

## Mortality among drug users: Guidelines for carrying out, analysing and reporting key figures

## 2012

EMCDDA standard protocol to collect data and report figures for the mortality component of the Key indicator 'DRD and mortality'

by the Reitox Standard Tables

The full cohort guidelines as well as the template of Standard Table 18 (ST18), the SPSS® and Stata® scripts and the MS® Excel files necessary to compute the Standard Table (ST18) are available from http://www.emcdda.europa.eu/themes/key-indicators/drd

## STATA<sup>©</sup> script<sup>1</sup>

1) \*\*\*\*\*\*\*\* initiate cambridge revisited 2010 \*\*\*\*\*\*\*\*
use tmpthur, clear
sort cohort id
duplicates drop cohort id, force
cap drop if studyset != 5
cap drop \_\*

\*\*\*drop unwanted variables from previous Cambridge work\*\*\*
drop viol\_ cause\_ric
drop artot0one artotal yartot0one fut\_yrbeg fut\_yrend one cohortm cohortf
drop dthppaids effe\_date effx\_date fut\_agbeg fut\_agend
drop yre\_cohort yrf\_cohort
drop eta end\_date

<sup>&</sup>lt;sup>1</sup> This script was developed and updated by Colin Taylor, as part of the cohort guidelines. The work was initiated with the EMCDDA Cosmo group (pooled analysis of the so-called 'Cambridge dataset'). Section 1 of this script refers to the initial 'Cambridge script' and indicates which of the initial variables are dropped or renamed. Sections 2 to 5 explain how to re-structure the data file as "time-slices", construct basic tables of crude mortality and causes of death, and get reference population data for standardising ratios.

```
rename eta1 eta
rename end_date1 end_date
*note some variables kept for checking purposes with earlier results but otherwise not
needed: yartotal, eta,
*.. and also those many variables for yar by cal.yr, dth by cal.yr, yar by ageband, dth
by ageband
***analyse just data for Barcelona...
tab cohort
drop if (cohort != 2) & (cohort != 3)
***** Things to do once only to fit in with 2012 cohort guidelines names *******
rename id idno
gen access_no = 100000*cohort+idno
rename cohort country
*note Stata date variables have been retained, but could be generated anew for
completeness:
*... b_date, e_date, x_date (set from d_date, l_date, f_date, a_date), e_cohort, f_cohort
*these were generated from the (also retained) string variables: birth date,
enrolment_date, death_date, etc.
gen cohyar = yartotal
gen cohdth = (vital==3)
label define gender 1 "Male" 2 "Female"
label values gender gender
label define novesno 0 "No" 1 "yes" 2 "No"
label values treated noyesno
2) ****** re-structure data file as "time-slices" ********
*use b_date, e_date, x_date to time-slice data file, giving multiple records per
individual (access no)
* ... using cohdth to mark study exit by death or not and rescaling from days to years
(365.25 days)
gen i_date=x_date
sort access no
stset i_date, origin(time b_date) enter(e_date) scale(365.25) failure(cohdth)
id(access_no)
stsplit i_aged, every(1)
```

stsplit i\_obsd, every(1) after(e\_date)

stsplit i\_year, every(1) after(mdy(1,1,1960))

```
*time-slices are now indexed by individual, gender, year-of-age=i_aged, study-
year=i obsd, cal.year=i year
*set proper coding for cal.year index, recode missing death indicator, calculate yrs at
risk from system vbls
replace i year=i year+1960
replace cohdth=0 if cohdth==.
gen i yar= t- t0
*and (for future use) generate age-bands 15(10)65 indicator for each (time-slice of)
record ...
gen agegps 10 = min(65, 15+10*int((i_aged-15)/10))
*******check/demo list first 50 slices of records *******
*list b date e date x date access no gender i obsd i aged i year cohdth i date i yar
in 1/50, noo
3) *******construct basic tables of crude mortality and causes of death *******
*need to construct weight and 'working dummies' to get CMRs tabled directly
cap drop tmpw tmp1 tmpd
gen tmp1 = 1
gen tmpw = i_yar
gen tmpd = cohdth/tmpw
*Table ST? Mortality rates by gender and overall, (yrs risk, obs.deaths, obs.mean pa)
table gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd ) row
*Table ST? Mortality rates by primary drug, gender and overall, (yrs risk, obs.deaths,
obs.mean pa)
table prim_route gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row col
*Table ST? Mortality rates by calendar years, gender and overall, (yrs risk, obs.deaths,
obs.rate pa)
table i_year gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd ) row
*Table ST? Age-specific mortality rates by gender and overall, (yrs risk, obs.deaths,
obs.mean pa)
table agegps 10 gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row col
*Table ST? Causes of death: proportional mortality by five cateories (obs.deaths,
ave.latency)
table codeath5 gender [pw=tmpw], m contents(sum tmpd mean tmpd) row col
```

4) \*\*\*\*\*\*get ref. population data for standardising ratios \*\*\*\*\*\*\*

```
*get reference population data (gender, age, refpopn, refdths, refyars, refrate)
cap drop age
gen age=i age
sort gender i_aged i_year i obsd
*also refpopdata.dta file needs to be sorted by gender then age
*!*merge gender age using refpopdata.dta
*!*drop merge
*!*temporary fix since no ref.pop data yet ...
cap drop refpopn refdths refyar refrate
gen refpopn=(1000.0 - 0.1*age^2)
gen refdths=0.1*age^2 - 0.1*(age-1)^2
gen refyars=refpopn-0.5*refdths
gen refrate=refdths/refvars
*... end of temporary fix
*******construct tables of excess mortality ratios (EMRs == SMRs)*******
*need to construct weight and 'working dummies' to get SMRs tabled directly
cap drop tmpy
cap drop tmpw tmp1 tmpd
gen tmp1 = 1
gen tmpw = i_yar*refrate
gen tmpd = cohdth/tmpw
*Table ST? Age-specific EMR by gender and overall, (exp.deaths, obs.deaths, EMR)
table agegps 10 gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row col
*Table ST? EMR by gender and overall, (exp.deaths, obs.deaths, EMR)
table gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd ) row
*Table ST? EMR by primary drug, gender and overall, (exp.deaths, obs.deaths, EMR)
table prim_route gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row col
*Table ST? EMR by calendar years, gender and overall, (exp.deaths, obs.deaths,
EMR)
table i year gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd ) row
col
*******construct tables of directly standardised rates (DSMRs)*******
*calc weights to project cohort exposures to those of ref.popn
*here standardisation (and weighting) is by each gender, age-band
cap drop agy_ref agy_coh
cap drop agy_adj
egen agy_ref = mean(refyar), by(gender agegps10)
egen agy\_coh = sum(i\_yar), by(gender agegps10)
gen agy_adj = agy_ref/agy_coh
```

```
*need to construct weight and 'working dummies' to get DSMRs tabled directly
cap drop tmpw tmp1 tmpd
gen tmp1 = 1
gen tmpw = i_yar^*(agy_adj)
gen tmpd = (cohdth/i yar)
***NB OR EQUIVALENTLY: gen tmpd = agy_adj*cohdth/tmpw
*Table ST? Age-specific DSMR by gender and overall, (adj.yar, adj.deaths, resulting
MR)
table agegps 10 gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row col
*Table ST? DSMR by gender and overall, (adj.yar, adj.deaths, resulting MR)
table gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd ) row
*Table ST? DSMR by primary drug, gender and overall, (adj.yar, adj.deaths, resulting
table prim_route gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row col
*Table ST? DSMR by calendar years, gender and overall, (adj.yar, adj.deaths,
resulting MR)
table i_year gender [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd ) row
col
5) ****** Also can do .... *******
cap drop tmpw tmp1 tmpd
gen tmp1 = 1.0
gen tmpw = i_yar
gen tmpd = cohdth/tmpw
*Table ST? Males: mortality rates by calendar years, (yrs risk, n deaths, rate pa)
table i year if gender==1 [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row
*Table ST? Females: mortality rates by calendar years, (yrs risk, n deaths, rate pa)
table i_year if gender==2 [pw=tmpw], m contents( sum tmp1 sum tmpd mean tmpd )
row
*Table ST? Mortality rates over the observation period by whether previously treated,
table i_obsd treated gender if treated<9 [pw=tmpw], m contents( mean tmpd ) row
*Table ST? CMR over the observation period: trend significance tests by 'Gender' &
'Previously treated'
xi: poisson cohdth i_obsd i.gender*i.treated if treated<9, exp(i_yar) irr
```