Complex survey samples in R

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Why are surveys special?

- Probability samples come with a lot of meta-data that has to be linked correctly to the observations, so software was specialized

- Interesting data sets tend to be large, so hardware was specialized

- Design-based inference literature is largely separate from rest of statistics, doesn't seem to have a unifying concept such as likelihood to rationalize arbitrary choices.

In part, too, the specialized terminology has formed barriers around the territory. At one recent conference, I heard a speaker describe methods used in his survey with the sentence, ”We used BRR on a PPS sample of PSU’s, with MI after NRFU”

(Sharon Lohr, American Statistician 5/2004)

Survey package

http://faculty.washington.edu/tlumley/survey/

Version 3.6-9 is current, containing approximately 6000 lines of interpreted R code. (cf 250,000 lines of Fortran for VPLX)

Version 2.3 was published in Journal of Statistical Software. Major changes since then are finite population corrections for multistage sampling, calibration and generalized raking, tests of independence in contingency tables, better tables of results, simple two-phase designs.

Other relevant R packages: pps, sampling, sampfling, all focus on design, in particular PPS sampling without replacment.

Design principles

- Ease of maintenance and debugging by code reuse
- Speed and memory use not initially a priority: don't optimize until there are real use-cases to profile.
- Rapid release, so that bugs and other infelicities can be found and fixed.
- Emphasize features that look like biostatistics (regression, calibration, survival analysis)

Intended market

- Methods research (because of programming features of R)
- Teaching (because of cost, use of R in other courses)
- Secondary analysis of national surveys (regression features, R is familiar to non-survey statisticians)

Overview

- Describing survey designs: `svydesign()`
- Replicate weights: `svrepdesign()`, `as.svrepdesign`
- Summary statistics: mean, total, quantiles, design effect
- Tables of summary statistics, domain estimation.
- Graphics: histograms, hexbin scatterplots, smoothers.
- Regression modelling: `svyglm()`
- Calibration of weights: `postStratify()`, `calibrate()`

Objects and Formulas

Collections of related information should be kept together in an object. For surveys this means the data and the survey meta-data.

The way to specify variables from a data frame or object in R is a formula

```
~a + b + I(c < 5*d)
```

The survey package always uses formulas to specify variables.

Weights and probabilities

The basic estimation idea is that individuals are sampled with known probabilities π_i, so that the population total for a variable can be estimated by

$$T = \sum_{i=1}^{n} \frac{1}{\pi_i} X_i$$

Other statistics follow from this: if the statistic on the whole population would solve

$$\sum_{i=1}^{N} U_i(\theta) = 0$$

then we solve

$$\sum_{i=1}^{n} \frac{1}{\pi_i} U_i(\theta) = 0$$

Standard errors

Standard errors for totals follow from elementary formulas for the variance of a sum.

Standard errors for more complicated statistics come from the delta method. If $\widehat{\theta}$ solves

$$\sum_{i=1}^{n} \frac{1}{\pi_i} U_i(\theta) = 0$$

then its variance can be estimated by

$$\widehat{\mathrm{var}}[\widehat{\theta}] = A^{-1} B A^{-1}$$

where

$$A = \sum_{i=1}^{n} \frac{1}{\pi_i} \frac{\partial U_i(\theta)}{\partial \theta}\bigg|_{\theta=\widehat{\theta}}$$

and B is an estimate of the variance of

$$\sum_{i=1}^{n} \frac{1}{\pi_i} U_i(\theta)$$

Standard errors

Another approach extends the idea of jackknife or bootstrap resampling: evaluate the statistic on a lot of slightly different weights and use the variability between these to estimate the variance. (replicat{e,ion} weights)

Technical details are in the code: `svyrecvar` and `svrVar`, references are in the help pages (Särndal, Swensson & Wretman is the most important).

Types of designs

The calculations are correct for multistage stratified random sampling with or without replacements.

Taylor expansion is correct for unequal probability sampling with replacement (eg PPS with replacement). I don't think the replicate weights are correct in this case, but they are probably not bad.

I am working on Horvitz–Thompson and Yates–Grundy estimators for more general designs (including PPS without replacement), using the fact that the covariance matrix of sampling indicators is often a projection times a sparse matrix.

Describing survey designs

Stratified independent sample (without replacement) of schools

```
dstrat <- svydesign(id=~1,strata=~stype, weights=~pw,
                    data=apistrat, fpc=~fpc)
```

- `stype` is a factor variable for elementary/middle/high school
- `fpc` is a numeric variable giving the number of schools in each stratum. If omitted we assume sampling with replacement
- `id=∼1` specifies independent sampling.
- `apistrat` is the data frame with all the data.
- `pw` contains sampling weights ($1/\pi_i$). These could be omitted since they can be computed from the population size.

Describing survey designs

```
> dstrat
Stratified Independent Sampling design
svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
    fpc = ~fpc)
> summary(dstrat)
Stratified Independent Sampling design
svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
    fpc = ~fpc)
Probabilities:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.02262 0.02262 0.03587 0.04014 0.05339 0.06623
Stratum Sizes:
             E  H  M
obs        100 50 50
design.PSU 100 50 50
actual.PSU 100 50 50
Population stratum sizes (PSUs):
   E    M    H
4421 1018  755
Data variables:
 [1] "cds"      "stype"    "name"     "sname"    "snum"     "dname"
 [7] "dnum"     "cname"    "cnum"     "flag"     "pcttest"  "api00"
 ...
```

Describing survey designs

Cluster sample of school districts, using all schools within a district.

```
dclus1 <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
```

- `dnum` is a (numeric) identifier for school district
- No stratification

```
> summary(dclus1)
1 - level Cluster Sampling design
With (15) clusters.
svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)
Probabilities:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.02954 0.02954 0.02954 0.02954 0.02954 0.02954
Population size (PSUs): 757
Data variables:
 [1] "cds"        "stype"      "name"       "sname"      "snum"       "dname"
 [7] "dnum"       "cname"      "cnum"       "flag"       "pcttest"    "api00"
...
```

Describing survey designs

Two-stage sample: 40 school districts and up to 5 schools from each

```
dclus2 <- svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)
```

- `dnum` identifies school district, `snum` identifies school
- `fpc1` is the number of school districts in population, `fpc2` is number of schools in the district.
- Weights are computed from `fpc1` and `fpc2`

```
> summary(dclus2)
2 - level Cluster Sampling design
With (40, 126) clusters.
svydesign(id = ~dnum + snum, fpc = ~fpc1 + fpc2, data = apiclus2)
Probabilities:
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
0.003669 0.037740 0.052840 0.042390 0.052840 0.052840
Population size (PSUs): 757
Data variables:
 [1] "cds"        "stype"     "name"       "sname"      "snum"       "dname"
 [7] "dnum"       "cname"     "cnum"       "flag"       "pcttest"    "api00"
...
```

Prespecified replicate weights

`svrepdesign` creates an object using prespecified replicate weights.

Some survey institutions prefer using replicate weights rather strata/cluster information for confidentiality reasons, or because it is easier to handle calibration/post-stratification.

Unless the replicate weights are a type that R knows about (BRR, JK1, JKn, Fay, bootstrap) it is also necessary to specify how to scale the variance: From `survey:::svrVar`

```
meantheta <- mean(thetas[rscales > 0])
v <- sum((thetas - meantheta)^2 * rscales) * scale
```

Here `scale` is a single number (a) and `rscales` is a vector (b_i). For JKn `scale` is the finite population correction and `rscales` is $n/n-1$ for the stratum.

Example

California Health Interview Survey public use data files (http://www.chis.ucla.edu) supplies a data set with 80 sets of replicate weights. Their documentation says

“WesVar, SUDAAN, and Stata are software packages that allow variance estimation using replicate weights ... As of September 2005, SAS and SPSS do not contain features that allow use of replicate weights ... There are other possibilities, like R for utilizing replicate weights but these are not as commonly used as other software”

```
rchis<-svrepdesign(chis[,-(216+(1:80))],
    repweights=chis[,216+(1:80)],
    weights=chis$RAKED0, combined.weights=TRUE,
    scale=1, rscales=rep(1,80),type="other")
```

Example

Alcohol and Drug Services Study (ADSS) conducted for the Substance Abuse and Mental Health Services Administration. Data and documentation available from the (`http://www.icpsr.umich.edu/`).

The data files contain 200 replicate weights that are based on a stratified jackknife (JKn) with modifications to reduce very large weights, account for nonresponse, and for other reasons. Separate files contain the finite population correction factors and the quantity we have called b_i or `rscales`.

```
adss<-svrepdesign(data = adssdata, repweights = adssdata[, 782:981],
    scale = 1, rscales = adssjack, type = "other",
    weights = ~PH1FW0, combined.weights = TRUE, fpc=adssfpc,
    fpctype="correction")
```

Constructing replicate weights

`as.svrepdesign` converts a `svydesign` to replicate weights. Default is jackknife.

```
rclus1 <- as.svrepdesign(dclus1)
bclus1 <- as.svrepdesign(dclus1, type="bootstrap", replicates=100)
```

Bootstrap and jackknife replicate weights incorporate the finite-sampling correction, BRR doesn't.

Replicate weights

- Jackknife, leaving out one PSU (JK1, JKn)
- Bootstrap of PSUs within strata (best with large strata).
- Half-sample for designs with 2 PSUs/stratum (BRR)

Rather than leaving out PSUs we actually set the weight to zero. If θ_i^* is the estimate with the ith set of weights then

$$\widehat{\mathrm{var}}[\hat{\theta}] = a \sum_{i=1}^{K} b_i (\theta_i^* - \bar{\theta}^*)^2$$

where a and b_i depend on the weighting design.

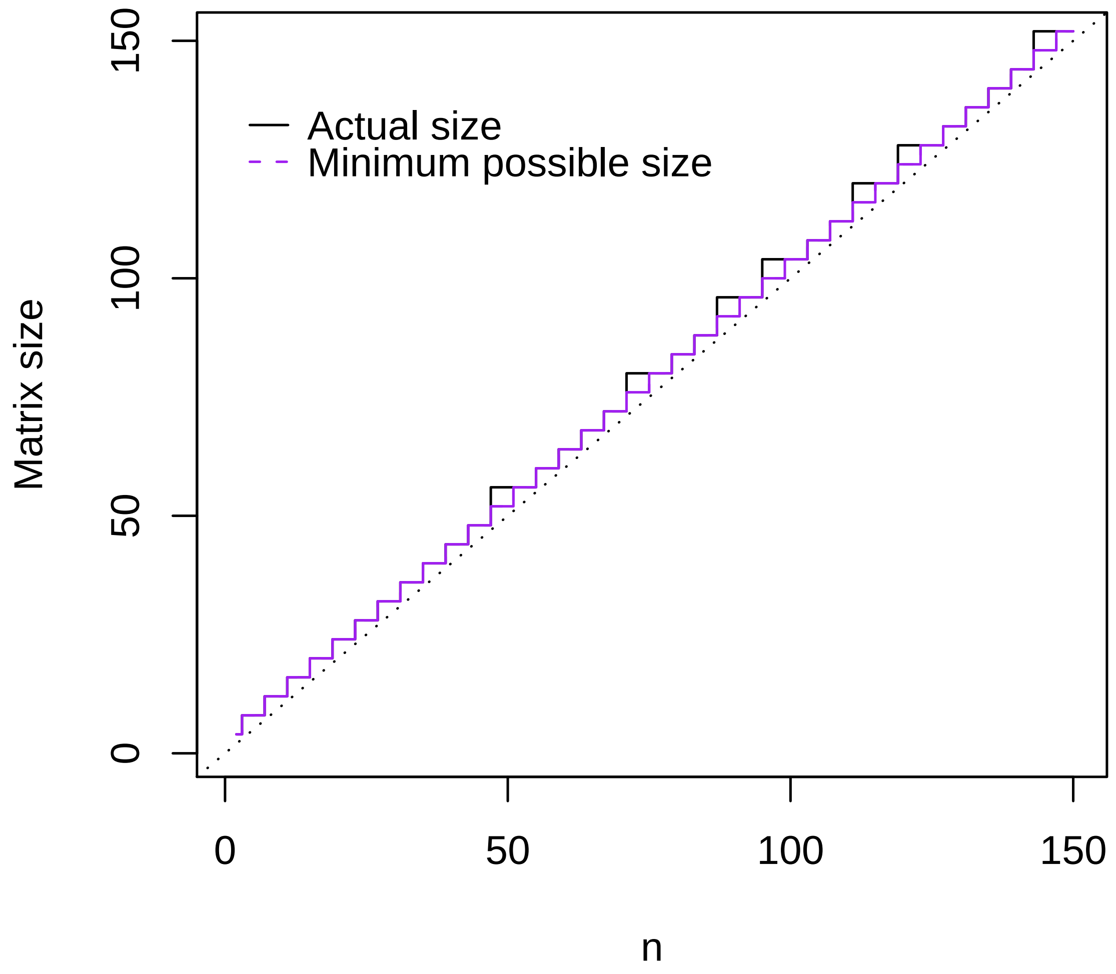
Plackett–Burman designs

BRR splits the same in halves so that all PSUs appear in 50% of the half-samples and all pairs of PSUs from different strata appear together in 25% of the half-samples. [full orthogonal balance, Plackett–Burman design, Hadamard matrix]

Under this condition the standard error of the population mean or total is the same as if all 2^{nstrata} half-samples were used.

The number of half-samples has to be a multiple of 4, greater than the number of strata. Constructing the half-samples is hard in general and trivial if the number is a power of 2. The survey package also knows how to generate sets of $2^k(p+1)$ half-samples where p is a prime and $p+1$ is a multiple of 4. This gets close to the minimum possible number of half-samples in most cases.

Plackett–Burman designs



Summary statistics

`svymean`, `svytotal`, `svyratio`, `svyvar`, `svyquantile`

All take a formula and design object as arguments, return an object with `coef`, `vcov`, `SE`, `cv` methods.

Mean and total on factor variables give tables of cell means/totals. Mean and total have `deff` argument for design effects and the return object has a `deff` method.

```
>       svymean(~api00, dclus1, deff=TRUE)
         mean       SE   DEff
api00 644.169  23.542 9.3459
>         svymean(~factor(stype),dclus1)
                   mean     SE
factor(stype)E 0.786885 0.0463
factor(stype)H 0.076503 0.0268
factor(stype)M 0.136612 0.0296
```

Summary statistics

```
>        svymean(~interaction(stype, comp.imp), dclus1)
                                             mean      SE
interaction(stype, comp.imp)E.No   0.174863 0.0260
interaction(stype, comp.imp)H.No   0.038251 0.0161
interaction(stype, comp.imp)M.No   0.060109 0.0246
interaction(stype, comp.imp)E.Yes 0.612022 0.0417
interaction(stype, comp.imp)H.Yes 0.038251 0.0161
interaction(stype, comp.imp)M.Yes 0.076503 0.0217
>        svyvar(~api00, dclus1)
      variance     SE
api00    11183 1386.4
>        svytotal(~enroll, dclus1, deff=TRUE)
         total       SE   DEff
enroll 3404940  932235 31.311
```

Summary statistics

```
> mns <- svymean(~api00+api99,dclus1)
> mns
        mean     SE
api00 644.17 23.542
api99 606.98 24.225
> coef(mns)
   api00    api99
644.1694 606.9781
> SE(mns)
   api00    api99
23.54224 24.22504
> vcov(mns)
         api00    api99
api00 554.2371 565.7856
api99 565.7856 586.8526
> cv(mns)
     api00      api99
0.03654666 0.03991090
```

Ratio estimators

Estimating the ratio of population means/totals: `svyratio` takes two formulas specifying numerator and denominator variables.

```
>         svyratio(~api.stu, ~enroll, dclus1)
Ratio estimator: svyratio.survey.design2(~api.stu, ~enroll, dclus1)
Ratios=
           enroll
api.stu 0.8497087
SEs=
             enroll
api.stu 0.008386297
```

Ratio estimators

Ratio estimation of population total uses `predict`

```
> sep<-svyratio(~api.stu,~enroll, dstrat,separate=TRUE)
> com<-svyratio(~api.stu, ~enroll, dstrat)
> stratum.totals<-list(E=1877350, H=1013824, M=920298)
> predict(sep, total=stratum.totals)
$total
         enroll
api.stu 3190022

$se
          enroll
api.stu 29756.44

>  predict(com, total=3811472)
$total
         enroll
api.stu 3190038

$se
          enroll
api.stu 29565.98
```

Some details

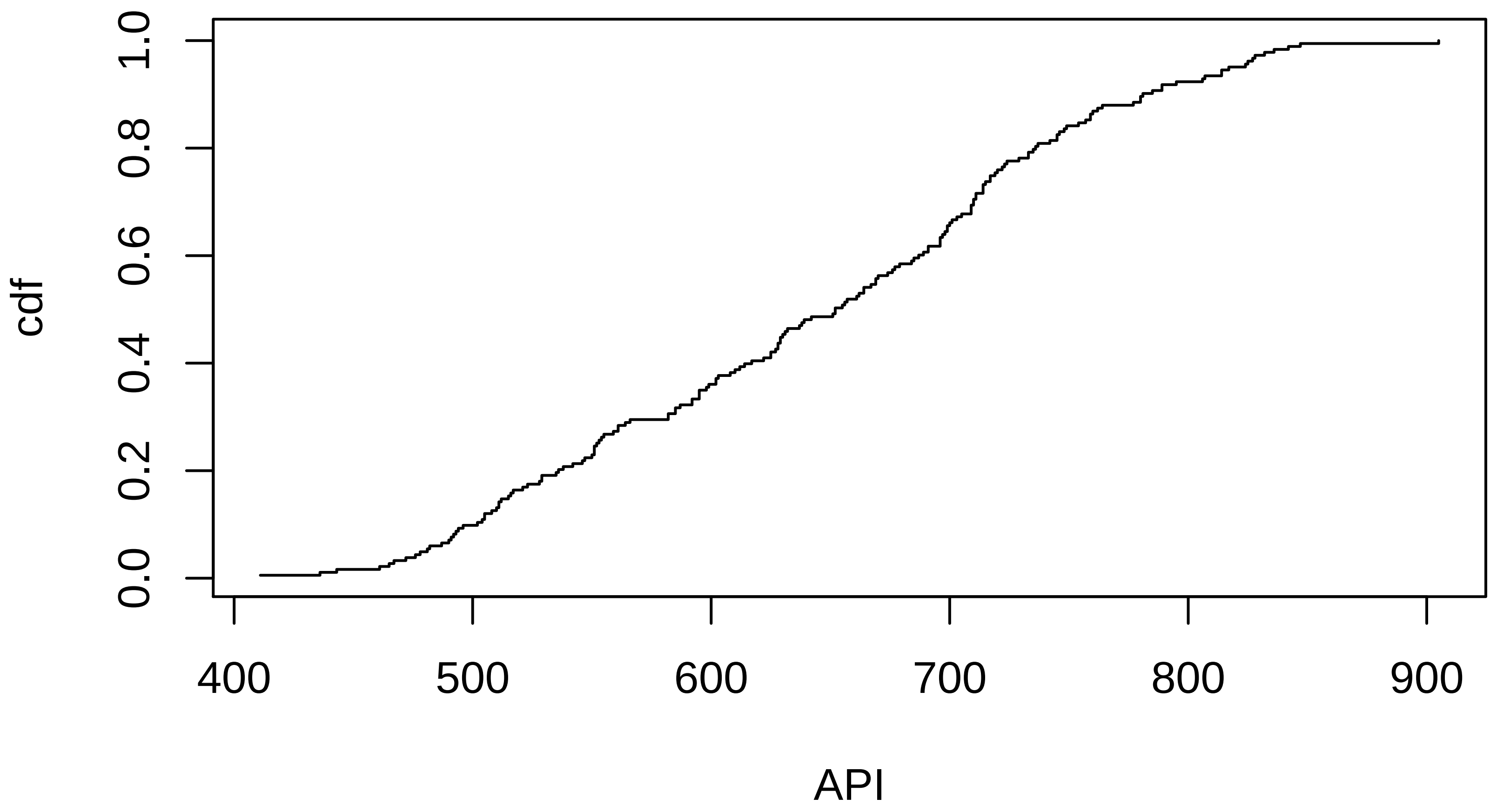
- `svyratio` uses the Taylor expansion std error, which has larger unconditional but small conditional bias than the main alternative.
- Design effects can be calculated compared to with-replacement (DEFT) or without-replacement (DEFF) designs, without-replacement is the default.

Quantiles

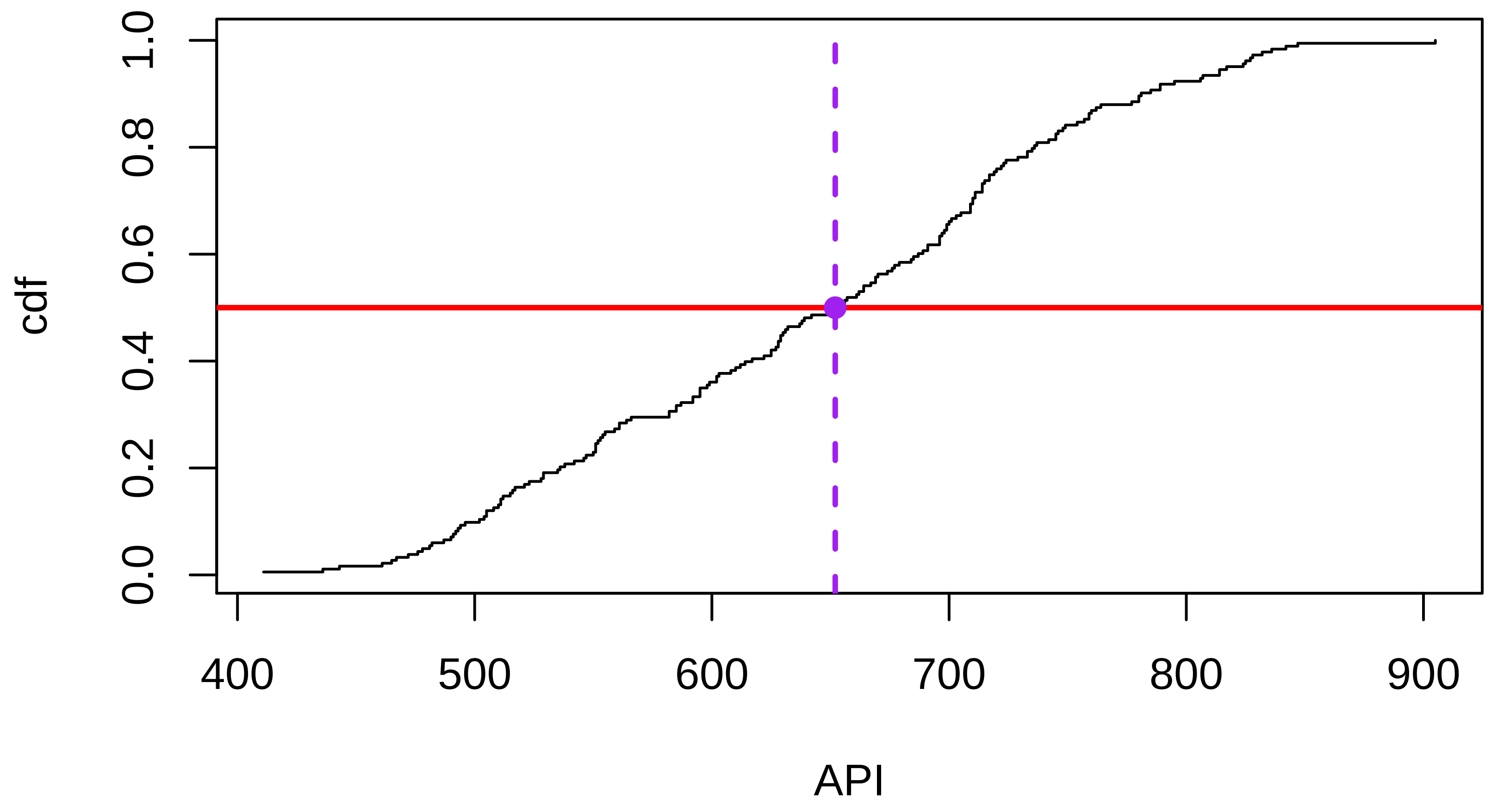
```
> library(survey)
> data(api)
> dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

> index<-order(apiclus1$api00)
> cdf<-cumsum(apiclus1$pw)/sum(apiclus1$pw)
> plot(apiclus1$api00[index], cdf,xlab="API", type="s")
> abline(h=0.5,col="red",lwd=2)
> points(652,0.5,pch=19,col="purple")
> abline(v=652,col="purple",lty=2,lwd=2)
```

Quantiles



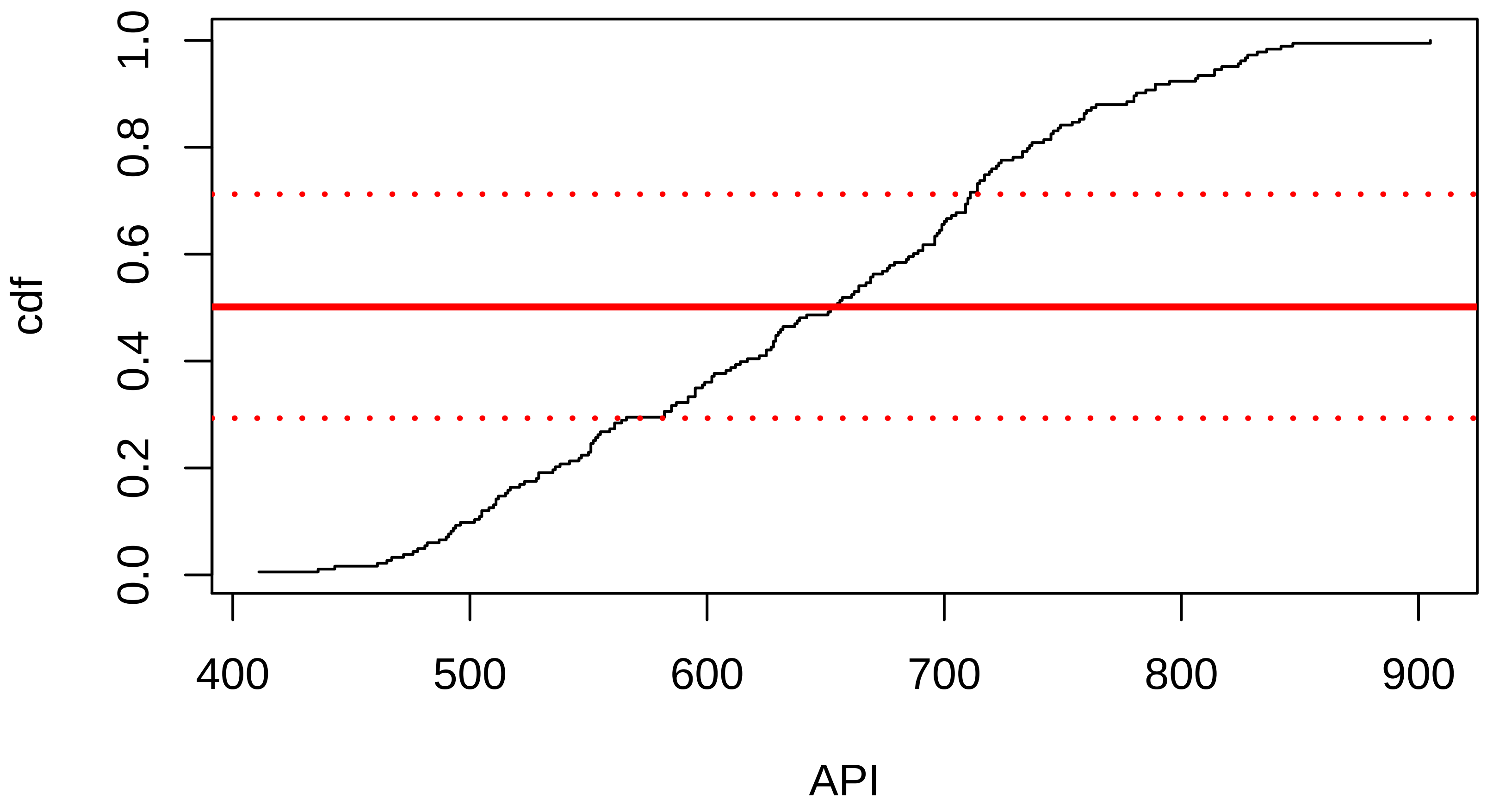
Quantiles



Quantiles

```
> svymean(~I(api00>652),dclus1)
                          mean     SE
I(api00 > 652)FALSE 0.50273 0.1069
I(api00 > 652)TRUE  0.49727 0.1069
> abline(h=0.50273,col="red",lwd=2)
> abline(h=0.50273-1.96*0.1069,col="red",lwd=2,lty=3)
> abline(h=0.50273+1.96*0.1069,col="red",lwd=2,lty=3)
```

Quantiles



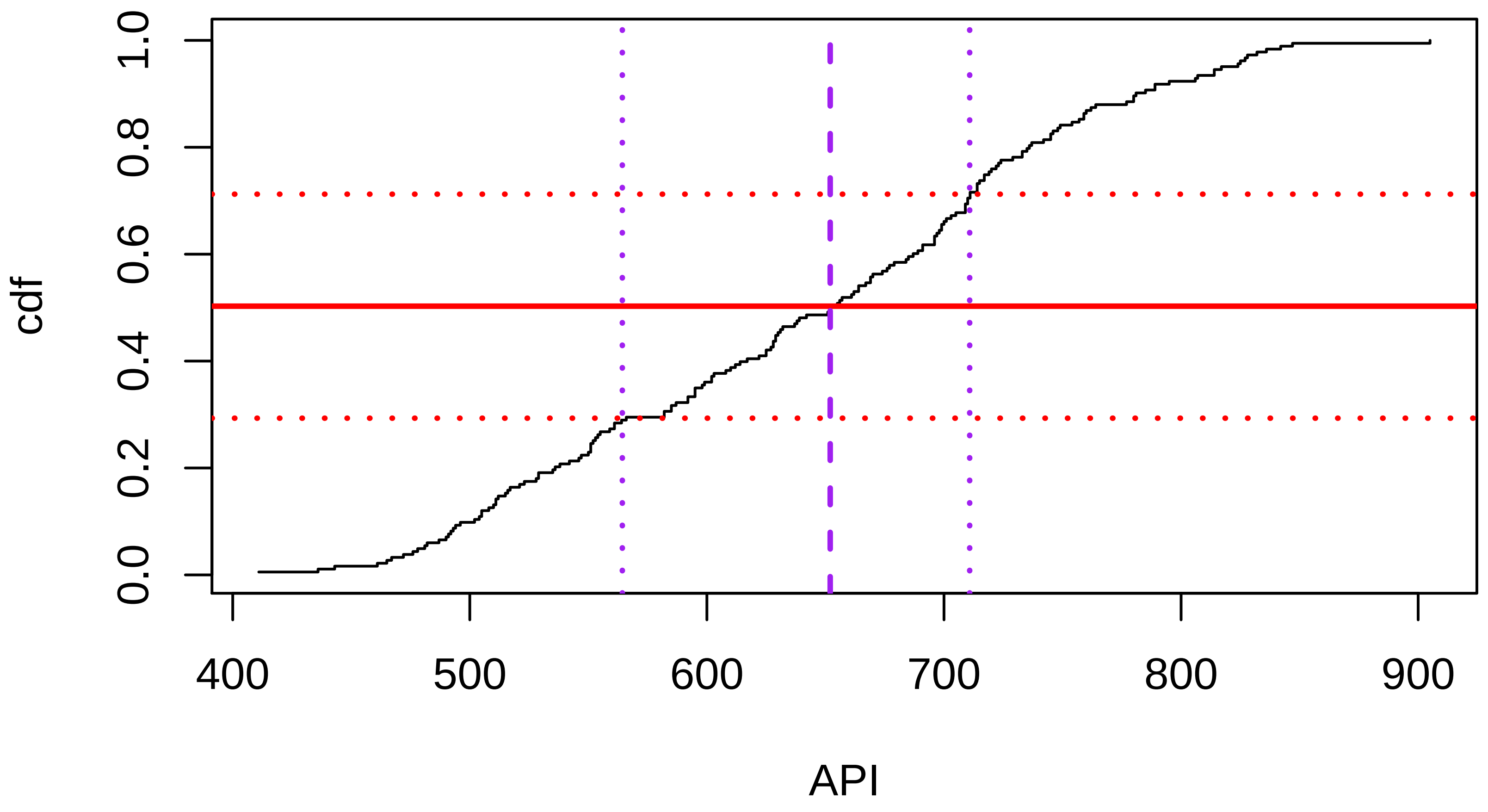
Quantiles

```
> abline(v=652,col="purple",lty=2,lwd=2)
> abline(v=564.325,col="purple",lty=3,lwd=2)
> abline(v=710.8375,col="purple",lty=3,lwd=2)
> svyquantile(~api00, dclus1, 0.5, ci = TRUE)
$quantiles
      0.5
api00 652

$CIs
, , api00

             0.5
(lower 564.3250
upper) 710.8375
```

Quantiles



Quantiles

This approach gives asymmetric confidence intervals. A proposed standard error estimator is the 95% confidence interval length divided by 2×1.96.

There is an option is to invert a score test (Francisco–Fuller) but this is slower and appears to be less accurate.

The same approach to confidence intervals in estimating function estimates has been promoted more recently by Kalbfleisch and colleagues — the idea is the the Normal approximation should work better on the estimating function scale since that is where the central limit theorem is applied.

This method works with replicate weight or design information and is the default in R.

Choice of quantile

With a reasonably complex design and a continuous variable it is very unlikely that the equation for the pth quantile

$$\sum_{i=1}^{n} \frac{1}{\pi_i} (\{x_i < q\} - p) = 0$$

will be exactly true, so we will always be in a setting analogous to estimating the median from a sample of even size.

Hyndman and Fan (1996, TAS) describe **9** definitions of the quantile (for iid data) involving different rules for interpolating the order statistics to the left and right of the quantile. If the left and right order statistics are the same the quantile is equal to them.

Choice of quantile

`svyquantile()` interpolates linearly between order statistics.

I think SUDAAN interpolates linearly between unique order statistics (ie does not distinguish between two observations with weight w and one with weight $2w$).

This appears to be done for convenience but would make sense if the measurements were from a continuous variable rounded to a small number of digits.

Domain estimation

The correct standard error estimate for a subpopulation that isn't a stratum is not just obtained by pretending that the subpopulation was a designed survey of its own.

However, the `subset` function and `"["` method for survey design objects handle all these details automagically, so you can ignore this problem.

The package test suite (`tests/domain.R`) verifies that subpopulation means agree with the ratio estimator and regression estimator derivations. Some more documentation is in the `domain` vignette.

Note: subsets of design objects are not necessary smaller than the whole objects.

Pretty tables

Two main types:

- totals or proportions cross-classified by multiple factors
- arbitrary statistics in subgroups

Computing over subgroups

`svyby` computes a statistic for subgroups specified by a set of factor variables:

```
>     svyby(~api99, ~stype, dclus1, svymean)
  stype statistics.api99 se.api99
E     E         607.7917 22.81660
H     H         595.7143 41.76400
M     M         608.6000 32.56064
```

`~api99` is the variable to be analysed, `~stype` is the subgroup variable, `dclus1` is the design object, `svymean` is the statistic to compute.

Lots of options for eg what variance summaries to present (mostly requests from `ine.pt`).

Computing over subgroups

```
> svyby(~api99, ~stype, dclus1, svyquantile, quantiles=0.5,ci=TRUE)
  stype statistics.quantiles     statistics.CIs        se      var
E     E                  615 525.6174, 674.1479 37.89113 1435.738
H     H                  593 428.4810, 701.0065 69.52309  4833.46
M     M                  611 527.5797, 675.2395 37.66903 1418.955
M     M       611
>  svyby(~api99, list(school.type=apiclus1$stype), dclus1, svymean)
  school.type statistics.api99 se.api99
E           E         607.7917 22.81660
H           H         595.7143 41.76400
M           M         608.6000 32.56064
> svyby(~api99+api00, ~stype, dclus1, svymean, deff=TRUE)
  stype statistics.api99 statistics.api00 se.api99 se.api00 DEff.api99
E     E         607.7917         648.8681 22.81660 22.36241   5.895734
H     H         595.7143         618.5714 41.76400 38.02025   2.211866
M     M         608.6000         631.4400 32.56064 31.60947   2.226990
  DEff.api00
E   6.583674
H   2.228259
M   2.163900
```

Computing over subgroups

```
>  svyby(~api99+api00, ~stype+sch.wide, dclus1, svymean, keep.var=FALSE)
      stype sch.wide statistic.api99 statistic.api00
E.No      E       No        601.6667        596.3333
H.No      H       No        662.0000        659.3333
M.No      M       No        611.3750        606.3750
E.Yes     E      Yes        608.3485        653.6439
H.Yes     H      Yes        577.6364        607.4545
M.Yes     M      Yes        607.2941        643.2353
```

Computing over subgroups

```
>  (a<-svyby(~enroll, ~stype, rclus1, svytotal, deff=TRUE,
      vartype=c("se","cv","cvpct","var")))
  stype statistics.enroll       se cv.enroll cv%.enroll          var       DEff
E     E         2109717.1 631349.4 0.2992578   29.92578 398602047550 125.039075
H     H          535594.9 226716.6 0.4232987   42.32987  51400414315   4.645816
M     M          759628.1 213635.5 0.2812369   28.12369  45640120138  13.014932
> deff(a)
[1] 125.039075   4.645816  13.014932
> SE(a)
[1] 631349.4 226716.6 213635.5
> cv(a)
[1] 0.2992578 0.4232987 0.2812369
> coef(a)
[1] 2109717.1  535594.9  759628.1
>   svyby(~api00,~comp.imp+sch.wide,design=dclus1,svymean,
             drop.empty.groups=FALSE)
        comp.imp sch.wide statistics.api00 se.api00
No.No         No       No         608.0435 28.98769
Yes.No       Yes       No               NA       NA
No.Yes        No      Yes         654.0741 32.66871
Yes.Yes      Yes      Yes         648.4060 22.47502
```

Functions of estimates

`svycontrast` computes linear and nonlinear combinations of estimated statistics (in the same object).

```
> a <- svytotal(~api00 + enroll + api99, dclus1)
> svycontrast(a, list(avg = c(0.5, 0, 0.5), diff = c(1,
    0, -1)))
     contrast     SE
avg   3874804 873276
diff   230363  54921

> svycontrast(a, list(avg = c(api00 = 0.5, api99 = 0.5),
    diff = c(api00 = 1, api99 = -1)))
     contrast     SE
avg   3874804 873276
diff   230363  54921
```

Functions of estimates

```
> svycontrast(a, quote(api00/api99))
          nlcon     SE
contrast 1.0613 0.0062

> svyratio(~api00, ~api99, dclus1)
Ratio estimator: svyratio.survey.design2(~api00, ~api99, dclus1)
Ratios=
         api99
api00 1.061273
SEs=
            api99
api00 0.006230831
```

Functions of estimates

Contrasts of arbitrary statistics across subgroups after `svyby` are supported with replicate weights. Here we compare proportion of hypertension treated by insurance status from CHIS

```
> a<-svyby(~I(AB30==1),~INS, denominator=~I(AB29==1),
    design=rchis,svyratio, covmat=TRUE)
> a
  INS statistics          se
1   1  0.7124663 0.006109845
2   2  0.3548040 0.022022222
> svycontrast(a, quote(`1`-`2`))
           nlcon     SE
contrast 0.35766 0.0235
```

Contrasts of means across subgroups can always be computed by regression.

Domain and ratio estimators

Ratio estimators of domain means agree with the result from subsetting the design object:

```
> dstrat<-update(dstrat,imp=as.numeric(comp.imp=="Yes"))
> svyratio(~I(api.stu*imp),~imp,dstrat)
Ratio estimator: svyratio.survey.design2(~I(api.stu * imp), ~imp, dstrat)
Ratios=
                      imp
I(api.stu * imp) 439.9305
SEs=
                      imp
I(api.stu * imp) 19.24367
> svymean(~api.stu, subset(dstrat, comp.imp=="Yes"))
          mean     SE
api.stu 439.93 19.244
```

Formatting

svyby or svymean and svytotal with interaction will produce the numbers, but the formatting is not pretty.

ftable provides formatting:

```
>  d<-svyby(~api99 + api00, ~stype + sch.wide, rclus1, svymean, keep.var=TRUE,
+        vartype=c("se","cvpct"))
>  round(ftable(d),1)
      sch.wide                No                                Yes
            statistics.api99 statistics.api00 statistics.api99 statistics.api00
stype
E     svymean          601.7            596.3            608.3            653.6
      SE                70.0             64.5             23.7             22.4
      cv%               11.6             10.8              3.9              3.4
H     svymean          662.0            659.3            577.6            607.5
      SE                40.9             37.8             57.4             54.0
      cv%                6.2              5.7              9.9              8.9
M     svymean          611.4            606.4            607.3            643.2
      SE                48.2             48.3             49.5             49.3
      cv%                7.9              8.0              8.2              7.7
```

Formatting

svyby knows enough to structure the table without help. For other analyses more information is needed

```
>  a <- svymean(~interaction(stype,comp.imp), design=dclus1, deff=TRUE)
>  b <- ftable(a, rownames=list(stype=c("E","H","M"),comp.imp=c("No","Yes")))
>  round(100*b,1)
              stype     E     H     M
comp.imp
No         mean      17.5   3.8   6.0
           SE         2.6   1.6   2.5
           Deff      87.8 131.7 200.4
Yes        mean      61.2   3.8   7.7
           SE         4.2   1.6   2.2
           Deff     137.2 131.4 124.7
```

Tests for two-way tables

`svychisq` does four variations on the Pearson χ^2 test

- First- and second-order Rao–Scott corrections: first order (`statistic="Chisq"`) corrects the mean of Pearson's X^2, second order (`statistic="F"`) corrects the variance as well.

- Wald-type tests that all the interaction parameters in a saturated log-linear model are zero. Original Koch et al proposal is `statistic="Wald"`, modified version for small numbers of PSUs is `statistic="adjWald"`.

Also works with replicate weights, where $n_{PSU} - n_{strata}$ is replaced by the rank of the matrix of weights minus 1.

Tests for two-way tables

```
> svychisq(~stype+sch.wide,dclus1)

        Pearson's X^2: Rao & Scott adjustment

data:  svychisq(~stype + sch.wide, dclus1)
F = 5.1934, ndf = 1.495, ddf = 20.925, p-value = 0.02175

> svychisq(~stype+sch.wide,dclus1,statistic="adjWald")

        Design-based Wald test of association

data:  svychisq(~stype + sch.wide, dclus1, statistic = "adjWald")
F = 2.2296, ndf = 2, ddf = 13, p-value = 0.1471
```

Tests for two-way tables

The actual asymptotic distribution is a linear combination of χ^2_1 variables, which is not hard to compute by numerical inversion of the characteristic function.

I plan to add this for two-way tables, but more importantly for tests i regression models based on population estimated deviance.

Graphics

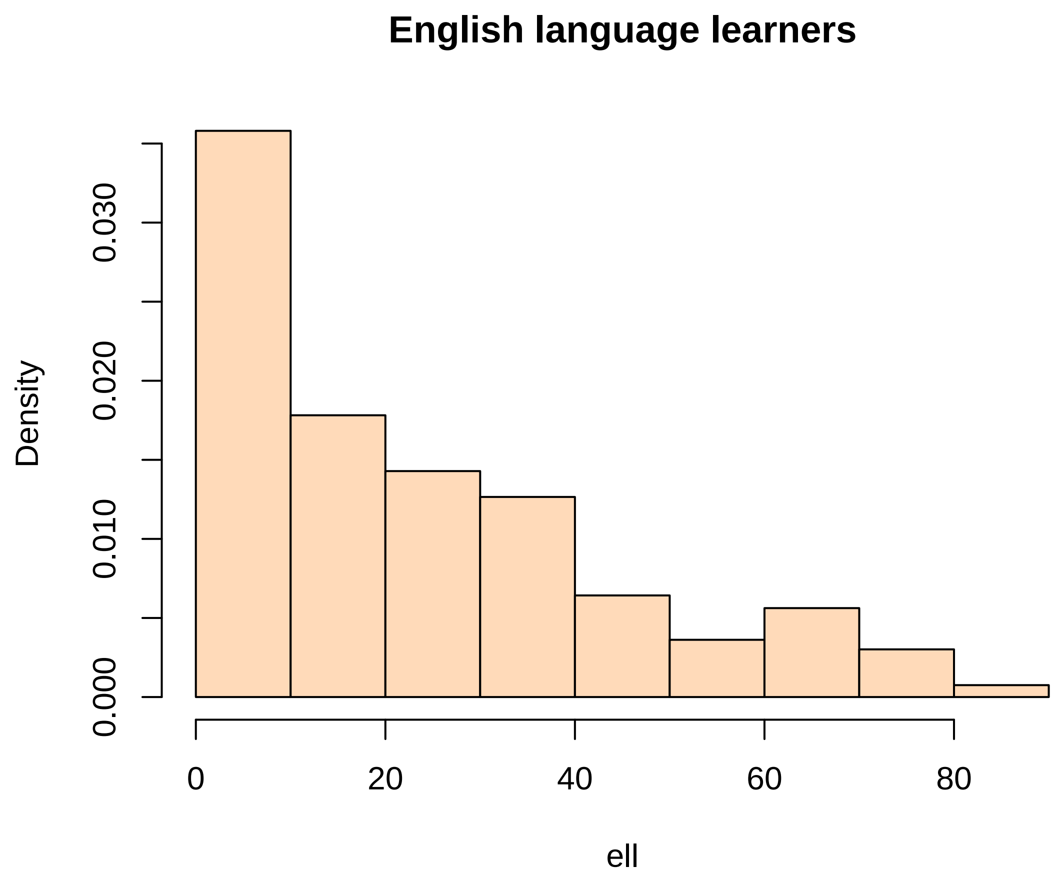
Two difficulties in graphics: large sample size, sampling weights.

- ‘Bubble’ plots with circle area proportional to weight
- histograms, boxplots, smoothers using sample weights
- Hexagonal binning plots, estimating population number over areas of plot

`svyhist` and `svyboxplot` do histograms and boxplots, `svyplot()` does scatterplots, `svysmooth()` does kernel smoothing.

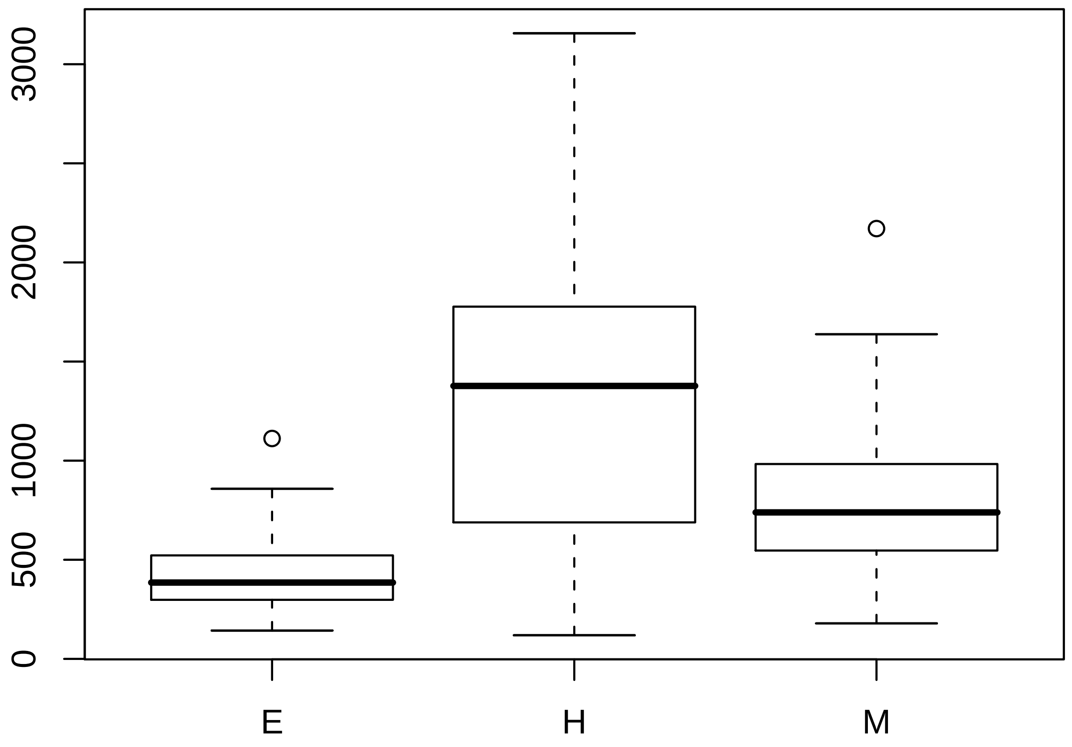
Graphics

```
svyhist(~ell, dstrat, main = "English language learners",
        col = "peachpuff")
```



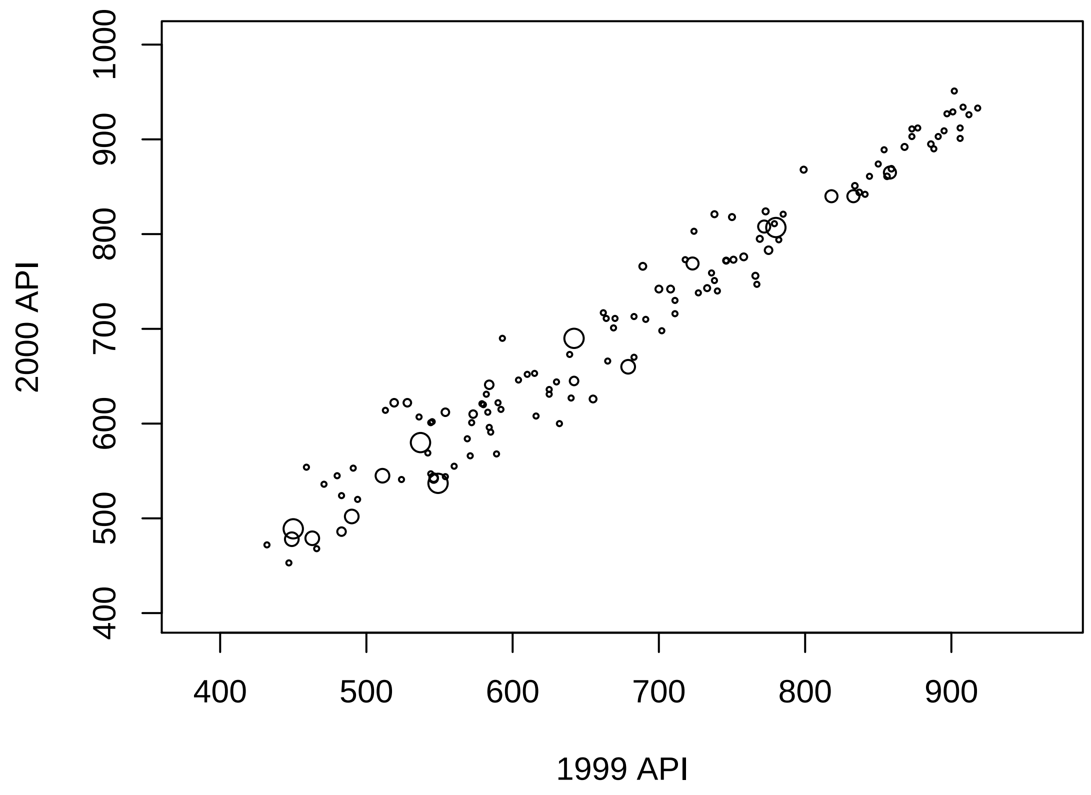
Graphics

```
svyboxplot(enroll ~ stype, dstrat)
```



Graphics

```
svyplot(api00~api99, design=dclus2, style="bubble",
         xlab="1999 API",ylab="2000 API")
```



Synthetic data

A related approach is to estimate the joint empirical distribution that is being graphed and take a simple random sample with replacement from it.

Jittering the data may then be necessary (eg for scatterplots), since it is very likely that multiple copies of the same point will be included.

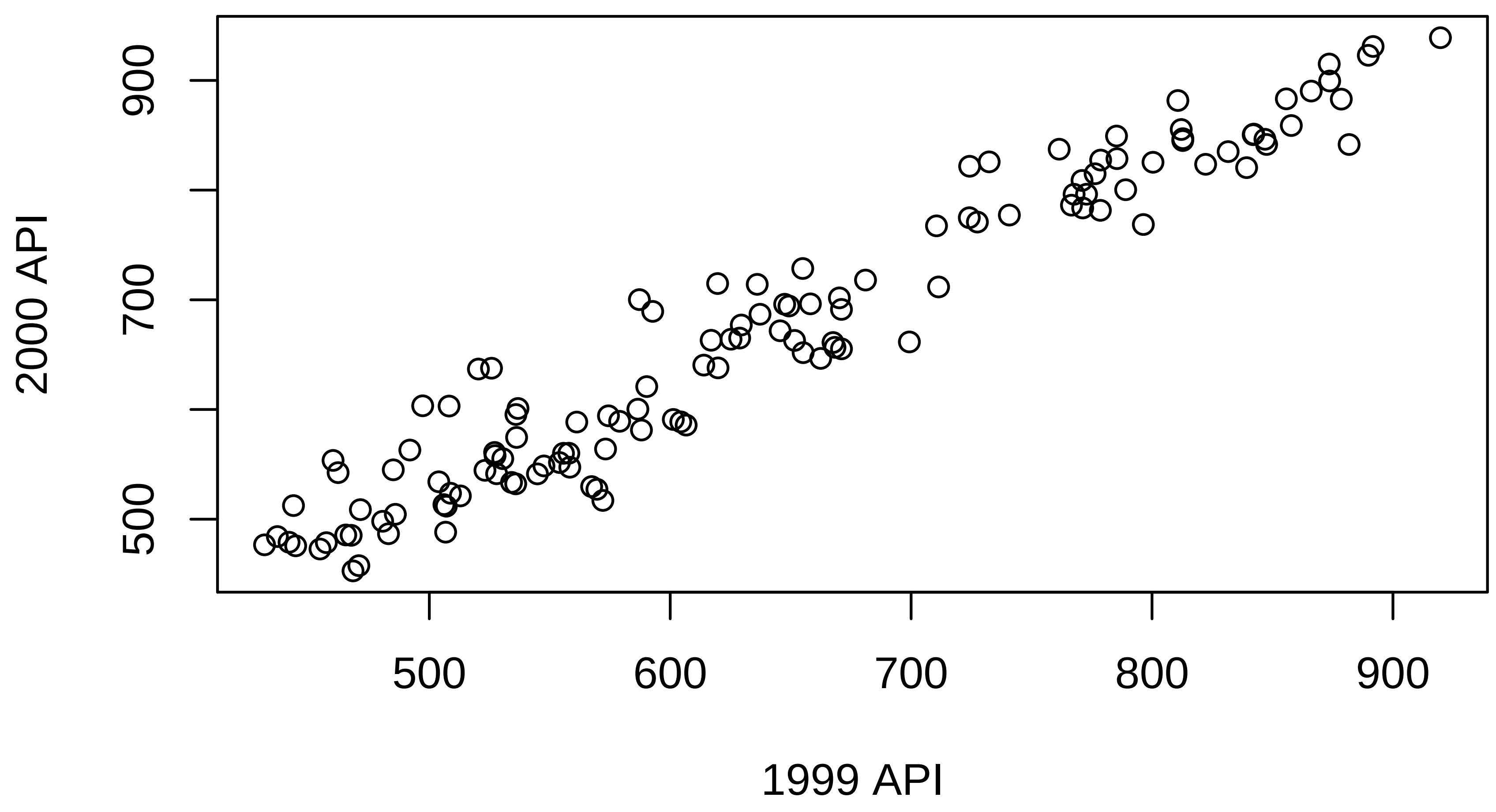
The graph may look different for different random samples and will look different depending on jittering, so it may be necesssary to do several plots and look for consistent features

Synthetic data

In the example, the jittering was $U(0, 25)$ noise: 25 is approximately the median absolute deviation of the change from 1999 to 2000 and so is a reasonable "measurement error" variability.

A more sophisticated approach would distinguish between two observations with weight w and one observation with weight $2w$ when jittering, to preserve any true discreteness in the data (eg digit preference in blood pressures).

Synthetic data



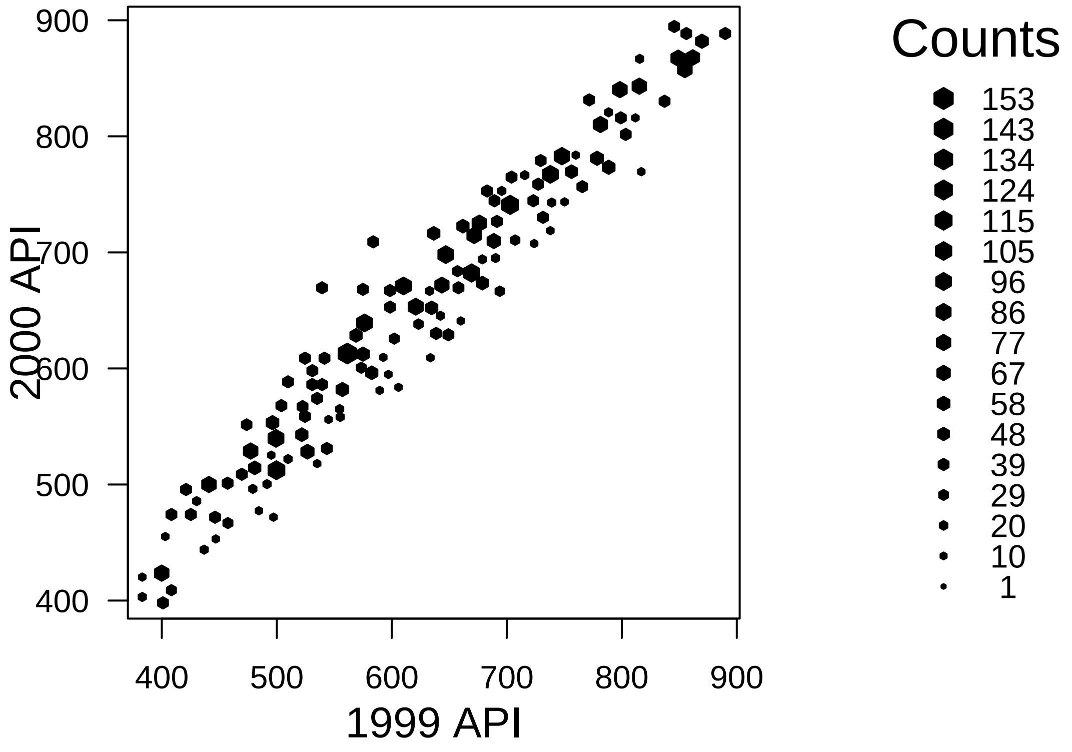
Hexagonal binning

To handle large SRS data sets, divide plot region into hexagons and count points in each hex.

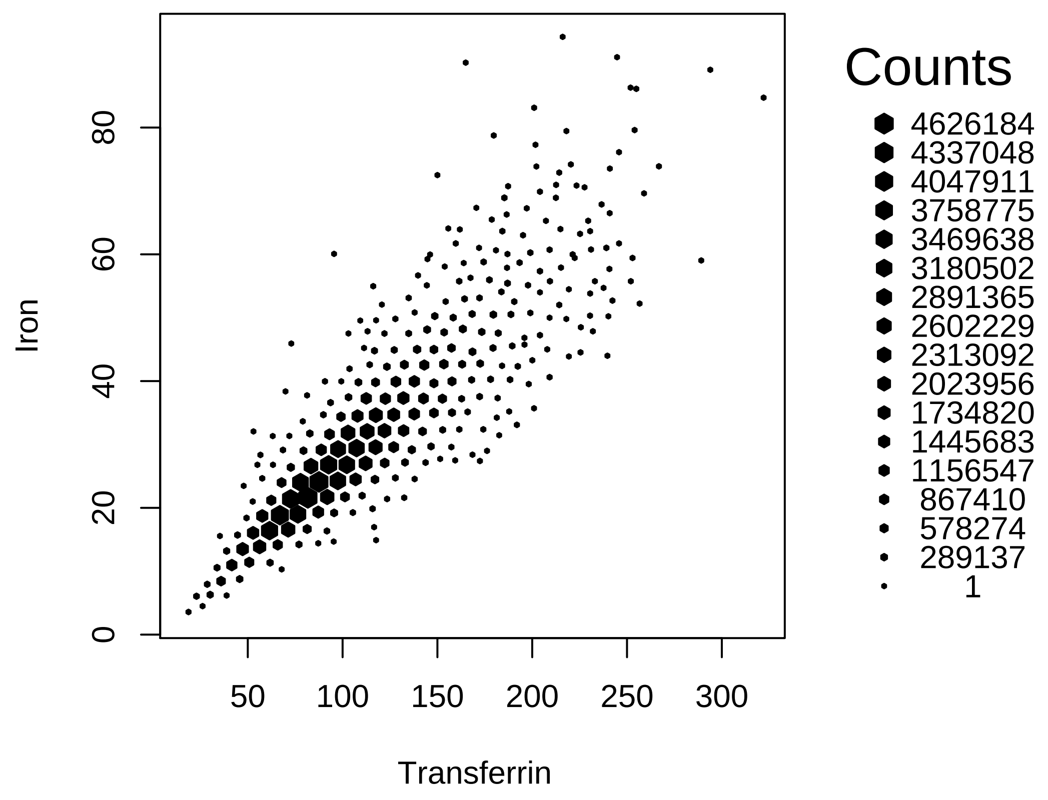
Generalizes to complex samples by estimating population total in each hex.

Hexagonal binning

```
svyplot(api00~api99, design=dstrat, style="hex",
   xlab="1999 API",ylab="2000 API")
```



Hexagonal binning



Smoothing

Extending smoothing methods to survey data is typically straightforward (unless you need standard errors)

R implements a local linear smoother with Gaussian kernel weights, based on Matt Wand's `KernSmooth` package

That is, the estimated mean of Y at $x = x_0$ is obtained by fitting a straight line to the data, with weights proportional to

$$w_i = \frac{1}{\pi_i}\phi((x_i = x_0)/h)$$

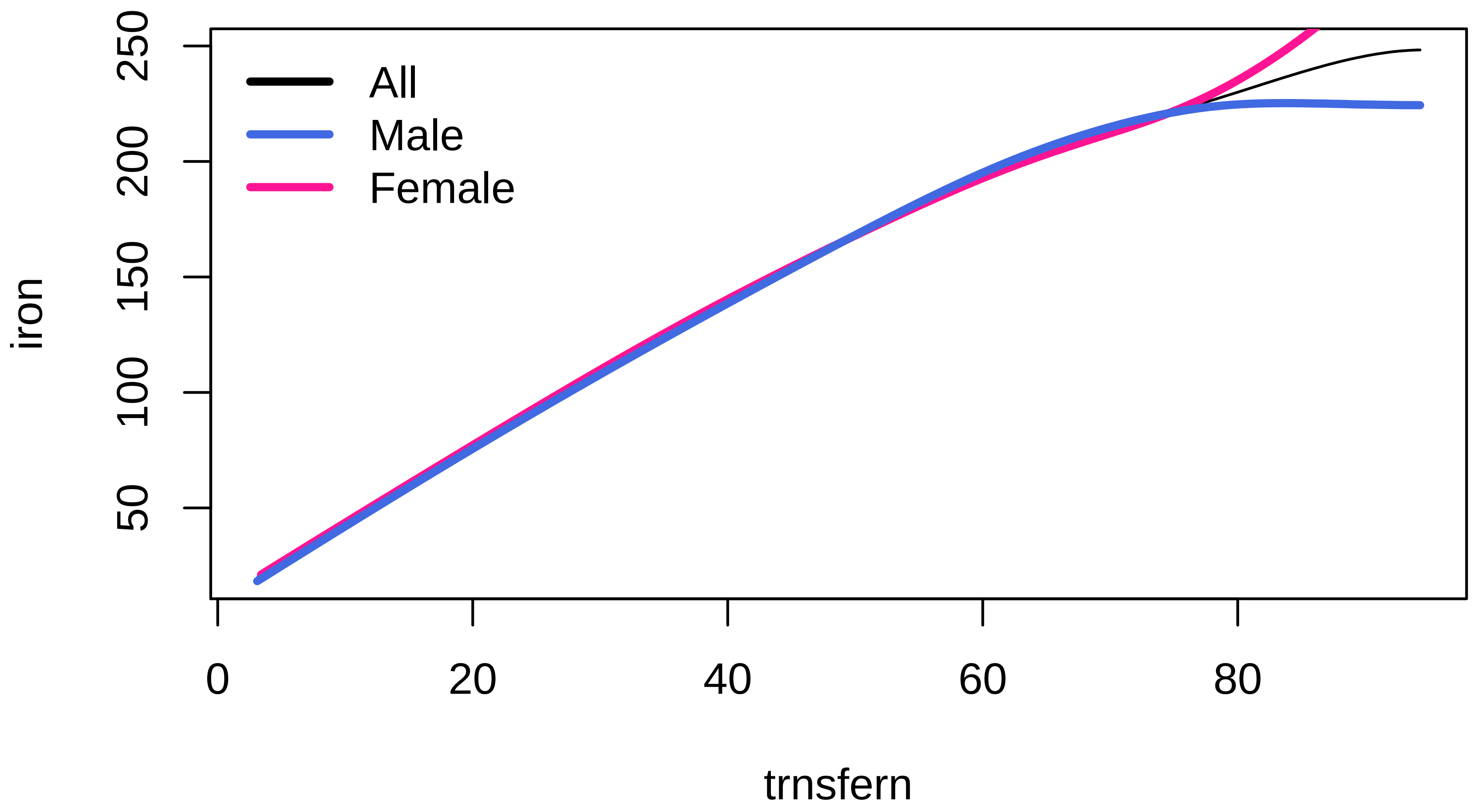
where h is the smoothing bandwidth.

This takes n^2 computations for n points so the code actually lays down a discrete grid, assigns each point pro rata to the nearest two grid points, and fits with these grid points rather than x_i and y_i.

Smoothing

```
pdf("~/TEACHING/survey/iron-smooth.pdf",height=4,width=6)
plot(svysmooth(iron~trnsfern,design=dhanes,bandwidth=10))
lines(svysmooth(iron~trnsfern,design=subset(dhanes,sex=="Female"),
      bandwidth=10),col="deeppink",lwd=3)
lines(svysmooth(iron~trnsfern,design=subset(dhanes,sex=="Male"),
      bandwidth=10),col="royalblue",lwd=3)
legend("topleft",lwd=3,col=c("black","royalblue","deeppink"),
       legend=c("All","Male","Female"),bty="n")
dev.off()
```

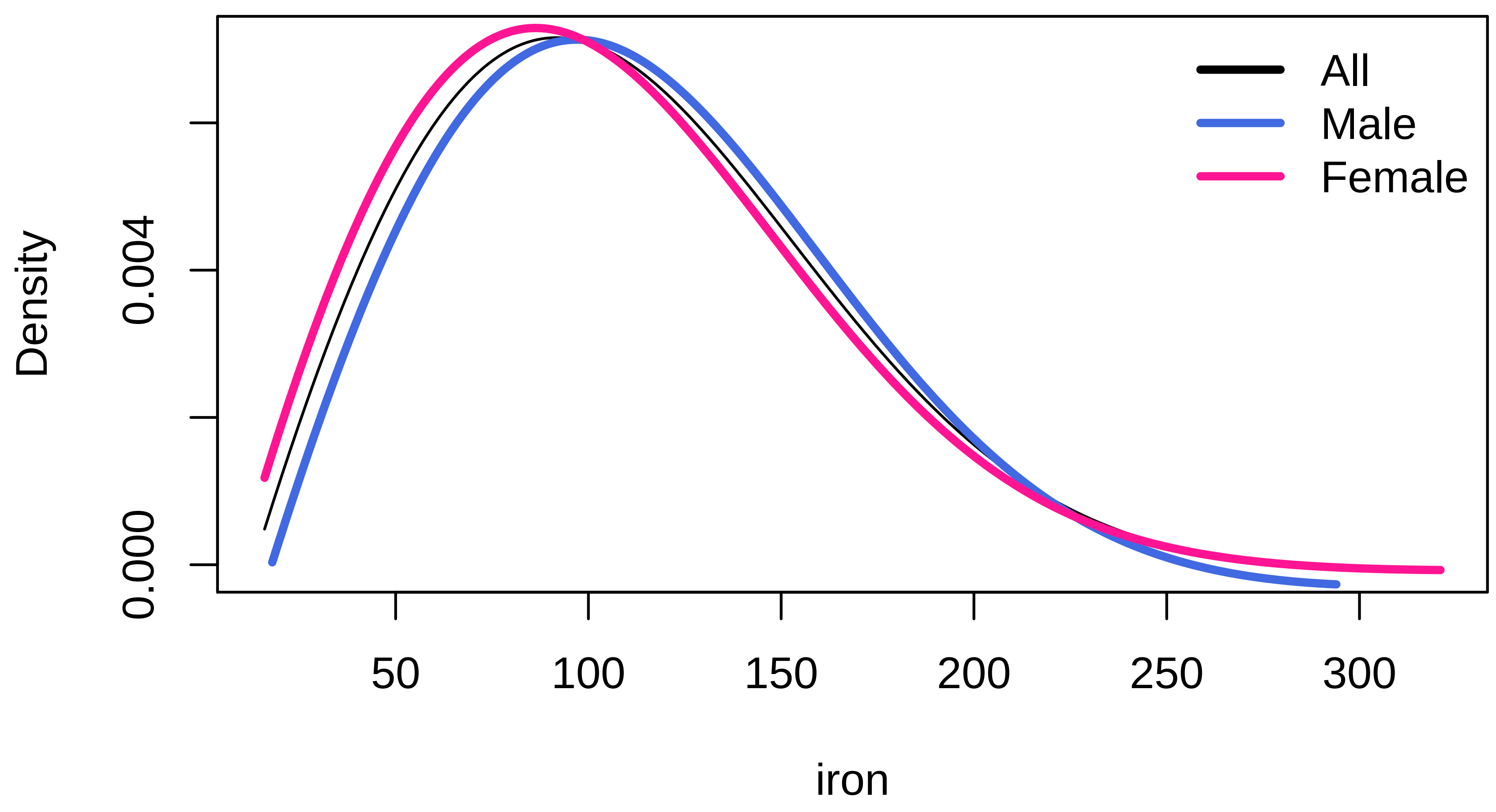
Smoothing



Smoothing

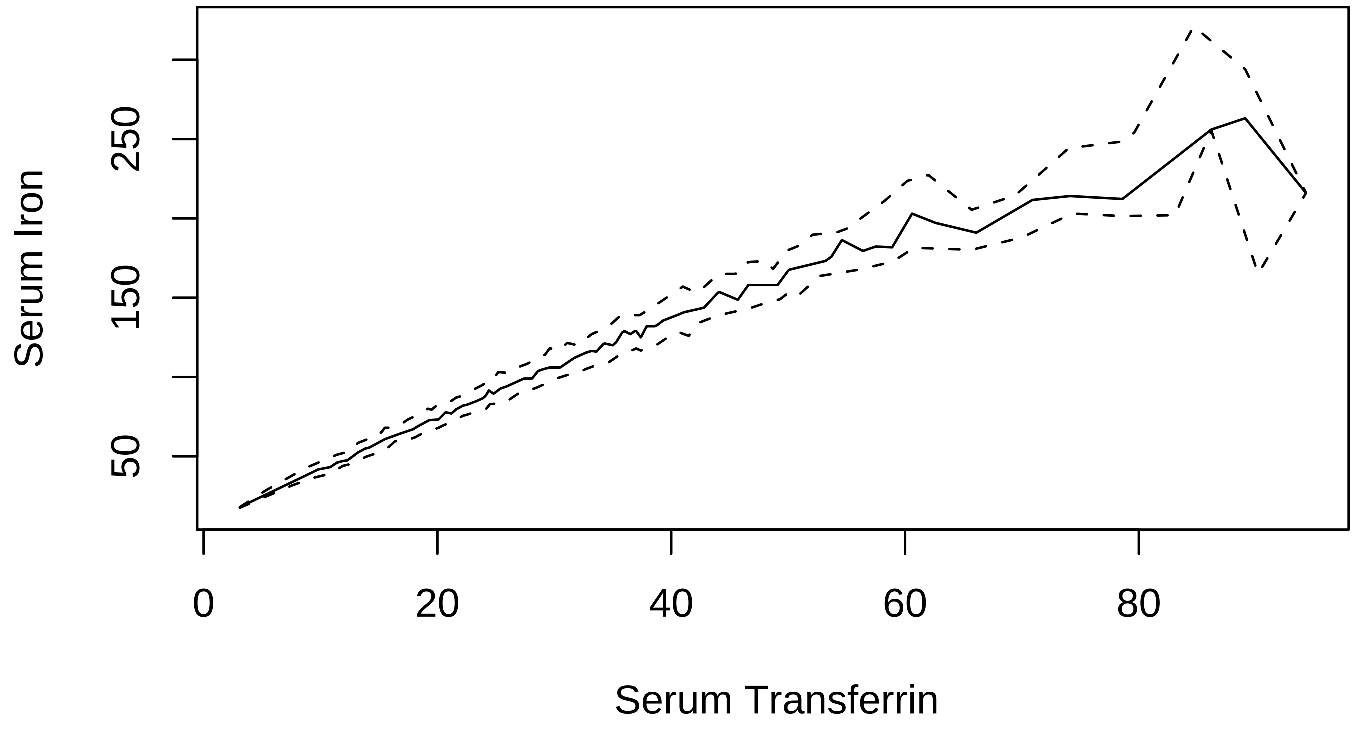
```
plot(svysmooth(~iron,design=dhanes,bandwidth=50))
lines(svysmooth(~iron,design=subset(dhanes,sex=="Male"),
      bandwidth=50),lwd=3,col="royalblue")
lines(svysmooth(~iron,design=subset(dhanes,sex=="Female"),
      bandwidth=50),lwd=3,col="deeppink")
legend("topright",lwd=3,col=c("black","royalblue","deeppink"),
      legend=c("All","Male","Female"),bty="n")
```

Smoothing



Regression quantiles

Other smoothing methods that allow weights can also be used, eg regression quantiles based on splines (quantreg package).



Regression models

- `svyglm` for linear and generalized linear models

- `svycoxph` for Cox model (no std errors on survival curves yet)

Some other models, eg censored parametric regression models, could be fitted with `svymle` (`svydesign` objects only) or `withReplicates` (replicate weight designs only).

Regression and domain estimators

Academic Performance Index in schools with more or less than 20% "English language learners"

```
> svyby(~api00,~I(ell>20), dclus1,svymean)
      I(ell > 20) statistics.api00 se.api00
FALSE       FALSE         717.9661 15.53905
TRUE         TRUE         609.0565 25.55300

> summary(svyglm(api00~I(ell>20), dclus1))
Call:
svyglm(api00 ~ I(ell > 20), dclus1)

Survey design:
svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)       717.97      15.54   46.20 8.33e-16 ***
I(ell > 20)TRUE  -108.91      19.48   -5.59 8.78e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 8577.366)
```

Regression and domain estimators

```
> summary(svyglm(api00~I(ell>20)+0, dclus1))

Call:
svyglm(api00 ~ I(ell > 20) + 0, dclus1)

Survey design:
svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
I(ell > 20)FALSE   717.97      15.54   46.20 8.33e-16 ***
I(ell > 20)TRUE    609.06      25.55   23.84 4.11e-12 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 8577.366)

Number of Fisher Scoring iterations: 2
```

Logistic regression

Do school type and socioeconomic variables predict attaining school-wide performance target?

```
> summary(svyglm(sch.wide~stype+ell+mobility,dclus1,
      family=quasibinomial))

Call:
svyglm(sch.wide ~ stype + ell + mobility, dclus1,
      family = quasibinomial)

Survey design:
svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.057e+00  4.064e-01   5.062 0.000491 ***
stypeH      -9.291e-01  6.886e-01  -1.349 0.207026
stypeM      -1.571e+00  6.167e-01  -2.547 0.029009 *
ell          1.209e-02  1.111e-02   1.089 0.301698
mobility    -8.177e-05  1.673e-02  -0.005 0.996195
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Tests

Likelihood ratio tests are not available, so multi-coefficient tests have to use the Wald method. `regTermTest()` packages this.

```
> model <- svyglm(sch.wide~stype+ell+mobility,dclus1, family=quasibinomial)

> regTermTest(model, ~stype)
Wald test for stype
 in svyglm(sch.wide ~ stype + ell + mobility, dclus1, family = quasibinomial)
Chisq =  6.638399  on  2  df: p= 0.036182

> regTermTest(model, ~ell+mobility)
Wald test for ell mobility
 in svyglm(sch.wide ~ stype + ell + mobility, dclus1, family = quasibinomial)
Chisq =  1.329623  on  2  df: p= 0.51437
```

Cox model

The Cox proportional hazards model is the most popular model for time-to-event in biostatistics. Here we use a two-phase design in sampling from a cohort that is in turn a simple random sample from a large population.

Event is relapse in Wilm's Tumour: `edrel` is observation time, `rel` is relapse indicator

`age` is known for everyone, but `histol` is determined from stored samples for everyone who relapses and a stratified random sample of others. [Case–cohort design]

We use `twophase()` to specify the two-phase study design: like `svydesign()` but two of everything.

Cox model

```
> library("survival")
Loading required package: splines
> data(nwtco)
> dcchs<-twophase(id=list(~seqno,~seqno), strata=list(NULL,~rel),
+              subset=~I(in.subcohort | rel), data=nwtco)
> svycoxph(Surv(edrel,rel)~factor(stage)+factor(histol)+I(age/12), design=dcchs)
Call:
svycoxph.survey.design(formula = Surv(edrel, rel) ~ factor(stage) +
    factor(histol) + I(age/12), design = dcchs)

                  coef exp(coef) se(coef)     z       p
factor(stage)2  0.6927      2.00    0.163  4.25 2.1e-05
factor(stage)3  0.6269      1.87    0.168  3.73 1.9e-04
factor(stage)4  1.2995      3.67    0.189  6.88 6.1e-12
factor(histol)2 1.4583      4.30    0.145 10.02 0.0e+00
I(age/12)       0.0461      1.05    0.023  2.00 4.5e-02
```

Two-phase designs

The `twophase()` function constructs two-phase design objects. Two-phase designs are currently limited to two cases:

- Simple or stratified sampling of individuals at both phases
- Cluster sampling at phase 1 with every cluster represented at phase 2.

The biostatistics applications are typically simple random sampling at phase 1 with stratification at phase 2.

Allowing arbitrary multiphase designs would still be nice and is a major reason for investigating sparse-matrix representations.

Calibration

Calibration adjusts the survey weights so that the estimated population total for a variable exactly matches the known true value.

The class of calibration estimators is the same as the Robins, Rotnitzky & Zhao (1994) incomplete data estimators for the nonparametric model, and so contains the efficient nonparametric estimator.

Simplest version is post-stratification: adjust the weights so that a categorical variable matches the population counts. Recovers most of the information lost by not stratifying the sampling.

`postStratify` takes a design, a formula, and a data frame or table giving population totals.

Post-stratification

```
> svymean(~api00, dclus1)
        mean     SE
api00 644.17 26.329
> svytotal(~enroll, dclus1)
          mean     SE
enroll 3404940 932235
>
>       pop.types <- data.frame(stype=c("E","H","M"), Freq=c(4421,755,1018))
>     rclus1p<-postStratify(rclus1, ~stype, pop.types)
>       summary(rclus1p)
Call: postStratify(rclus1, ~stype, pop.types)
Unstratified cluster jacknife (JK1) with 15 replicates.
Variables:
 [1] "cds"        "stype"      "name"       "sname"      "snum"       "dname"
 [7] "dnum"       "cname"      "cnum"       "flag"       "pcttest"    "api00"
...
```

Post-stratification

```
>      svymean(~api00, rclus1p)
        mean    SE
api00 642.31 26.45
>      svytotal(~enroll, rclus1p)
          mean     SE
enroll 3680893 346014
> svytotal(~stype,rclus1p)
       mean        SE
stypeE 4421 4.685e-12
stypeH  755 1.719e-13
stypeM 1018 2.877e-13
```

Raking

With population totals for two categorical variables but not the joint distribution, alternately post-stratify on each one until convergence — raking.

`rake` takes a design, a list of formulas, and a list of data frames or tables giving population totals.

```
> pop.types <- data.frame(stype=c("E","H","M"), Freq=c(4421,755,1018))
> pop.schwide <- data.frame(sch.wide=c("No","Yes"), Freq=c(1072,5122))
> dclus1r<-rake(dclus1, list(~stype,~sch.wide), list(pop.types, pop.schwide))
>
> svymean(~api00, dclus1r)
        mean     SE
api00 641.23 23.739
> svytotal(~enroll, dclus1r)
         total     SE
enroll 3647300 399094
```

Calibration

Regression calibration adjusts weights to match the totals of multiple variables by least squares

Generalized raking extends to iterative least squares adjustment, including raking as a special case.

All done by `calibrate()`

`calibrate()`

- `design` to be calibrated
- `formula` specifying calibration variables
- `population` vector specifying totals (as column totals of design matrix generated by `formula`)
- `aggregate.stage` optional level of sampling where weights must be constant within sampling units, or `aggregate.index` for replicate weight designs
- `calfun` is `"linear"`, `"logit"`, `"raking"`
- `bounds` are bounds for weights: optional except in `logit`

calibrate()

```
> pop.totals<-c(`(Intercept)`=6194, stypeH=755, stypeM=1018)
>
> help(calibrate)
>  (dclus1g3 <- calibrate(dclus1, ~stype+api99, c(pop.totals, api99=3914069)))
1 - level Cluster Sampling design
With (15) clusters.
calibrate(dclus1, ~stype + api99, c(pop.totals, api99 = 3914069))
>
>  svymean(~api00, dclus1g3)
       mean     SE
api00 665.31 3.4418
>  svytotal(~enroll, dclus1g3)
         total     SE
enroll 3638487 385524
>  svytotal(~stype, dclus1g3)
       total         SE
stypeE  4421 3.373e-14
stypeH   755 1.368e-14
stypeM  1018 2.609e-14
```

calibrate()

Logistic calibration, which is popular in Europe, uses `calfun="logit"`

```
> (dclus1g3d <- calibrate(dclus1, ~stype+api99, c(pop.totals,
         api99=3914069), calfun="logit",bounds=c(0.5,2.5)))
1 - level Cluster Sampling design
With (15) clusters.
calibrate(dclus1, ~stype + api99, c(pop.totals, api99 = 3914069),
    calfun = "logit", bounds = c(0.5, 2.5))
>      range(weights(dclus1g3d)/weights(dclus1))
[1] 0.5943692 1.9358791
> svytotal(~enroll, dclus1g3d)
         total     SE
enroll 3624254 385446
> svymean(~api00, dclus1g3d)
        mean     SE
api00 665.43 3.4325
```

Calibration and ratio

For linear calibration we can specify the variance as a linear combination of covariates in the working linear regression model. With a single covariate this can reproduce the ratio estimator of the total.

```
> pop<-3811472
> dstratg1<-calibrate(dstrat,~enroll-1, pop, variance=1)
> svytotal(~api.stu, dstratg1)
          total    SE
api.stu 3190038 29566
```

Two-phase calibration

Calibration the second phase of a two-phase design can give useful gains in information. Also useful as a way of handling missing data

In Wilm's Tumour example, calibrate on disease stage and local hospital histology classification

Two-phase calibration

```
> gcchs<-calibrate(dcchs, ~interaction(rel, instit, stage), phase=2)
> svycoxph(Surv(edrel,rel)~factor(stage)+factor(histol)+I(age/12),
     design=gcchs)
Call:
svycoxph.survey.design(formula = Surv(edrel, rel) ~ factor(stage) +
    factor(histol) + I(age/12), design = gcchs)


                  coef exp(coef) se(coef)     z       p
factor(stage)2  0.658      1.93   0.1352  4.86 1.1e-06
factor(stage)3  0.800      2.23   0.1356  5.90 3.6e-09
factor(stage)4  1.297      3.66   0.1522  8.52 0.0e+00
factor(histol)2 1.511      4.53   0.1287 11.74 0.0e+00
I(age/12)       0.037      1.04   0.0235  1.58 1.2e-01

Likelihood ratio test=NA  on 5 df, p=NA  n= 1154
```

Missing data

`estWeights` constructs a calibrated two-phase design from a data frame with missing data on some variables

```
>     data(airquality)
>
>      ## ignoring missingness, using model-based standard error
>      summary(lm(log(Ozone)~Temp+Wind, data=airquality))

Call:
lm(formula = log(Ozone) ~ Temp + Wind, data = airquality)

Residuals:
     Min       1Q   Median       3Q      Max
-2.34415 -0.25774  0.03003  0.35048  1.18640

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.531932   0.608901  -0.874  0.38419
Temp         0.057384   0.006455   8.889 1.13e-14 ***
Wind        -0.052534   0.017128  -3.067  0.00271 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Missing data

```
> ## Without covariates to predict missingness we get
> ## same point estimates, but different (sandwich) standard errors
> daq<-estWeights(airquality, formula=~1,subset=~I(!is.na(Ozone)))
> summary(svyglm(log(Ozone)~Temp+Wind,design=daq))

Call:
svyglm(log(Ozone) ~ Temp + Wind, design = daq)

Survey design:
estWeights(airquality, formula = ~1, subset = ~I(!is.na(Ozone)))

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.531932   0.833602  -0.638   0.5247
Temp         0.057384   0.008453   6.789 5.51e-10 ***
Wind        -0.052534   0.020330  -2.584   0.0110 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.3130098)

Number of Fisher Scoring iterations: 2
```

Missing data

```
>  ## Reweighting based on weather, month
>  d2aq<-estWeights(airquality, formula=~Temp+Wind+Month,
+                        subset=~I(!is.na(Ozone)))
>  summary(svyglm(log(Ozone)~Temp+Wind,design=d2aq))

Call:
svyglm(log(Ozone) ~ Temp + Wind, design = d2aq)

Survey design:
estWeights(airquality, formula = ~Temp + Wind + Month,
                     subset = ~I(!is.na(Ozone)))

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.577759   0.812118  -0.711   0.4783
Temp         0.057689   0.008213   7.024 1.72e-10 ***
Wind        -0.048750   0.019729  -2.471   0.0150 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.3232150)

Number of Fisher Scoring iterations: 2
```

Simple simulations

One benefit of incorporating survey features into R is the availability of the rest of R for simulations.

For example, we can compare the default confidence interval for quantiles to the alternative `interval.type="score"`, which chooses the confidence interval endpoints $[m_l, m_u]$ so that a test of $m == m_l$ just rejects at the $\alpha/2$ level. (Francisco & Fuller, 1991, Ann Stat; Binder, 1991, Proc ASA SRMS).

The analogous strategy works well in simple random simples for the binomial mean, so we might expect it to do better than the default method.

Simple simulations

To get a variety of simulation conditions we will look at the 10th, 25th, 50th, 75th and 90th percentiles of 1999 API based on stratified samples.

```
apipop$stratsize <- ave(apipop$snum, apipop$stype, FUN=length)

truth<-quantile(apipop$api99, probs=c(0.1,0.25,0.5,0.75,0.9))

one.sample<-function(strats=c(100,50,50)) {
               E <- sample(which(apipop$stype=="E"),size=strats[1])
               M <- sample(which(apipop$stype=="M"),size=strats[2])
               H <- sample(which(apipop$stype=="H"),size=strats[3])
               svydesign(id=~1, strat=~stype, data=apipop[c(E,M,H),],
                         fpc=~stratsize)
              }
```

Simple simulations

```
one.result<-function(design){
             qwald <- svyquantile(~api99, design,
                      quantiles=c(0.1,0.25,0.5,0.75,0.9),
                      ci=TRUE)$CIs
             qscore <- svyquantile(~api99, design,
                      quantiles=c(0.1,0.25,0.5,0.75,0.9),
                      ci=TRUE, interval.type="score")$CIs
             wald.covers <- (qwald[1,,] < truth) & (qwald[2,,] > truth)
             score.covers <- (qscore[1,,] < truth) & (qscore[2,,] > truth)
             c(wald.covers, score.covers)
             }
```

Simple simulations

Now we test the function and work out how long a simulation will take

```
> system.time(results <- replicate(2 , one.result(one.sample())))
[1] 2.278 0.093 2.372 0.000 0.000
> results
     [,1] [,2]
0.1  TRUE TRUE
0.25 TRUE TRUE
0.5  TRUE TRUE
0.75 TRUE TRUE
0.9  TRUE TRUE
0.1  TRUE TRUE
0.25 TRUE TRUE
0.5  TRUE TRUE
0.75 TRUE TRUE
0.9  TRUE TRUE
> system.time(results <- replicate(200 , one.result(one.sample())))
[1] 241.447   9.522 251.034   0.000   0.000

> round(rowMeans(results)*100)
 0.1 0.25  0.5 0.75  0.9   0.1 0.25  0.5 0.75  0.9
  97   93   90   96   97    95   94   90   96   96
```

Simple simulations

```
> system.time(results2 <- replicate(500 , one.result(one.sample())))
[1] 614.744  25.341 646.318   0.000   0.000

> a<-rowMeans(cbind(results,results2))
> round(a*100)
 0.1 0.25  0.5 0.75  0.9  0.1 0.25  0.5 0.75  0.9
  96   95   94   94   96   94   95   94   94   95
```

Example: case-control

Compare maximum likelihood analysis of case-control study to design-based analysis in estimating superpopulation parameters

```
population<-data.frame(x=rnorm(10000))
expit <- function(eta) exp(eta)/(1+exp(eta))

population$y<- rbinom(10000, 1, expit(population$x-4))
population$wt<-ifelse(population$y==1, 1,(10000-sum(population$y))/600)

one.sample<-function(){
                  cases<-which(population$y==1)
                  controls<-sample(which(population$y==0),600)
                  population[c(cases,controls),]
                  }

mle<-function(sample) coef(glm(y~x, data=sample, family=binomial()))

svy<-function(sample){
               design<-svydesign(id=~1,strat=~y, weight=~wt, data=sample)
               coef(svyglm(y~x, design=design, family=quasibinomial()))
               }
```

Example: case-control

Testing gives plausible results, and 10 replicates takes about 1 second

```
> replicate(3, {d<-one.sample(); c(mle(d), svy(d))})
                  [,1]       [,2]       [,3]
(Intercept) -1.1953152 -1.1959160 -1.1827224
x            0.8862800  0.8984955  0.8236619
(Intercept) -3.9981844 -3.9920772 -3.9812051
x            0.9140028  0.9135195  0.8405922
```

Example: case-control

```
> results<-replicate(1000, {d<-one.sample(); c(mle(d), svy(d))})
> apply(results,1,median)
(Intercept)           x (Intercept)           x
 -1.1912635   0.8705304  -3.9820481   0.8724667
> apply(results,1,mad)
(Intercept)           x (Intercept)           x
 0.01284982  0.05258391  0.02755323  0.07461405
> round(apply(results,1,median)-c(-4,1), 2)
(Intercept)           x (Intercept)           x
       2.81       -0.13        0.02       -0.13
> round(apply(results,1,mad), 2)
(Intercept)           x (Intercept)           x
       0.01        0.05        0.03        0.07
```

As expected in this correctly specified model, the MLE is more efficient for the slope but biased for the intercept. We can easily look at misspecified models by changing how `y` is generated.

Wishlist

Many features of the survey package result from requests from unsatisfied users.

For new methods the most important information is a reference that gives sufficient detail for implementation. A data set is nice but not critical.

For slowness/memory problems a data set is vital so I can actually measure the time and memory use. Optimization without profiling is like estimating population totals from a convenience sample. It doesn't have to be a real data set, but it does have to be slow for the same reasons as the real data set.