpoint == "CV"
90  replace endpoint = "Type 2 Diabetes Mellitus" if endpoint == "DM"
91  tabstat events part, statistics( sum ) by(endpoint)
92  sencode endpoint, replace
93  bys endpoint: gen sumev = sum(events)
94  bys endpoint: gen sumpa = sum(part)
95  replace events = sumev if (id == "zCV" | id == "zDM")
96  replace part = sumpa if (id == "zCV" | id == "zDM")
97
98  **forest plot
```

```
   metan lnest seln, randomi by(endpoint) lcols(id events part) nosubgroup nowt nooverall eform xlabel(0.1, 0.3, 0.7, 2, 4, 8, 16, 32)
    force xsize(3) ysize(4.5) scale(1.5) classic ciopt(lwidth(vthin))

   **pub_bias_adjusted estimates - https://vevealab.shinyapps.io/WeightFunctionModel/
   import excel "Pub_bias_adjusted.xlsx", sheet("Sheet1") firstrow clear
   gen ec =  RR if [out == "CV" & pvalue == "Unadjusted"]
   gen lc = l95 if [out == "CV" & pvalue == "Unadjusted"]
   gen uc = u95 if [out == "CV" & pvalue == "Unadjusted"]
   gen ed =  RR if [out == "DM" & pvalue == "Unadjusted"]
   gen ld = l95 if [out == "DM" & pvalue == "Unadjusted"]
   gen ud = u95 if [out == "DM" & pvalue == "Unadjusted"]
   foreach var of varlist ec-ud {
       replace `var' = `var'[_n-1] if `var' == .
       }
   drop if pvalue == "Unadjusted"
   sencode pvalue, replace
   twoway (scatter RR pvalue, mcolor(black)) (rspike l95 u95 pvalue, lcolor(black) lwidth(vthin)) (rarea lc uc pvalue, fcolor(blue%30)
    lwidth(none)) (line ec pvalue, lcolor(red) lwidth(vthin)) if out == "CV", /*
   */yscale(log) ylabel(0(1)5, labsize(small) angle(horizontal)) xlabel(, labsize(small) valuelabel grid) legend(off) name(cvd,
   replace)
   twoway (scatter RR pvalue, mcolor(black)) (rspike l95 u95 pvalue, lcolor(black) lwidth(vthin)) (rarea ld ud pvalue, fcolor(blue%30)
    lwidth(none)) (line ed pvalue, lcolor(red) lwidth(vthin)) if out == "DM", /*
   */yscale(log) ylabel(0(1)5, labsize(small) angle(horizontal)) xlabel(, labsize(small) valuelabel grid) legend(off) name(dm, replace)
   graph close _all
   graph combine cvd dm, ycommon

   **metareg
   cls
   use "Rdb1", clear
   merge 1:1 pmid using "sex"
   drop _merge
   egen float miss = rowmiss(region adj year age fu_years events men_p)

   foreach o in DM CV {
       xi:metareg lnest i.region i.adj year age fu_years events if endpoint == "`o'", wsse(seln) knapphartung
       }

   foreach o in DM CV {
       xi:metareg lnest i.region if endpoint == "`o'", wsse(seln) knapphartung
       }

   foreach o in DM CV {
       xi:metareg lnest i.adj if endpoint == "`o'", wsse(seln) knapphartung
       }

   foreach o in DM CV {
       foreach var of varlist year age fu_years events  {
           metareg lnest `var' if endpoint == "`o'", wsse(seln) knapphartung
       }
   }

```

```
146   metan lnest seln, randomi by(endpoint) nooverall eform nograph /*to generate _WT*/
147   sort region
148   sencode region, replace
149   labelbook region
150   sort adj
151   tostring adj, replace
152   sencode adj, replace
153   labelbook adj
154   foreach o in DM CV {
155       foreach var of varlist region year age fu_years events adj {
156           twoway (scatter lnest `var' [aweight = _WT] if endpoint == "`o'", mcolor(navy%40) msize(vsmall) mlcolor(black) mlwidth(
      vthin)), ytitle("Ln Relative Risk", size(small)) xtitle(, size(small))/*
157           */ ylabel(-1(1)3, labsize(vsmall) angle(horizontal)) xlabel(, labsize(vsmall) valuelabel grid) name(mr_`o'_`var', replace)
      title("`o'", size(small)) graphregion(fcolor(white))
158       }
159   }
160   graph close _all
161   graph combine   mr_CV_region    mr_DM_region    /*
162   */              mr_CV_year      mr_DM_year      /*
163   */              mr_CV_age       mr_DM_age       /*
164   */              mr_CV_fu_years  mr_DM_fu_years  /*
165   */              mr_CV_events    mr_DM_events    /*
166   */              mr_CV_adj       mr_DM_adj,      /*
167   */ cols(2) xsize(4.8) ysize(7.5) ycommon
168
169   **funnel plot
170   foreach o in DM CV {
171       metabias lnest seln if endpoint == "`o'", egger
172       metafunnel lnest seln if endpoint == "`o'", eform legend(cols(5)) xsize(4) name(funnel_`o', replace) title(`o')
173       }
174   graph close _all
175   graph combine funnel_CV funnel_DM, cols(2) xsize(7)
176
177
178   ******************************
179   ***sensitivity analyses in R***
180   ******************************
181
182   use resCV, clear
183   gen out = "CV"
184   append using resDM
185   replace out = "DM" if out == ""
186   rename exp_B_ biasf
187   gen g = biasf + (biasf^2 - biasf)^0.5
188   tostring g, gen(g1) format(%7.2f) force
189   gen k = out + "_" + g1
190   reshape long y l h, i(k) j(q)
191   drop k g1
192   replace q = 1.05 if q == 1
193   replace q = 1.10 if q == 2
194   replace q = 1.15 if q == 3
```

```
195   replace q = 1.20 if q == 4
196   replace q = 1.25 if q == 5
197   replace q = 1.50 if q == 6
198   replace q = 1.75 if q == 7
199   replace q = 2.00 if q == 8
200   tostring q, format(%7.2f) replace force
201   sort out q g
202
203   *with CI
204   preserve
205   drop if g>3
206   twoway (rarea l h g, fcolor(ltblue%60) lcolor(white) lwidth(vvvthin)) (line y g, lcolor(blue)), ytitle("Estimated proportion of
      studies with true RR") ytitle(, size(small)) ylabel(0(0.2)1, labsize(vsmall) angle(horizontal) /*
207   */ format(%7.1f)) ymtick(##2) xtitle("Confounding strength (RR)") xtitle(, size(small)) xlabel(1(0.25)3, labsize(vsmall) grid
      format(%7.2f)) xmtick(##2) by(, legend(off)) xline(1.25 1.50, lwidth(vthin)) by(out q, note("")) subtitle(, size(small) lcolor(
      black) lwidth(vthin))
208
209   *without CI
210   sepscatter y g, sep(q) legend(cols(8) size(small) symxsize(8)) by(out, note("")) recast(line) ytitle("Estimated proportion of
      studies with true RR") ytitle(, size(small)) ylabel(0(0.1)1, labsize(small) angle(horizontal) /*
211   */ format(%7.1f)) ymtick(##2) xtitle("Confounding strength (RR)") xtitle(, size(small)) xlabel(1(1)9, labsize(small) grid) xmtick(
      ##2) subtitle(, size(small) lcolor(black) lwidth(vthin)) xsize(6)
212
213
214   ************************************
215   ********changing sigma B***************
216   ************************************
217
218   use resCV_R1, clear
219   gen out = "CV"
220   append using resDM_R1
221   replace out = "DM" if out == ""
222   rename exp_B_ biasf
223   gen g = biasf + (biasf^2 - biasf)^0.5
224   tostring g, gen(g1) format(%7.2f) force
225   gen k = out + "_" + g1
226   reshape long y l h, i(k) j(q)
227   drop k g1
228
229   gen sigma = 0       if (q == 10 | q == 20 | q == 30 | q == 40)
230   replace sigma = 0.1 if (q == 11 | q == 21 | q == 31 | q == 41)
231   replace sigma = 0.2 if (q == 12 | q == 22 | q == 32 | q == 42)
232   replace sigma = 0.3 if (q == 13 | q == 23 | q == 33 | q == 43)
233
234   replace q = 1.10    if (q == 10 | q == 11 | q == 12 | q == 13)
235   replace q = 1.20    if (q == 20 | q == 21 | q == 22 | q == 23)
236   replace q = 1.50    if (q == 30 | q == 31 | q == 32 | q == 33)
237   replace q = 1.75    if (q == 40 | q == 41 | q == 42 | q == 43)
238
239   drop biasf
240   order out
```

```
241   tostring g, format(%7.2f) replace force
242   tostring q, format(%7.2f) replace force
243   tostring sigma, format(%7.2f) replace force
244   keep if g == "1.25"
245   drop g
246   sort out q sigma
247
248   egen float x = seq(), from(1) to(4) block(1)
249   replace x = x+7  if q == "1.20"
250   replace x = x+14 if q == "1.50"
251   replace x = x+21 if q == "1.75"
252
253   replace out = "Cardiovascular Events" if out == "CV"
254   replace out = "Type 2 Diabetes Mellitus" if out == "DM"
255
256   twoway  (scatter y x if sigma == "0.00",    mcolor(black)   msymbol(square))    (rspike l h x if sigma == "0.00",   lcolor(black)
         lwidth(vthin)) /*
257   */      (scatter y x if sigma == "0.10",    mcolor(red)     msymbol(square))    (rspike l h x if sigma == "0.10",   lcolor(red)
          lwidth(vthin)) /*
258   */      (scatter y x if sigma == "0.20",    mcolor(blue)    msymbol(square))    (rspike l h x if sigma == "0.20",   lcolor(blue)
         lwidth(vthin)) /*
259   */      (scatter y x if sigma == "0.30",    mcolor(green)   msymbol(square))    (rspike l h x if sigma == "0.30",   lcolor(green)
         lwidth(vthin)), /*
260   */      ytitle("Estimated proportion of studies with true Relative Risk") ytitle(, size(small)) ylabel(0(0.2)1.2, angle(horizontal)
        format(%7.1f))  /*
261   */      xtitle("Increased risk of outcome, NAFLD vs no-NAFLD") xtitle(, size(small))
                                                                                  /*
262   */      by(, legend(off)) xsize(6) ysize(2.5) by(out, note("")) play(rec1)
263
```