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 or 0.5; *a
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 or 0.5;
VAR bmi_p;
BY racehpr2 srsex; *b
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 $([# \text{ replicate weights} - 1]/[# \text{ replicate weights}])$; for CHIS, this would be $[(80 - 1)/80] = 0.9875$.

Following external statistical consultation and research on two-PSU-per-stratum paired jackknife replicate designs, **CHIS recommends that data users use a jackknife coefficient of 0.5 instead of the historical 0.9999 beginning in 2019**, in conjunction with the methodological redesign. The use of a jackknife coefficient algebraically equivalent to 1 for paired jackknife replicates has produced more conservative estimates of standard errors in recent years. This change will be reflected in all CHIS data products including AskCHIS and Data Access Center (DAC) projects using CHIS 2019 data as well as all subsequent years moving forward.

*b* This produces $racehpr2*srsex$ grouping.

**SUDAAN:**

```
PROC DESCRIPT DATA = data FILETYPE=SAS DESIGN=JACKKNIFE;
WEIGHT rakedw0;
JACKWGTS rakedw1-rakedw80/ADJJACK=1 or 0.5;
VAR bmi_p;
TABLES racehpr2 racehpr2*srsex;
SUBGROUP racehpr2 srsex;
LEVELS 7 2;
RUN;
```
**Stata:**

*Sample design specification step*

```stata
use "DATASET LOCATION"
svyset [pw=rakedw0], jkrw(rakedw1-rakedw80, multiplier(1 or 0.5))
vce(jack) mse
```

*Analysis*

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

* In Stata, the sample design specification step should be included before conducting any analysis.