Tutorial: Sampling, Weighting and Estimation
Day 4

Stefan Zins, Matthias Sand
and Jan-Philipp Kolb

GESIS - Leibniz Institute
for the Social Sciences

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Computation of contrasts

- Using the multi-stage sample of day 3 (`mul.surv`)

```
means <-svymean(~api00+api99,mul.surv)
means
```

```
      mean   SE
api00  644 11.4
api99  613 13.2
```

```
svycontrast(means,quote(api00-api99))
```

```
         nlcon   SE
contrast  30.6 3.19
```

- The command `svycontrast()` can be used to estimate contrasts for linear and nonlinear survey statistics and their standard error

```
svycontrast(means,quote(api00/api99))
```

```
         nlcon   SE
contrast  1.05 0.01
```

⇒ `svyratio(~0 api00,~0 api99,mul.surv)` generates the same results gesis Leibniz Institute for the Social Sciences

Weighted regression

summary(svyglm(api00~enroll+meals+api99,mul.surv))

```
Call:
svyglm(formula = api00 ~ enroll + meals + api99, mul.surv)

Survey design:
svydesign(id = ~cds + id, fpc = ~fpc + fpc2, strata = NULL, data = DATA.s,
    pps = "brewer")

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 114.31730   38.64877    2.96   0.0049 **
enroll       -0.00535    0.00472   -1.13   0.2623
meals         0.06558    0.18715    0.35   0.7277
api99         0.86531    0.04505   19.21   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 406.9)

Number of Fisher Scoring iterations: 2
```

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Weighted regression

summary(svyglm(api00~enroll+meals+api99,mul.surv))

- The `svyglm()` function fits linear and generalized lin. models to the data stored in a survey object
- syntax almost identical to the glm, except that the data argument is replaced by a design argument → weighted least square
- Main difference to `glm()`: `svyglm()` doe not use a maximum likelihood approach

Survey weighted contingency tables and chi squared tests

```
tab1 <- svytable(~stype+sch.wide,mul.surv)
tab1
```

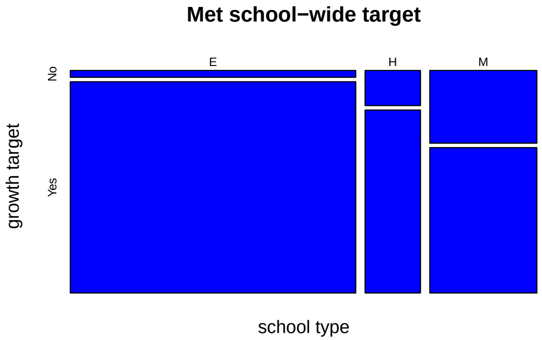
```
     sch.wide
stype    No   Yes
    E  2003 62108
    H  2003 10441
    M  8014 16028
```

- Creates the weighted contingency table of two or more variables

```
plot(tab1, col="blue",xlab = "school type",
+       ylab = "growth target",cex.lab=0.25)
```

- Such contingency tables can easily be visualized to learn more about the sampled variables

Survey weighted contingency tables and chi squared tests



Survey weighted contingency tables and chi squared tests

```
chi <- svychisq(~stype+sch.wide,mul.surv,statistic="adjWald")
chi

       Design-based Wald test of association

data:  svychisq(~stype + sch.wide, mul.surv, statistic = "adjWald")
F = 4.071, ndf = 2, ddf = 48, p-value = 0.02327
```

- Tests for the association of sample variables
- Numerous tests are applicable
- In this case it is tested for independence under the consideration of the number of PSUs

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Estimation of subpopulations

- Within a stratified random sample, subtotals for each stratum are easy to compute, since every stratum can be treated like a separate srs

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- For an unstratified design or subpopulations that are no strata, the situation is more complicated, since the joint inclusion probabilities π_{kl} are unequal to those that would be, if this group had been a stratum
- Sampling weights would be correct, but pairwise sampling probability would be incorrect

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$\Rightarrow$ Unbiased point estimates; but standard errors would be wrong

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Estimation of subpopulations

- The survey package deals with these problems without any further specification as long as the full sample is used to define a survey object
- Subpopulations either by subset or svyby

```
sub1 <- subset(mul.surv,sch.wide=="Yes")
svymean(~api00+api99,sub1)
```

```
      mean   SE
api00  638 12.7
api99  602 14.4
```

```
sub2 <- svyby(~api00,~stype,svymean,design = mul.surv)
print(sub2)
```

```
  stype api00    se
E     E 645.1 16.69
H     H 619.9 11.10
M     M 653.6 16.26
```

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The ratio estimator

$$\frac{\hat{t}_{y,HT}}{\hat{t}_{x,HT}}$$

- Drawing a sample of $n = 130$ from bm

```
bm$pik <- inclusionprobabilities(bm$Tot03,130)
s <- UPmaxentropy(bm$pik)
ratioest(y=bm$TaxableIncome[s==1],x=bm$averageincome[s==1],
+          Tx=sum(bm$averageincome),pik=bm$pik[s==1])
```

```
[1] 1.385e+11
```

- Returns the ratio estimator of the population total

⇒ Another way to calculate the ratio estimator is implemented in the survey package

The ratio estimator

```
 samp <- bm[s==1,]
 IPkl <-UPmaxentropypi2(bm$pik)
 obj <- svydesign(id=~1,fpc = ~pik,data=samp,
+                  pps = ppsmat(IPkl[s==1,s==1]),variance="YG")
 svyratio(~TaxableIncome,~averageincome,obj)
```

```
Ratio estimator: svyratio.pps(~TaxableIncome, ~averageincome, obj)
Ratios=
              averageincome
TaxableIncome          9370
SEs=
              averageincome
TaxableIncome         474.5
```

- The svyratio() command returns the ratio between the two weighted sampling variables.

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The ratio estimator

- To obtain an estimator for the total, the ratio must be multiplied with the population total of the auxiliary variable

```
 as.numeric(svyratio(~TaxableIncome,~averageincome,obj))*
+   sum(bm$averageincome)
```

```
[1] 1.385e+11 3.327e+12
```

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Variance estimation

- Estimating the Variance of the ratio estimator via *Taylor Linearization* with the sampling package

```
 vartaylor_ratio(Ys=samp$TaxableIncome,Xs=samp$averageincome,
+                  pikls = IPkl[s==1,s==1])

$ratio
[1] 9370

$estvar
[1] 234061

[1] 483.8
```

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```

- The survey package uses *Taylor Linearization* by default to estimate standard errors based on design information
- The `vartaylor_ratio()` returns the HT-estimator of the variance, not the YG-type

- Within the survey package all of the *common* strategies are implemented and easy to use
- First step: redefine the survey object as a replicate weights object with the `as.svrepdesign()` command
- Second step: choosing a strategy with the `type=` argument

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$\Rightarrow$ Most of the strategies cannot create replicate weights under unequal inclusion probabilities and resample only the PSUs to create replicate weights

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Jackknife

```
 dclus1 <- svydesign(id=~dnum,weights=~pw,data=apiclus1,
+                    fpc= rep(757/15,times=nrow(apiclus1)))
 clus.rep <- as.svrepdesign(dclus1,type = "JK1")
 svyquantile(~api00 , clus.rep, c (.25 ,.5 ,.75) ,
+             interval.type ="probability")
```

```
Statistic:
      api00
q0.25 551.8
q0.5  652.0
q0.75 717.5
SE:
      api00
q0.25 30.34
q0.5  34.21
q0.75 15.83
```

- Allows the estimation of standard errors for quantiles, etc.
- In case of estimates for the totals and means, the estimates for the standard error are comparable to those of the Taylor Linearization

Bootstrap

```
 rep.clus2 <- as.svrepdesign(dclus1,type = "bootstrap",
+                                replicates = 100)
 svyquantile(~api00,rep.clus2,c (.25 ,.5 ,.75) ,
+              interval.type ="probability")
```

```
Statistic:
      api00
q0.25 551.8
q0.5  652.0
q0.75 717.5
SE:
      api00
q0.25 29.33
q0.5  30.90
q0.75 15.75
```

$\Rightarrow$ Reduces the standard error

- design weights are the starting weights multiplied by the times they have been sampled within each iteration (srswr!)

Balanced Repeated Replicates (BRR)

- BRR is appealing because it requires less computational effort than the Jackknife method
- BRR standard errors are valid for quantiles and median, while the Jackknife method might produce invalid results

```
 dstrat <- svydesign(id=~1,weights=~pw,strata = ~stype,
+                     data = apistrat,fpc = ~fpc)
 rep3 <- as.svrepdesign(dstrat,type = "BRR")
 svyquantile(~api00,rep3,c (.25 ,.5 ,.75) ,
+               interval.type ="probability")

Statistic:
      api00
q0.25 562.2
q0.5  667.2
q0.75 755.1
SE:
      api00
q0.25 15.05
q0.5  11.33
q0.75 13.18
```

Summary: replicate weights and single stage sampling

- All three methods can only be applied to single-stage samples or resample only on the PSU-level
- All three approaches ignore the fpc

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- All three methods can only be applied to single-stage samples or resample only on the PSU-level
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$\Rightarrow$ BRR can only be applied for samples with two clusters per stratum

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- All three methods can only be applied to single-stage samples or resample only on the PSU-level
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⇒ BRR can only be applied for samples with two clusters per stratum

⇒ All three approaches have problems with multi-stage samples and unequal inclusion probabilities

Multi-stage samples and replicate weights

- In case of multi-stage samples, the *mrb* or *mrbbootstrap* method of Preston should be employed

$\Rightarrow$ Resamples PSUs and SSUs rather than only PSUs

```
summary(svyglm(api00~enroll+meals+api99,mul.surv))

Call:
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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 406.9)

Number of Fisher Scoring iterations: 2
```

Multi-stage samples and replicate weights

```
rep4 <- as.svrepdesign(mul.surv,type = "mrbbootstrap")
summary(svyglm(api00~enroll+meals+api99,rep4))
```

```
Call:
svyglm(formula = api00 ~ enroll + meals + api99, rep4)

Survey design:
as.svrepdesign(mul.surv, type = "mrbbootstrap")

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 114.31730   19.95635    5.73  7.4e-07 ***
enroll       -0.00535    0.00256   -2.09    0.042 *
meals         0.06558    0.09243    0.71    0.482
api99         0.86531    0.02384   36.30  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 406.7)

Number of Fisher Scoring iterations: 2
```

- Reduces standard error of the estimates
- Estimates are far more significant
- Needs more computational time then other resampling strategies

⇒ But: correct approach for multi-stage samples