Example 1: Mean Calculation

In the following sample code, the distribution of BMI (bmi_p) is examined by race (racehpr2) and by race and sex (racehpr2*srsex).

**SAS:**

```sas
PROC SORT DATA = data;
   BY racehpr2;
   RUN;
PROC SURVEYMEANS DATA = data VARMETHOD=JACKKNIFE;
   WEIGHT rakedw0;
   REPWEIGHT rakedw1-rakedw80/JKCOEFS=1;  *
   VAR bmi_p;
   BY racehpr2;
   RUN;
PROC SORT DATA = data;
   BY racehpr2 srsex;
   RUN;
PROC SURVEYMEANS DATA = data VARMETHOD=JACKKNIFE;
   WEIGHT rakedw0;
   REPWEIGHT rakedw1-rakedw80/JKCOEFS=1;
   VAR bmi_p;
```

* Jackknife coefficients are necessary for accurate variance calculations, and jackknife coefficients of 1 in SAS will produce equal variance calculations as those produced in SUDAAN. However, for SAS V.9.2(TS1M0) and earlier, a value of 1 will not be accepted; as a substitute, 0.9999 can be entered. Without this specification, the default value of the jackknife coefficients will be [(# replicate weights - 1)/# replicate weights]; for CHIS, this would be [(80 - 1)/80] = 0.9875.

**SUDAAN:**

```sas
PROC DESCRIPT DATA = data FILETYPE=SAS DESIGN=JACKKNIFE;
   WEIGHT rakedw0;
   JACKWGTS rakedw1-rakedw80/ADJJACK=1;
   VAR bmi_p;
   TABLES racehpr2 racehpr2*srsex;
   SUBGROUP racehpr2 srsex;
   LEVELS 7 2;
   RUN;
```

This produces racehpr2*srsex grouping.
In Stata, the sample design specification step should be included before conducting any analysis.

Stata:

*Sample design specification step*

```
use "DATASET LOCATION"
svyset [pw=rakedw0], jkrw(rakedw1-rakedw80, multiplier(1)) vce(jack) mse
```

*Analysis*

```
svy: mean bmi_p, over(racehr2)
svy: mean bmi_p, over(srsex racehr2)
```