**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:**

```
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;
BY racehpr2 srsex;
RUN;
```

\(^a\) 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.

\(^b\) This produces racehpr2*srsex grouping.

**SUDAAN:**

```
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;
```

**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(racehpr2)
svy: mean bmi_p, over(srsex racehpr2)
```

\(^c\) In Stata, the sample design specification step should be included before conducting any analysis.