

Biostat 212: 2017

Example Final Project

```
. webuse nhanes2, clear
```

TABLE 1 Code

```
. label define diabetes_label 1 "Diabetics" 0 "Non diabetics"
. label values diabetes diabetes_label
. tabstat zinc copper vitaminc iron, by(diabetes) stat(n mean sd) save
    Summary statistics: N, mean, sd
    by categories of: diabetes (diabetes, 1=yes, 0=no)

```

diabetes	zinc	copper	vitaminc	iron
Non diabetics	8750 86.65074 14.49493	8679 125.3898 32.72976	9486 1.032933 .5774621	9850 99.85706 34.14416
Diabetics	451 83.69845 13.8738	450 130.04 27.80633	485 1.072784 .6534093	499 91.34269 31.77103
Total	9201 86.50603 14.47842	9129 125.619 32.51881	9971 1.034871 .5814126	10349 99.44652 34.08093

```

. return list
    macros:
        r(name2) : "Diabetics"
        r(name1) : "Non diabetics"
    matrices:
        r(Stat2) : 3 x 4
        r(Stat1) : 3 x 4
        r(StatTotal) : 3 x 4
. matrix list r(StatTotal)
    r(StatTotal)[3,4]
      zinc      copper      vitaminc      iron
    N      9201      9129      9971      10349
  mean 86.506032 125.61902 1.0348711 99.446517
   sd 14.478417 32.518809 .58141263 34.080933
. matrix stats1 = r(Stat1)
. matrix stats2 = r(Stat2)
. local d_n : display %9.0f stats2[1,1]
. local d_z : display %9.2f stats2[2,1] "("%9.1f stats2[3,1] ")"
. local d_c : display %9.2f stats2[2,2] "("%9.1f stats2[3,2] ")"
. local d_v : display %9.2f stats2[2,3] "("%9.1f stats2[3,3] ")"
. local d_i : display %9.2f stats2[2,4] "("%9.1f stats2[3,4] ")"
. local nd_n : display %9.0f stats1[1,1]
. local nd_z : display %9.2f stats1[2,1] "("%9.1f stats1[3,1] ")"
. local nd_c : display %9.2f stats1[2,2] "("%9.1f stats1[3,2] ")"
. local nd_v : display %9.2f stats1[2,3] "("%9.1f stats1[3,3] ")"
. local nd_i : display %9.2f stats1[2,4] "("%9.1f stats1[3,4] ")"
```

TABLE 1

Table 1: Serum Zinc, Copper, Vitamin C and Iron levels (mcg/dL) for Diabetics and Non-Diabetics in NHANES

Mean (SD)	N	Zinc	Copper	Vitamin C	Iron
Diabetics	451	83.70(13.9)	130.04(27.8)	1.07(0.7)	91.34(31.8)
Non diabetics	8750	86.65(14.5)	125.39(32.7)	1.03(0.6)	99.86(34.1)

FIGURE 1 Code

you will need to install 1 add-on package that combines legends called grc1leg

net install grc1leg, from(<http://www.stata.com/users/vwiggins>)

```
. twoway
///
    kdensity zinc if diabetes==1
    , lcolor(gray) ||
    kdensity zinc if diabetes==0
    , lcolor(black) lpattern(dash)
    , yscale(off)
    graphregion(color(white) lcolor(none) ilcolor(none))
    legend(lab(1 "Diabetics") lab(2 "Non-diabetics"))
    ytitle("Density") xtitle("Serum Zinc (mcg/dL)")
    name(zinc_plot, replace)
///
. twoway
///
    kdensity copper if diabetes==1
    , lcolor(gray) ||
    kdensity copper if diabetes==0
    , lcolor(black) lpattern(dash)
    , yscale(off)
    graphregion(color(white) lcolor(none) ilcolor(none))
    legend(lab(1 "Non diabetics") lab(2 "Diabetics"))
    ytitle("Density") xtitle("Serum Copper (mcg/dL)")
    legend(off)
```

```

name(copper_plot, replace)
. twoway
///
    kdensity vitaminc if diabetes==1
    , lcolor(gray) ||
    kdensity vitaminc if diabetes==0
    , lcolor(black) lpattern(dash)
    , yscale(off)
    graphregion(color(white) lcolor(none) ilcolor(none))
    legend(lab(1 "Non diabetics") lab(2 "Diabetics"))
    ylabel("Density") xlabel("Serum Vitamin C (mcg/dL)")
    legend(off)
    name(vc_plot, replace)
.
///
    kdensity iron if diabetes==1
    , lcolor(gray) ||
    kdensity iron if diabetes==0
    , lcolor(black) lpattern(dash)
    , yscale(off)
    graphregion(color(white) lcolor(none) ilcolor(none))
    legend(lab(1 "Non diabetics") lab(2 "Diabetics"))
    ylabel("Density") xlabel("Serum Iron (mcg/dL)")
    legend(off)
    name(iron_plot, replace)
.
grc1leg zinc_plot copper_plot vc_plot iron_plot
, legendfrom(zinc_plot)
title("Figure 1 : K-density Distribution for Serum Zinc, Copper, Vitamin C" and Iron levels in Diabetics and Non-diabetics")
note("Data source: NHANES2")

```

FIGURE 1

Figure 1: K-density Distribution for Serum Zinc, Copper, Vitamin and Iron levels in Diabetics and Non-diabetics

