```
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           drop _at1-_contrast2_1_uci
 177
 178
       }
 179
       keep if age_diag != .
 180
 181
       keep age_diag-cont_uci
       gen scale = "Absolute"
 182
       gen out = "All cause"
 183
       gen sens = "BMI"
 184
       save "...Results/abs_all_bmi", replace
 185
 186
 187
       **#*MAIN: Cause-specific absolute difference***
 188
 189
       cap use "...m3_survival_data.dta", clear
       drop cancer date-str cva
 190
 191
       gen death cvd=0
       replace death_cvd=1 if death_ihd==1 | death_str_cva==1
       drop death ihd death str cva
 193
       gen end_date="31/10/2020"
 194
 195
       gen d end=date(end date, "DMY")
 196
       replace d end=deathn if died==1
       gen time = (d_end-indexn)/365.25
 197
 198
       replace time = .00136895 if time==0
 199
 200
       gen event=.
       replace event=0 if died==0
 202
       replace event=1 if death_cancer==1
       replace event=2 if death cvd==1 | death renal==1
 203
 204
       replace event=3 if death_other==1
       tab event, m
 205
 206
 207
       gen age_exp = age_index*exp
       replace sex = sex-1
 208
       tab eth, gen(d_eth)
 209
 210
       tab imd, gen(d imd)
 211
       stset time, failure(event=1)
 212
       stpm2 exp age_index age_exp sex d_eth2-d_eth11 d_imd2-d_imd5 smoke hypertension_5, df(4) scale(hazard) eform nolog
 213
       estimates store cancer
 214
 215
       stset time, failure(event=2)
       stpm2 exp age_index age_exp sex d_eth2-d_eth11 d_imd2-d_imd5 smoke hypertension_5, df(4) scale(hazard) eform nolog
 216
       estimates store cvd
 217
 218
       stset time, failure(event=3)
       stpm2 exp age_index age_exp sex d_eth2-d_eth11 d_imd2-d_imd5 smoke hypertension_5, df(4) scale(hazard) eform nolog
 219
 220
       estimates store other
 221
       gen timep = 10 in 1
 222
 223
                                   before(patid)
 224
       gen age_diag= .,
 225
       gen exp cancer = .,
                                   before(patid)
                                   before(patid)
 226
       gen exp_cancer_lci = .,
       gen exp_cancer_uci = .,
                                   before(patid)
       gen unexp cancer = .,
                                   before(patid)
 228
 229
       gen unexp_cancer_lci = .,
                                   before(patid)
 230
       gen unexp_cancer_uci = .,
                                   before(patid)
 231
       gen cancer_diff= .,
                                   before(patid)
       gen cancer_diff_lci= .,
 232
                                   before(patid)
       gen cancer_diff_uci= .,
                                   before(patid)
       gen exp_cvd = .,
                                   before(patid)
 234
                                   before(patid)
 235
       gen exp_cvd_lci = .,
```

```
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       gen exp_cvd_uci = .,
                                    before(patid)
       gen unexp cvd = .,
                                    before(patid)
 238
       gen unexp_cvd_lci = .,
                                    before(patid)
 239
       gen unexp_cvd_uci = .,
                                    before(patid)
 240
       gen cvd_diff= .,
                                    before(patid)
 241
       gen cvd_diff_lci= .,
                                    before(patid)
 242
       gen cvd diff uci= .,
                                    before(patid)
                                    before(patid)
 243
       gen exp_oth = .,
 244
       gen exp_oth_lci = .,
                                    before(patid)
 245
       gen exp_oth_uci = .,
                                    before(patid)
                                    before(patid)
 246
       gen unexp_oth = .,
 247
       gen unexp_oth_lci = .,
                                    before(patid)
                                    before(patid)
       gen unexp_oth_uci = .,
       gen oth diff= .,
                                    before(patid)
 249
 250
       gen oth_diff_lci= .,
                                    before(patid)
 251
       gen oth_diff_uci= .,
                                    before(patid)
 252
 253
       forval i=16/50 {
 254
            qui replace age_diag =`i' in `i'
 255
            qui standsurv, crmodels(cancer cvd other) cif ci timevar(timep)
                                                                                                                  ///
 256
            at1(exp 0 age_index `i' age_exp 0) at2(exp 1 age_index `i' age_exp `i') atvar(F_unexp F_exp) contrast(difference) contrastvar(cif_diff)
 257
            qui replace exp_cancer
                                            = F exp cancer[1]
                                                                         in `i'
 258
           qui replace exp cancer lci
                                            = F_exp_cancer_lci[1]
                                                                         in `i'
 259
            qui replace exp cancer uci
                                            = F_exp_cancer_uci[1]
                                                                         in `i'
 260
            qui replace unexp_cancer
                                            = F_unexp_cancer[1]
                                                                         in `i'
 261
            qui replace unexp_cancer_lci
                                            = F_unexp_cancer_lci[1]
                                                                         in `i'
                                            = F_unexp_cancer_uci[1]
                                                                         in `i'
 262
            qui replace unexp cancer uci
 263
            qui replace cancer_diff
                                            = cif_diff_cancer[1]
                                                                         in `i'
                                                                         in `i'
 264
            qui replace cancer diff lci
                                            = cif diff cancer lci[1]
 265
            qui replace cancer_diff_uci
                                            = cif_diff_cancer_uci[1]
                                                                         in `i'
 266
            qui replace exp_cvd
                                                                         in `i'
                                            = F_exp_cvd[1]
                                                                         in `i'
 267
            qui replace exp cvd lci
                                            = F_exp_cvd_lci[1]
                                                                         in `i'
 268
            qui replace exp_cvd_uci
                                            = F_exp_cvd_uci[1]
 269
            qui replace unexp cvd
                                            = F unexp cvd[1]
                                                                         in `i'
            qui replace unexp_cvd lci
                                                                         in `i'
 270
                                            = F_unexp_cvd_lci[1]
 271
                                                                         in `i'
            qui replace unexp_cvd_uci
                                            = F_unexp_cvd_uci[1]
                                                                         in `i'
 272
            qui replace cvd_diff
                                            = cif_diff_cvd[1]
                                                                         in `i'
 273
            qui replace cvd_diff_lci
                                            = cif_diff_cvd_lci[1]
                                                                         in `i'
 274
            qui replace cvd diff uci
                                            = cif diff cvd uci[1]
 275
            qui replace exp_oth
                                            = F_exp_other[1]
                                                                         in `i'
 276
                                                                         in `i'
            qui replace exp_oth_lci
                                            = F_exp_other_lci[1]
                                                                         in `i'
 277
            qui replace exp oth uci
                                            = F exp other uci[1]
 278
            qui replace unexp_oth
                                            = F_unexp_other[1]
                                                                         in `i'
 279
                                                                         in `i'
            qui replace unexp oth lci
                                            = F_unexp_other_lci[1]
 280
            qui replace unexp_oth_uci
                                            = F_unexp_other_uci[1]
                                                                         in `i'
            qui replace oth diff
                                            = cif diff other[1]
                                                                         in `i'
 281
 282
            qui replace oth diff lci
                                            = cif diff other lci[1]
                                                                         in `i'
                                                                         in `i'
 283
            qui replace oth_diff_uci
                                            = cif_diff_other_uci[1]
 284
            qui drop F unexp cancer- cif diff other uci
 285
 286
           di "Age = `i' | sens = MAIN --- $S TIME $S DATE"
 287
       }
 288
 289
       keep if age_diag != .
 290
       keep age diag-oth diff uci
 291
       gen scale = "Absolute"
       gen out = "Cause_specific"
       gen sens = "MAIN"
 293
 294
       save "...abs_cs_main", replace
```

```
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 295
       **#*SENSITIVITY: Cause-specific absolute difference + BMI***
 297
       cap use "...m3_survival_data.dta", clear
 298
 299
       drop cancer_date-str_cva
       drop if bmi == .
 300
 301
 302
       gen death_cvd=0
       replace death cvd=1 if death ihd==1 | death str cva==1
 303
 304
       drop death ihd death str cva
 305
       gen end_date="31/10/2020"
       gen d end=date(end date, "DMY")
 306
       replace d_end=deathn if died==1
       gen time = (d end-indexn)/365.25
 308
 309
       replace time = .00136895 if time==0
 310
 311
       gen event=.
       replace event=0 if died==0
 312
 313
       replace event=1 if death cancer==1
       replace event=2 if death cvd==1 | death renal==1
 314
 315
       replace event=3 if death_other==1
       tab event, m
 317
 318
       gen age exp = age index*exp
       replace sex = sex-1
 320
       tab eth, gen(d_eth)
       tab imd, gen(d imd)
 321
 322
 323
       stset time, failure(event=1)
 324
       stpm2 exp age_index age_exp sex d_eth2-d_eth11 d_imd2-d_imd5 smoke hypertension_5 bmi, df(4) scale(hazard) eform nolog
 325
       estimates store cancer
       stset time, failure(event=2)
 326
       stpm2 exp age_index age_exp sex d_eth2-d_eth11 d_imd2-d_imd5 smoke hypertension_5 bmi, df(4) scale(hazard) eform nolog
 327
 328
       estimates store cvd
       stset time, failure(event=3)
 329
 330
       stpm2 exp age_index age_exp sex d_eth2-d_eth11 d_imd2-d_imd5 smoke hypertension_5 bmi, df(4) scale(hazard) eform nolog
 331
       estimates store other
 332
 333
       gen timep = 10 in 1
 334
                                   before(patid)
 335
       gen age_diag= .,
                                   before(patid)
 336
       gen exp cancer = .,
       gen exp_cancer_lci = .,
                                   before(patid)
 337
 338
       gen exp cancer uci = .,
                                   before(patid)
       gen unexp_cancer = .,
                                   before(patid)
                                   before(patid)
 340
       gen unexp cancer lci = .,
 341
       gen unexp_cancer_uci = .,
                                   before(patid)
       gen cancer_diff= .,
                                   before(patid)
 343
       gen cancer diff lci= .,
                                   before(patid)
       gen cancer_diff_uci= .,
                                   before(patid)
 344
       gen exp_cvd = .,
                                   before(patid)
       gen exp cvd lci = .,
                                   before(patid)
 346
 347
       gen exp_cvd_uci = .,
                                   before(patid)
       gen unexp_cvd = .,
                                   before(patid)
 349
       gen unexp cvd lci = .,
                                   before(patid)
 350
       gen unexp cvd uci = .,
                                   before(patid)
       gen cvd_diff= .,
                                   before(patid)
       gen cvd_diff_lci= .,
                                   before(patid)
 352
       gen cvd_diff_uci= .,
                                   before(patid)
```

```
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       gen exp_oth = .,
                                    before(patid)
       gen exp oth lci = .,
                                    before(patid)
 356
       gen exp_oth_uci = .,
                                    before(patid)
 357
       gen unexp_oth = .,
                                    before(patid)
 358
       gen unexp_oth_lci = .,
                                    before(patid)
 359
       gen unexp_oth_uci = .,
                                    before(patid)
 360
       gen oth diff= .,
                                    before(patid)
       gen oth_diff_lci= .,
                                    before(patid)
 361
 362
       gen oth_diff_uci= .,
                                    before(patid)
 363
 364
       forval i=16/50 {
 365
            qui replace age diag =`i' in `i'
 366
            qui standsurv, crmodels(cancer cvd other) cif ci timevar(timep)
                                                                                                                  ///
 367
            at1(exp 0 age index `i' age exp 0) at2(exp 1 age index `i' age exp `i') atvar(F unexp F exp) contrast(difference) contrastvar(cif diff)
 368
            qui replace exp cancer
                                            = F_exp_cancer[1]
                                                                         in `i'
                                                                         in `i'
 369
            qui replace exp_cancer_lci
                                            = F_exp_cancer_lci[1]
 370
            qui replace exp cancer uci
                                                                         in `i'
                                            = F exp cancer uci[1]
 371
            qui replace unexp_cancer
                                                                         in `i'
                                            = F_unexp_cancer[1]
 372
            qui replace unexp cancer lci
                                            = F_unexp_cancer_lci[1]
                                                                         in `i'
 373
            qui replace unexp cancer uci
                                            = F unexp cancer uci[1]
                                                                         in `i'
                                                                         in `i'
 374
            qui replace cancer_diff
                                            = cif_diff_cancer[1]
 375
            qui replace cancer_diff_lci
                                            = cif diff cancer lci[1]
                                                                         in `i'
 376
           qui replace cancer diff uci
                                            = cif diff cancer uci[1]
                                                                         in `i'
 377
            qui replace exp cvd
                                            = F exp cvd[1]
                                                                         in `i'
 378
            qui replace exp_cvd_lci
                                            = F_exp_cvd_lci[1]
                                                                         in `i'
                                            = F_exp_cvd_uci[1]
 379
            qui replace exp_cvd_uci
                                                                         in `i'
                                                                         in `i'
 380
            qui replace unexp cvd
                                            = F unexp cvd[1]
           qui replace unexp_cvd_lci
                                                                         in `i'
 381
                                            = F_unexp_cvd_lci[1]
            qui replace unexp cvd uci
                                                                         in `i'
 382
                                            = F unexp cvd uci[1]
            qui replace cvd diff
 383
                                            = cif_diff_cvd[1]
                                                                         in `i'
 384
            qui replace cvd_diff_lci
                                            = cif_diff_cvd_lci[1]
                                                                         in `i'
                                                                         in `i'
 385
            qui replace cvd diff uci
                                            = cif diff cvd uci[1]
                                                                         in `i'
 386
            qui replace exp_oth
                                            = F_exp_other[1]
 387
            qui replace exp oth lci
                                            = F exp other lci[1]
                                                                         in `i'
                                                                         in `i'
            qui replace exp oth uci
 388
                                            = F_exp_other_uci[1]
 389
                                                                         in `i'
            qui replace unexp_oth
                                            = F_unexp_other[1]
 390
            qui replace unexp_oth_lci
                                            = F_unexp_other_lci[1]
                                                                         in `i'
                                                                         in `i'
            qui replace unexp_oth_uci
 391
                                            = F_unexp_other_uci[1]
                                                                         in `i'
 392
            qui replace oth diff
                                            = cif diff other[1]
                                                                         in `i'
 393
           qui replace oth_diff_lci
                                            = cif_diff_other_lci[1]
 394
                                            = cif_diff_other_uci[1]
                                                                         in `i'
            qui replace oth diff uci
            qui drop F unexp cancer- cif diff other uci
 395
 396
            di "Age = `i' | sens = BMI --- $$ TIME $$ DATE"
 397
 398
 399
       }
 400
       keep if age_diag != .
 402
       keep age diag-oth diff uci
       gen scale = "Absolute"
 403
 404
       gen out = "Cause_specific"
 405
       gen sens = "BMI"
 406
       save "...abs_cs_bmi", replace
 407
 408
       ***MAIN/SENSITIVITY: All-cause & cause-specific relative hazard MAIN + BMI***
 409
 410
       cap use "...m3 survival data.dta", clear
       egen float agegr = cut(age_index), at(16 28 32 36 40 44 48 51) icodes
 411
       lab define agegr 1 0 "16-27" 1 "28-31" 2 "32-35" 3 "36-39" 4 "40-43" 5 "44-47" 6 "48-50"
 412
```

```
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       lab values agegr agegr_1
       tab agegr, m
 414
 415
       tabstat age_index, statistics(mean median min max count) by(agegr)
       gen end_date="31/10/2020"
 416
 417
       gen d_end=date(end_date, "DMY")
       replace d end=deathn if died==1
 418
       gen time = (d end-indexn)/365.25
 419
       replace time = .00136895 if time==0
 420
       keep patid time died exp age index sex eth imd smoke hypertension_5 agegr bmi death_str_cva death_ihd death_renal death_cancer death_other
 421
       lab define exp lab 0 "no" 1 "yes"
 422
       lab values exp exp_lab
 423
       gen death_cardioren=0
 424
 425
       replace death_cardioren=1 if death_str_cva==1 | death_ihd==1 | death_renal==1
 426
       foreach nm in died death cancer death cardioren death other {
 427
 428
 429
           stset time, f(`nm'==1)
 430
 431
           preserve
 432
           set showbaselevels on
           stpm2 i.exp#i.agegr i.agegr sex i.eth i.imd smoke hypertension_5, df(4) scale(hazard) eform nolog
 433
 434
           parmest, fast eform
           split parm, p(#)
 435
 436
           keep if parm1 == "1.exp"
 437
           sencode parm2, replace
 438
           replace parm2 = parm2 - 1
 439
           drop parm1
 440
           gen agegr
                        = "16-27" if parm2 == 0
           replace agegr = "28-31" if parm2 == 1
 441
 442
           replace agegr = "32-35" if parm2 == 2
 443
           replace agegr = "36-39" if parm2 == 3
           replace agegr = "40-43" if parm2 == 4
 444
           replace agegr = "44-47" if parm2 == 5
 445
 446
           replace agegr = "48-50" if parm2 == 6
 447
           drop parm2 parm eq
 448
           gen scale = "Relative"
 449
           gen out = "`nm'"
 450
           gen sens = "MAIN"
 451
           tempfile rel `nm' main
 452
           save `rel_`nm'_main', replace
 453
           restore
 454
 455
           preserve
 456
           drop if bmi == .
 457
           set showbaselevels on
           stpm2 i.exp#i.agegr i.agegr sex i.eth i.imd smoke hypertension 5 bmi, df(4) scale(hazard) eform nolog
 458
 459
           parmest, fast eform
           split parm, p(#)
 460
 461
           keep if parm1 == "1.exp"
           sencode parm2, replace
 462
 463
           replace parm2 = parm2 - 1
           drop parm1
 464
 465
           gen agegr
                       = "16-27" if parm2 == 0
 466
           replace agegr = "28-31" if parm2 == 1
 467
           replace agegr = "32-35" if parm2 == 2
           replace agegr = "36-39" if parm2 == 3
 468
 469
           replace agegr = "40-43" if parm2 == 4
           replace agegr = "44-47" if parm2 == 5
 470
           replace agegr = "48-50" if parm2 == 6
 471
```

```
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 472
          drop parm2 parm eq
 473
          gen scale = "Relative"
         gen out = "`nm'"
 474
          gen sens = "BMI"
 475
 476
         tempfile rel_`nm'_bmi
          save `rel_`nm'_bmi', replace
 477
 478
          restore
 479
 480
      **************
 481
 482
      *COMBINED RELATIVE - BMI*
      **********
 483
 484
      foreach nm in died death cancer death cardioren death other {
 485
 486
          append using `rel `nm' main'
 487
          append using `rel_`nm'_bmi'
 488
 489
      save "...Results/Relative_all_cs_main_BMI", replace
 490
 491
      492
      493
 494
 495
      ***SENSITIVITY: All-cause absolute difference + hypertension***
 496
 497
      cap use "...m3_survival_data.dta", clear
      gen end date="31/10/2020"
 498
 499
      gen d_end=date(end_date, "DMY")
 500
      replace d end=deathn if died==1
      keep patid exp age_index sex eth imd smoke hypertension_5 bmi d_end indexn died death_cancer-death_other antihyp
      gen death_cvd=0
 502
      replace death cvd=1 if death ihd==1 | death str cva==1
 503
      drop death_ihd death_str_cva
 504
 505
      gen death cr=0
      replace death cr=1 if death cvd==1 | death renal==1
 506
 507
      drop death_renal death_cvd
 508
      gen time = (d end-indexn)/365.25
 509
      replace time = .00136895 if time==0
 510
      stset time, f(died==1)
 511
 512
 513
      gen age exp = age index*exp
      replace sex = sex-1
 514
 515
      tab eth, gen(d_eth)
      tab imd, gen(d_imd)
 516
      stpm2 exp age index age exp sex d eth2-d eth11 d imd2-d imd5 smoke antihyp, df(4) scale(hazard) eform nolog
 517
 518
      gen timep = 10 in 1
 519
      gen age diag = .,
                       before(patid)
 520
                           before(patid)
 521
      gen unexp_surv = .,
 522
      gen unexp_lci = ., before(patid)
 523
      gen unexp uci = .,
                       before(patid)
 524
      gen exp_surv = .,
                       before(patid)
 525
      gen exp_lci = .,
                       before(patid)
 526
      gen exp uci = ..
                       before(patid)
 527
      gen cont = .,
                       before(patid)
 528
      gen cont_lci = .,
                       before(patid)
      gen cont_uci = .,
                       before(patid)
 529
 530
```

```
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      forval i = 16/50 {
 532
           replace age diag =`i' in `i'
           standsurv, at1(exp 0 age_index `i' age_exp 0) at2(exp 1 age_index `i' age_exp `i') timevar(timep) ci contrast(difference)
 533
 534
           replace unexp_surv = _at1[1] in `i'
 535
           replace unexp_lci = _at1_lci[1] in `i'
           replace unexp_uci = _at1_uci[1] in `i'
 536
           replace exp surv
 537
                              = at2[1] in `i'
 538
           replace exp_lci
                               = _at2_lci[1] in `i'
           replace exp_uci
                               = _at2_uci[1] in `i'
 539
 540
           replace cont
                               = _contrast2_1[1] in `i'
 541
           replace cont_lci
                             = _contrast2_1_lci[1] in `i'
                             = contrast2 1 uci[1] in `i'
 542
           replace cont uci
 543
           drop _at1-_contrast2_1_uci
 544
 545
 546
       keep if age_diag != .
       keep age diag-cont uci
 547
       gen scale = "Absolute"
 548
 549
       gen out = "All cause"
       gen sens = "HYP"
 550
       cap save "...Results/abs_all_hyp", replace
 551
 552
 553
 554
       **#*SENSITIVITY: Cause-specific absolute difference + hypertension***
 555
       cap use "...m3 survival data.dta", clear
 556
       drop cancer_date-str_cva
 557
       gen death cvd=0
       replace death_cvd=1 if death_ihd==1 | death_str_cva==1
 558
       drop death ihd death str cva
 559
 560
       gen end_date="31/10/2020"
       gen d_end=date(end_date, "DMY")
 561
 562
       replace d end=deathn if died==1
       gen time = (d_end-indexn)/365.25
 563
 564
       replace time = .00136895 if time==0
 565
       gen event=.
 566
 567
       replace event=0 if died==0
       replace event=1 if death cancer==1
 568
       replace event=2 if death cvd==1 | death renal==1
 569
 570
       replace event=3 if death_other==1
       tab event, m
 571
 572
       gen age_exp = age_index*exp
 573
 574
       replace sex = sex-1
 575
       tab eth, gen(d_eth)
       tab imd, gen(d imd)
 576
 577
 578
       stset time, failure(event=1)
 579
       stpm2 exp age index age exp sex d eth2-d eth11 d imd2-d imd5 smoke antihyp, df(4) scale(hazard) eform nolog
       estimates store cancer
 580
       stset time, failure(event=2)
 582
       stpm2 exp age index age exp sex d eth2-d eth11 d imd2-d imd5 smoke antihyp, df(4) scale(hazard) eform nolog
 583
       estimates store cvd
 584
       stset time, failure(event=3)
 585
       stpm2 exp age_index age_exp sex d_eth2-d_eth11 d_imd2-d_imd5 smoke antihyp, df(4) scale(hazard) eform nolog
       estimates store other
 586
 587
 588
       gen timep = 10 in 1
 589
```

```
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 649
           qui replace oth diff uci
                                           = cif_diff_other_uci[1]
                                                                       in `i'
 650
           qui drop F unexp cancer- cif diff other uci
 651
           di "Age = `i' | sens = HYP --- $S_TIME $S_DATE"
 652
 653
       }
 654
 655
       keep if age diag != .
       keep age_diag-oth_diff_uci
 656
       gen scale = "Absolute"
 657
 658
       gen out = "Cause specific"
       gen sens = "HYP"
 659
 660
       save "...Results/abs cs hyp", replace
 661
 662
       ***SENSITIVITY: All-cause & cause-specific relative hazard hypertension***
 663
       cap use "...m3 survival data.dta", clear
 664
       egen float agegr = cut(age index), at(16 28 32 36 40 44 48 51) icodes
 665
       lab define agegr 1 0 "16-27" 1 "28-31" 2 "32-35" 3 "36-39" 4 "40-43" 5 "44-47" 6 "48-50"
 666
 667
       lab values agegr agegr 1
       tab agegr, m
 668
       tabstat age_index, statistics(mean median min max count) by(agegr)
 669
 670
       gen end date="31/10/2020"
       gen d end=date(end date, "DMY")
 671
 672
       replace d end=deathn if died==1
 673
       gen time = (d end-indexn)/365.25
 674
       replace time = .00136895 if time==0
       keep patid time died exp age index sex eth imd smoke hypertension 5 agegr bmi death str cva death ihd death renal death cancer death other antihyp
 675
 676
       lab define exp_lab 0 "no" 1 "yes"
       lab values exp exp lab
 677
 678
       gen death cardioren=0
 679
       replace death_cardioren=1 if death_str_cva==1 | death_ihd==1 | death_renal==1
 680
       foreach nm in died death_cancer death_cardioren death_other {
 681
 682
 683
           stset time, f(`nm'==1)
 684
 685
           preserve
 686
           set showbaselevels on
           stpm2 i.exp#i.agegr i.agegr sex i.eth i.imd smoke antihyp, df(4) scale(hazard) eform nolog
 687
 688
           parmest, fast eform
           split parm, p(#)
 689
           keep if parm1 == "1.exp"
 690
 691
           sencode parm2, replace
 692
           replace parm2 = parm2 - 1
 693
           drop parm1
                       = "16-27" if parm2 == 0
 694
           gen agegr
 695
           replace agegr = "28-31" if parm2 == 1
           replace agegr = "32-35" if parm2 == 2
 696
           replace agegr = "36-39" if parm2 == 3
 697
 698
           replace agegr = "40-43" if parm2 == 4
 699
           replace agegr = "44-47" if parm2 == 5
           replace agegr = "48-50" if parm2 == 6
 700
 701
           drop parm2 parm eq
           gen scale = "Relative"
 702
           gen out = "`nm''
 703
           gen sens = "HYP"
 704
 705
           tempfile rel_`nm'_hyp
           save `rel_`nm'_hyp', replace
 706
 707
           restore
```

```
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 708
 709
      ***********
 710
 711
       *COMBINED RELATIVE - HYPERTENSION*
       **********
 712
 713
 714
       foreach nm in died death cancer death cardioren death other {
 715
           append using `rel_`nm'_hyp'
 716
      save "...Results/Relative all cs HYP", replace
 717
 718
       *************
 719
 720
      ***Figure 2 | Absolute - All-cause by group**
      use "...Results/Absolute all main BMI HYP", clear
 721
      foreach var of varlist unexp surv-cont uci {
 722
           replace `var' = `var'*100
 723
 724
 725
      keep if sens == "MAIN"
      set scheme white tableau
 727
      twoway (line unexp surv age diag, sort lcolor(red)) (rarea unexp lci unexp uci age diag, sort fcolor(red%30) lwidth(none)) ///
 728
              (line exp_surv age_diag, sort lcolor(blue)) (rarea exp_lci exp_uci age_diag, sort fcolor(blue%30) lwidth(none))
                                                                                                                            ///
 729
              , ytitle("10-year survival (%)") ylabel(93(1)100) xtitle("Age at diagnosis (years)") xlabel(16(2)50)
                                                                                                                            ///
 730
             legend(order(3 "Type 2 diabetes" 1 "No type 2 diabetes") rows(1) position(7)) xsize(5) ysize(4)
 731
       graph save "Graph" "...Figure 2 R1.gph", replace
 732
      graph close all
 733
       *************
 734
 735
      ***Figure 3 | Absolute - Cause-specific by group**
      use "...Results/Absolute cs main BMI HYP", clear
 736
 737
      foreach var of varlist exp cancer-oth diff uci {
 738
           replace `var' = `var'*100
 739
      keep if sens == "MAIN"
 740
 741
      keep age diag exp* unexp*
      foreach nm in cancer cvd oth {
 742
 743
          rename exp_`nm' exp_`nm'_est
 744
           rename unexp_`nm' unexp_`nm'_est
 745
 746
      foreach nm in cancer cvd oth {
 747
           foreach j in est lci uci {
 748
              rename exp_`nm'_`j' exp_`j'_`nm'
 749
              rename unexp_`nm'_`j' unexp_`j'_`nm'
 750
          }
 751
       reshape long exp_est_ exp_lci_ exp_uci_ unexp_est_ unexp_lci_ unexp_uci_, i(age_diag) j(cause) string
 752
      replace cause = "Cardiorenal" if cause == "cvd"
 753
 754
      replace cause = "Noncancer/cardiorenal" if cause == "oth"
      replace cause = "Cancer" if cause == "cancer"
 756
      set scheme white tableau
      sencode cause, replace
 757
 758
       twoway (line unexp est age diag, sort lcolor(red)) (rarea unexp lci unexp uci age diag, sort fcolor(red%30) lwidth(none))
                                                                                                                                            111
             (line exp est age diag, sort lcolor(blue)) (rarea exp lci exp uci age diag, sort fcolor(blue%30) lwidth(none))
 759
                                                                                                                                            ///
              , ytitle("10-year cumulative incidence (%)") xtitle("Age at diagnosis (years)") xlabel(16(2)50, labsize(7pt)) ylab(0(0.5)4, format(%3.1f)) ///
 760
             by(cause, cols(3) note("")) legend(order(3 "Type 2 diabetes" 1 "No type 2 diabetes") rows(1) position(7)) xsize(8) ysize(4)
 761
 762
      graph save "Graph" "...Figure_3_R1.gph", replace
 763
      graph close all
 764
       *************
 765
      ***Figure S4 | Absolute - All-cause difference**
 766
```

```
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       use "...Results/Absolute_all_main_BMI_HYP", clear
 768
       foreach var of varlist unexp surv-cont uci {
           replace `var' = `var'*100
 769
 770
       keep if sens == "MAIN"
 771
       keep age diag cont*
 772
       twoway (line cont age diag, sort lcolor(red)) (rarea cont lci cont uci age diag, sort fcolor(red%30) lwidth(none)) ///
 773
 774
              , ytitle("10-year survival difference (%), T2DM vs noT2DM") xtitle("Age at diagnosis (years)")
 775
              xlabel(16(2)50, labsize(7pt)) ylab(0(-0.2)-2.6, format(\%3.1f) gmax labsize(8pt)) legend(off) xsize(6) ysize(5)
 776
       graph save "Graph" "...Figure S4 R1.gph", replace
 777
       graph close _all
 778
       ****************
 779
       ***Figure S5 | Absolute - Cause-specific difference**
 780
 781
       use "...Results/Absolute cs main BMI HYP", clear
       foreach var of varlist exp cancer-oth diff uci {
 782
           replace `var' = `var'*100
 783
 784
       keep if sens == "MAIN"
 786
       keep age diag cancer* cvd* oth*
       foreach nm in cancer cvd oth {
 787
 788
           rename `nm' diff `nm' diff est
 789
 790
       foreach nm in cancer cvd oth {
 791
           rename `nm' diff * * `nm'
 792
 793
       reshape long est_ lci_ uci_, i(age_diag) j(cause) string
       replace cause = "Cardiorenal" if cause == "cvd"
       replace cause = "Noncancer/cardiorenal" if cause == "oth"
 795
       replace cause = "Cancer" if cause == "cancer"
 796
 797
       set scheme white tableau
       sencode cause, replace
 798
 799
       twoway (line est_ age_diag, sort lcolor(red)) (rarea lci_ uci_ age_diag, sort fcolor(red%30) lwidth(none))
                                                                                                                       ///
 800
              , ytitle("10-year cumulative incidence difference (%), T2DM vs noT2DM") xtitle("Age at diagnosis (years)") ///
              xlabel(16(2)50, labsize(7pt)) ylab(0(0.25)2, format(%3.2f) gmax) by(cause, cols(3) note("") legend(off)) xsize(8) ysize(4)
 801
       graph save "Graph" "...Figure_S5_R1.gph", replace
 802
 803
       graph close all
 804
       *************************************
 805
 806
       ***Figure S7 | Absolute - SENSITIVITY: All-cause and cause-specific difference, MAIN/BMI/HYP**
       use "...Results/Absolute cs main BMI HYP", clear
 807
       foreach var of varlist exp cancer-oth diff uci {
 808
 809
           replace `var' = `var'*100
 810
       keep age_diag cancer* cvd* oth* sens
 811
       foreach nm in cancer cvd oth {
 812
 813
           rename `nm' diff `nm' diff est
 814
 815
       foreach nm in cancer cvd oth {
           rename `nm'_diff_* *_`nm'
 816
 817
       reshape long est lci uci , i(age diag sens) j(cause) string
 818
 819
       replace cause = "Cardiorenal" if cause == "cvd"
       replace cause = "Noncancer/cardiorenal" if cause == "oth"
 821
       replace cause = "Cancer" if cause == "cancer"
 822
       tempfile cs sens
 823
       save `cs sens', replace
 824
 825
       use "...Results/Absolute all main BMI HYP", clear
```

```
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       foreach var of varlist unexp surv-cont uci {
 827
           replace `var' = `var'*100
 828
 829
       keep age_diag sens out cont*
 830
       renames cont cont_lci cont_uci out \ est_ lci_ uci_ cause
 831
       order age diag sens cause est lci uci
 832
 833
       append using `cs_sens'
       sencode cause, replace
 834
 835
       sencode sens, replace
 836
       sort cause sens age_diag
       set scheme white tableau
 837
 838
       keep if inlist(age diag, 16, 20, 30, 40, 50)
 839
 840
       sort cause age diag sens
       label variable age diag "Age (years)"
 841
 842
       replace age diag = . if sens != 1
 843
       forestplot est_ lci_ uci_ if cause == 1, effect("Difference, %") lcols(age_diag)
                                                                                                                                                111
 844
 845
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
                                                                                                                                                 ///
          spacing(2) yline(3.5(3)12.5, lwidth(vthin) lpattern(vshortdash)) xtitle("10-year survival difference (%), T2DM vs noT2DM", size(5pt))
 846
                                                                                                                                                 111
 847
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(0(-0.4)-2.6, force labsize(4pt) nogrid format(%3.1f))
                                                                                                                                                ///
 848
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue)) ///
          title("All-cause", size(small)) name("All s", replace) xsize(4) ysize(5) scale(1.15) nodraw
 849
 850
 851
       forestplot est_ lci_ uci_ if cause == 2, effect("Difference, %") lcols(age_diag)
                                                                                                                                                             ///
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
 852
                                                                                                                                                             111
 853
          spacing(2) yline(3.5(3)12.5, lwidth(vthin) lpattern(vshortdash)) xtitle("10-year cumulative incidence difference (%), T2DM vs noT2DM", size(5pt))
                                                                                                                                                            ///
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(0(0.2)0.8, force labsize(4pt) nogrid format(%3.1f))
 854
                                                                                                                                                            ///
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue))
 855
                                                                                                                                                            111
          title("Cancer", size(small)) name("Cancer s", replace) xsize(4) ysize(5) scale(1.15) nodraw
 856
 857
       forestplot est_ lci_ uci_ if cause == 3, effect("Difference, %") lcols(age_diag)
 858
                                                                                                                                                            111
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
 859
                                                                                                                                                            ///
          spacing(2) yline(3.5(3)12.5, lwidth(vthin) lpattern(vshortdash)) xtitle("10-year cumulative incidence difference (%), T2DM vs noT2DM", size(5pt))
 860
                                                                                                                                                            111
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(0(0.1)0.5, force labsize(4pt) nogrid format(%3.1f))
 861
                                                                                                                                                            111
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue))
 862
                                                                                                                                                            ///
          title("Cardiorenal", size(small)) name("Cardiorenal s", replace) xsize(4) ysize(5) scale(1.15) nodraw
 863
 864
 865
       forestplot est_ lci_ uci_ if cause == 4, effect("Difference, %") lcols(age_diag)
                                                                                                                                                            111
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
                                                                                                                                                            111
 866
          spacing(2) yline(3.5(3)12.5, lwidth(vthin) lpattern(vshortdash)) xtitle("10-year cumulative incidence difference (%), T2DM vs noT2DM", size(5pt))
                                                                                                                                                            ///
 867
 868
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(\theta(0.2)1.8, force labsize(4pt) nogrid format(%3.1f))
                                                                                                                                                            ///
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue))
                                                                                                                                                            ///
 869
 870
          title("Noncancer/cardiorenal", size(small)) name("NCNC s", replace) xsize(4) ysize(5) scale(1.15) nodraw
 871
 872
       graph combine All s Cancer s Cardiorenal s NCNC s, cols(4) xsize(8) ysize(2.5)
       graph save "Graph" "...Figure_S7_R1.gph", replace
 873
 874
       graph close all
 875
 876
       ******************
 877
       *ALL COMBINED RELATIVE -- GRAPHS*************
 878
       **************
 879
 880
 881
 882
       cap use "...Results/Relative all cs main BMI.dta", clear
 883
       append using "...Results/Relative_all_cs_HYP.dta"
       drop if sens != "MAIN"
```

```
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 885
       drop sens
 886
       drop stderr z p scale
       replace out = "All-cause"
 887
                                             if out == "died"
 888
       replace out = "Cancer"
                                            if out == "death cancer"
 889
       replace out = "Cardiorenal"
                                            if out == "death cardioren"
       replace out = "Noncancer/cardiorenal" if out == "death other"
 890
 891
       sencode out, replace
 892
       sencode agegr, replace
 893
 894
       set scheme white tableau
 895
       twoway (scatter estimate agegr, sort mcolor(black) msize(small) msymbol(square)) (rspike min95 max95 agegr, sort lcolor(black)),
                                                                                                                                                                ///
               ytitle("Hazard Ratio") yscale(log) xtitle("Age group (years)") xlabel(1 "16-27" 2 "28-31" 3 "32-35" 4 "36-39" 5 "40-43" 6 "44-47" 7 "48-50")
                                                                                                                                                                111
 896
 897
               by(, legend(off) note("")) by(out, cols(2) yrescale) yline(1, lcolor(blue) lpattern(shortdash))
       graph save "Graph" "...Figure 1 R1.gph", replace
 898
 899
       ***Fig S6***
 900
       cap use "...Results/Relative all cs main BMI.dta", clear
 901
       append using "...Results/Relative_all_cs_HYP.dta"
 902
       drop stderr z p scale
 904
       replace out = "All-cause"
                                            if out == "died"
       replace out = "Cancer"
                                            if out == "death cancer"
 905
       replace out = "Cardiorenal"
                                          if out == "death cardioren"
 907
       replace out = "Noncancer/cardiorenal" if out == "death other"
 908
       sencode sens, replace
       sort out agegr sens
 910
       foreach var of varlist estimate-max95 {
 911
           gen ln `var' = ln(`var')
 912
       }
       replace agegr = "" if sens != 1
 913
 914
       label variable agegr "Age group at diagnosis (years)"
 915
 916
       set scheme white tableau
 917
 918
       forestplot ln estimate ln min95 ln max95 if out == "All-cause", eform effect("HR") lcols(agegr)
                                                                                                                                    ///
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
 919
                                                                                                                                    ///
 920
          spacing(2.5) yline(3.5(3)18.5, lwidth(vthin) lpattern(vshortdash)) xtitle("Hazard ratio, T2DM vs noT2DM", size(6pt))
                                                                                                                                    ///
 921
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(1 2 4 8, force labsize(6pt) nogrid)
                                                                                                                                    ///
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue)) ///
 922
          title("All-cause", size(small)) name("All", replace) xsize(4) ysize(5) scale(1) nodraw
 923
 924
 925
       forestplot ln estimate ln min95 ln max95 if out == "Cancer", eform effect("HR") lcols(agegr)
                                                                                                                                    111
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
                                                                                                                                    ///
 926
 927
          spacing(2.5) yline(3.5(3)18.5, lwidth(vthin) lpattern(vshortdash)) xtitle("Hazard ratio, T2DM vs noT2DM", size(6pt))
                                                                                                                                    ///
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(0.5 1 2 4 8 16, force labsize(6pt) nogrid)
 928
                                                                                                                                    ///
 929
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue)) ///
          title("Cancer", size(small)) name("Cancer", replace) xsize(4) ysize(5) scale(1) nodraw
 930
 931
       forestplot ln estimate ln min95 ln max95 if out == "Cardiorenal", eform effect("HR") lcols(agegr)
                                                                                                                                    111
 932
 933
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
                                                                                                                                    ///
          spacing(2.5) yline(3.5(3)18.5, lwidth(vthin) lpattern(vshortdash)) xtitle("Hazard ratio, T2DM vs noT2DM", size(6pt))
 934
                                                                                                                                    111
 935
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(1 2 4 8 16 32, force labsize(6pt) nogrid)
                                                                                                                                    111
 936
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue)) ///
          title("Cardiorenal", size(small)) name("Cardiorenal", replace) xsize(4) ysize(5) scale(1) nodraw
 937
 938
 939
       forestplot ln estimate ln min95 ln max95 if out == "Noncancer/cardiorenal", eform effect("HR") lcols(agegr)
                                                                                                                                    111
          nonames noov nosu nowt dp(2) classic boxscale(60) astext(40) textsize(105)
 940
                                                                                                                                    ///
          spacing(2.5) yline(3.5(3)18.5, lwidth(vthin) lpattern(vshortdash)) xtitle("Hazard ratio, T2DM vs noT2DM", size(6pt))
 941
                                                                                                                                    ///
 942
          leftjustify ciopts(lwidth(vthin)) plotid(sens) xlabel(1 2 4 8, force labsize(6pt) nogrid)
                                                                                                                                    ///
          box1opts(mcolor(red)) ci1opts(lcolor(red)) box2opts(mcolor(black)) ci2opts(lcolor(black)) box3opts(mcolor(blue)) ci3opts(lcolor(blue)) ///
 943
```

```
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       title("Noncancer/cardiorenal", size(small)) name("NCNC", replace) xsize(4) ysize(5) scale(1) nodraw
 945
     graph combine All Cancer Cardiorenal NCNC, rows(1) scale(0.9) xsize(6) ysize(4) name("FigS6", replace) nocopies
 946
 947
     graph export "...Figure_S6_R1.svg", as(svg) name("FigS6")
 948
     graph close all
 949
 950
     951
     952
     953
 954
     cap use "...m3_survival_data.dta", clear
 955
     gen end date="31/10/2020"
     gen d end=date(end date, "DMY")
     replace d end=deathn if died==1
 957
 958
     gen time = (d end-indexn)/365.25
 959
     replace time = .00136895 if time==0
     keep exp age index died time
 960
     sum age index
 961
 962
     egen float ageg = cut(age index), at(0 16 28 32 36 40 44 48 100) icodes label
 963
 964
     preserve
 965
     gen t25 = time
 966
     gen t50 = time
 967
     gen t75 = time
     collapse (p25) t25 (p50) t50 (p75) t75, by(ageg)
 969
     foreach var of varlist t25 t50 t75 {
 970
        tostring `var', format(%3.1f) force replace
 971
     }
     gen m igr = t50 + "(" + t25 + "-" + t75 + ")"
 972
 973
     gen agegr = "16-27" if ageg == 1
     replace agegr = "28-31" if ageg == 2
 975
     replace agegr = "32-35" if ageg == 3
     replace agegr = "36-39" if ageg == 4
 976
 977
     replace agegr = "40-43" if ageg == 5
     replace agegr = "44-47" if ageg == 6
 978
 979
     replace agegr = "48-50" if ageg == 7
 980
     order agegr m_iqr, first
     cap export excel using "...FollowUp_Agegroups.xls", firstrow(variables) replace
 981
 982
     restore
 983
 984
     sort ageg
 985
     gen agegr
               = "16-27" if ageg == 1
     replace agegr = "28-31" if ageg == 2
 987
     replace agegr = "32-35" if ageg == 3
 988
     replace agegr = "36-39" if ageg == 4
     replace agegr = "40-43" if ageg == 5
 989
 990
     replace agegr = "44-47" if ageg == 6
     replace agegr = "48-50" if ageg == 7
     tab ageg agegr
 992
     set scheme tab2
 993
 994
     distplot time, over(agegr) ylabel(0(10)100, labsize(8pt)) legend(rows(1) position(12)) trscale(100*@) xlabel(0(2)20, labsize(8pt)) xsize(5) ysize(5) xtitle("Follow-up time (years)")
     ytitle("Cumulative probability (%)")
 995
     cap graph export "...FollowUp_Agegroups.emf", as(emf) name("Graph") replace
     graph close all
 997
 998
     999
     1000
     1001
```

```
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1003
       ***RELATIVE: Cause-specific difference***
1004
       cap use "...m3 survival data.dta", clear
       egen float agegr = cut(age_index), at(16 28 32 36 40 44 48 51) icodes
1005
1006
       lab define agegr_1 0 "16-27" 1 "28-31" 2 "32-35" 3 "36-39" 4 "40-43" 5 "44-47" 6 "48-50"
1007
       lab values agegr agegr 1
1008
       tab agegr, m
       tabstat age_index, statistics(mean median min max count) by(agegr)
1009
1010
       gen end date="31/10/2020"
1011
       gen d end=date(end date, "DMY")
       replace d_end=deathn if died==1
1012
       gen time = (d end-indexn)/365.25
1013
       replace time = .00136895 if time==0
1014
       keep patid time died exp age index sex eth imd smoke hypertension 5 agegr bmi death str cva death ihd death renal death cancer death other
1015
       lab define exp_lab 0 "no" 1 "yes"
1016
1017
       lab values exp exp_lab
       gen death cvd=0
1018
       replace death_cvd=1 if death_ihd==1 | death_str_cva==1
1019
1020
       drop death ihd death str cva
       groups death cvd death renal died
1021
       renames death_cvd death_renal \ sdeath_cvd sdeath_renal
1022
1023
       groups sdeath_cvd agegr    if sdeath_cvd == 1, clean
1024
1025
       groups sdeath renal agegr if sdeath renal == 1, clean
1026
1027
       foreach nm in sdeath_cvd sdeath_renal {
1028
1029
           stset time, f(`nm'==1)
1030
1031
           preserve
1032
           set showbaselevels on
1033
           stpm2 i.exp#i.agegr i.agegr sex i.eth i.imd smoke hypertension 5, df(4) scale(hazard) eform nolog
1034
           parmest, fast eform
1035
           split parm, p(#)
1036
           keep if parm1 == "1.exp"
1037
           sencode parm2, replace
1038
           replace parm2 = parm2 - 1
1039
           drop parm1
1040
           gen agegr
                        = "16-27" if parm2 == 0
1041
           replace agegr = "28-31" if parm2 == 1
           replace agegr = "32-35" if parm2 == 2
1042
1043
           replace agegr = "36-39" if parm2 == 3
           replace agegr = "40-43" if parm2 == 4
1044
1045
           replace agegr = "44-47" if parm2 == 5
           replace agegr = "48-50" if parm2 == 6
1046
1047
           drop parm2 parm eq
1048
           gen scale = "Relative"
           gen out = "`nm'"
1049
1050
           gen sens = "MAIN"
           tempfile rel_`nm'_main
1051
1052
           save `rel_`nm'_main', replace
1053
           restore
1054
1055
       ***********
1056
1057
       *COMBINED RELATIVE - CARDIO RENAL*
       ***********
1058
1059
1060
       foreach nm in sdeath cvd sdeath renal {
```

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```
**********
1066
1067
      *TABLE RELATIVE - CARDIO RENAL*
      ***********
1068
      cap use "...Results/Relative_CR_main", clear
1069
      keep estimate min95 max95 agegr out
1070
1071
      foreach var of varlist estimate-max95 {
          tostring `var', replace force format(%20.2f)
1072
1073
      }
      gen hr_ci = estimate + " (" + min95 + " to " + max95 + ")"
1074
      order out agegr hr_ci
1075
      drop estimate-max95
1076
1077
      replace out = "CVD only" if out == "sdeath_cvd"
      replace out = "Renal only" if out == "sdeath_renal"
1078
      cap export excel using "...Cardio_Renal_Separate.xls", firstrow(variables) replace
1079
```