On several recent quasi-randomization approaches to estimation from non-probability samples

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Why consider non-probability samples

 Probability based samples have long been an established way of conducting surveys

 Problems with traditional probability-based surveys: Lowering response rates, increased burden and cost of data collection

New opportunities:

Availability of data from variety of sources, related to the Internet, computers, etc.

The demand for exploiting these resources is steadily growing.

- However, such "opportunistic" (non-probability based) data cannot be automatically regarded as representative, since this information is not based on a well designed random sample.
- Methods have been developed to account for potential selection bias

Quasi-randomization approach

- Assume the existence of a latent mechanism that governs the non-probability sample selection.
- Basic idea: use information from available probability-based ("reference") sample to uncover latent probabilities to participate in the non-probability survey

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- Use these participation probabilities in estimation of target finite population quantities.
- We compare several methods for estimation of participation probabilities



Setup and notation

 $U \quad {\rm target \ finite \ population \ of \ size \ } N$ $\mu = \sum_{i \in U} y_i / N \quad {\rm target \ quantity}$

 $\begin{array}{l} S_c \quad \text{non-probability (convenience) sample} \\ (y_i, \mathbf{x}_i) \quad \text{observed on } S_c \\ I_{ci} \quad \text{inclusion indicator for } S_c \\ \pi_{ci} = P\{I_{ci} = 1 \mid i \in U\} \text{ (not known)} \end{array}$

 S_r probability (*reference*) sample \mathbf{x}_i observed on S_r I_{ri} inclusion indicator for S_r , $\pi_{ri} = P\{I_{ri} = 1 \mid i \in U\}$ (known)

We wish to estimate π_{ci} , then *Inverse Propensity Weighted (IPW)* estimator of population mean μ is

S,

$$\hat{\mu} = \frac{\sum_{i \in S_c} y_i / \hat{\pi}_c}{\sum_{i \in S_c} 1 / \hat{\pi}_c}$$



Pseudo-likelihood approach of Chen, Li and Wu(2020)

Consider $I_{ci} \sim \text{Bernoulli}(\pi_{ci})$ on population U:

$$\ell^{CLW}(\boldsymbol{\beta}) = \sum_{i \in U} \left\{ I_{ci} \log \left[\pi_{ci}(\boldsymbol{\beta}) \right] + (1 - I_{ci}) \log \left[1 - \pi_{ci}\left(\boldsymbol{\beta}\right) \right] \right\}$$
$$= \sum_{i \in S_c} \log \left[\frac{\pi_{ci}(\boldsymbol{\beta})}{1 - \pi_{ci}\left(\boldsymbol{\beta}\right)} \right] + \sum_{i \in U} \log \left[1 - \pi_{ci}\left(\boldsymbol{\beta}\right) \right],$$

and logit $[\pi_{ci}(\boldsymbol{\beta})] = \boldsymbol{\beta}^T \mathbf{x}_i$.

Since U is not available, use pseudo-likelihood:

$$\hat{\ell}^{CLW}(oldsymbol{eta}) = \sum_{i \in S_c} \log\left[rac{\pi_{ci}(oldsymbol{eta})}{1 - \pi_{ci}\left(oldsymbol{eta}
ight)}
ight] + \sum_{i \in S_r} w_{ri} \log\left[1 - \pi_{ci}\left(oldsymbol{eta}
ight)
ight],$$

where $w_{ri} = \pi_{ri}^{-1}$.

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Sample based approach (under negligible sampling overlap)



Under "negligible" sampling overlap, approximate relationship holds:

$$\pi_{zi} \approx rac{\pi_{ci}}{\pi_{ci} + \pi_{ri}}.$$

A two-step procedure:

Step 1: Estimate π_{zi} using standard methods Step 2: Find π_{ci} from $\pi_{zi} \approx \pi_{ci}/(\pi_{ci} + \pi_{ri})$

Sample based approach (unknown overlap of any size) Savitsky, Williams, Gershunskaya and Beresovsky (2023)

Stacked sample: $S = S_c + S_r$ (overlapping units appear in S twice)



 $\pi_{zi} = P\{I_{zi} = 1 | i \in S\}$ is probability to be in S_c for units in stack S

Key relationship for independent sampling probabilities (KRISP): Under stacked samples setup, assuming S_c and S_r are independently selected from U, relationship

$$\pi_{zi} = \frac{\pi_{ci}}{\pi_{ci} + \pi_{ri}}$$

✓ holds exactly,✓ regardless of the size of sampling overlap.

Implicit Logistic Regression (ILR) Beresovsky(2019):

The log-likelihood for observed Bernoulli variable I_{zi} is

$$\ell^{ILR}(\boldsymbol{\beta}) = \sum_{i \in S_c} \log\left(\pi_{zi}[\pi_{ci}(\boldsymbol{\beta})]\right) + \sum_{i \in S_r} \log\left(1 - \pi_{zi}\left[\pi_{ci}(\boldsymbol{\beta})\right]\right),$$

where π_{zi} can be treated as a *composite function*, based on KRISP,

$$\pi_{zi} = \pi_{zi}[\pi_{ci}(oldsymbol{eta})] = rac{\pi_{ci}(oldsymbol{eta})}{\pi_{ri} + \pi_{ci}(oldsymbol{eta})}$$

and logit $[\pi_{ci}(\boldsymbol{\beta})] = \boldsymbol{\beta}^T \mathbf{x}_i$.

Take derivatives wrt β and solve estimating equations, thus estimating π_{ci} directly from the likelihood.

Asymptotic variances of the estimates of μ and β

$$\begin{aligned} \mathsf{Var}(\hat{\mu}) &\doteq \mathsf{Var}[U(\mu)] - 2\boldsymbol{b}^T \mathsf{Cov}[U(\mu), \boldsymbol{S(\beta)}] + \boldsymbol{b}^T \mathsf{Var}[\boldsymbol{S(\beta)}]\boldsymbol{b}, \\ \mathsf{Var}(\hat{\boldsymbol{\beta}}) &\doteq \boldsymbol{H}^{-1} \mathsf{Var}[\boldsymbol{S(\beta)}] \boldsymbol{H}^{-1}, \end{aligned}$$

where $\boldsymbol{b} = S_{\boldsymbol{\beta}}^{-1} U_{\boldsymbol{\beta}}^{T}$, $U_{\boldsymbol{\beta}} = E[\partial U(\mu)/\partial \boldsymbol{\beta}^{T}]$, $S_{\boldsymbol{\beta}} = E[\partial S(\boldsymbol{\beta})/\partial \boldsymbol{\beta}]$, $\boldsymbol{H} = -S_{\boldsymbol{\beta}}$.

Both methods, CLW and ILR, are asymptotically equivalent:

$$\operatorname{Var}\begin{pmatrix} \hat{\mu}\\ \hat{\beta} \end{pmatrix} \sim O\left(\frac{1}{n_r} + \frac{1}{n_c}\right) = O\left(\frac{1}{\min(n_r, n_c)}\right)$$

Note that

 $\operatorname{Var}[S(\boldsymbol{\beta})] = \operatorname{Var}[S_c(\boldsymbol{\beta})] + \operatorname{Var}[S_r(\boldsymbol{\beta})].$

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The methods differ mostly due to contributions from $Var[S_r(\beta)]$.



Relative efficiency of ILR and CLW estimates of propensity model parameter



Classification Trees

We can use ILR and CLW methods with a classification trees algorithm.

We expect: a sample-based likelihood would be more efficient compared to a pseudo-likelihood, especially as the regression tree grows and its nodes are based on progressively smaller samples

For a given node g, find an optimal binary split based on a given covariate:

- (1) find (π_{cgL}, π_{cgR}) , estimates of probabilities in left and right branches, on a grid of possible splits;
- (2) choose an optimal split based on an objective function



Homogeneous groups (based on CLW pseudo-likelihood)

The algorithm splits data into homogeneous groups g = 1, ..., G, so that all units in a given group have the same probabilities π_{cg} .

Under (CLW) pseudo-likelihood:

$$\hat{\pi}_{m{cg}} = rac{n_{m{cg}}}{\hat{N}_g}, ext{ where } \hat{N}_g = \sum_{i \in g} w_{ri}.$$

Estimated entropy impurity criteria:

$$\hat{I}^{CLW} = -\sum_{g=1}^{G} \frac{\hat{N}_g}{\hat{N}} \left[\hat{\pi}_{cg} \log(\hat{\pi}_{cg}) + (1 - \hat{\pi}_{cg}) \log(1 - \hat{\pi}_{cg}) \right]$$

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Homogeneous groups (based on **stacked-samples setup**)

For sample-based (ILR) approach: no explicit expression for π_{cg} . It can be found as a solution of equation

$$\sum_{i \in S_g} \frac{\pi_{ri}}{\pi_{ri} + \pi_{cg}} = n_{rg},$$

where S_g is the part of stacked sample S belonging to group g.

Estimated entropy impurity criteria:

$$\hat{I}^{ILR} = -\sum_{g=1}^{G} \left[\sum_{i \in S_{cg}} \log \hat{\pi}_{zi,g} + \sum_{i \in S_{rg}} \log(1 - \hat{\pi}_{zi,g}) \right],$$

where
$$\hat{\pi}_{zi,g}=rac{\hat{\pi}_{cg}}{\pi_{ri}+\hat{\pi}_{cg}}.$$

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Simulation example: setup

Suppose we already have a grown tree, up to some level g. We focus on splitting node g into two parts.

The setup is:

 $N_g = 1,000$ is population size Covariate: $x_{ig} \sim N(0,1)$ Study variable: $y_{ig} = 1 + x_{ig} + \epsilon_{ig}$, with $\epsilon_{ig} \sim N(0, 1.5^2)$

True convenience sample probabilities:

$$\begin{split} \pi_{cg,L} &= 0.80 \text{ for } i \text{ with } x_{ig} <= 0, \\ \pi_{cg,R} &= 0.20 \text{ for } i \text{ with } x_{ig} > 0. \\ \text{Hence, convenience sample size is } n_{cg} \approx 500. \end{split}$$

PPS design for *probability* sample $\pi_{rg,i} \propto x_{ig}$ Scenarios: $n_{rg} = 100,500$

1000 simulation runs

Reference sample scenarios: $n_{rg} \in \{100, 500\}$ Estimators: CLW, ILR (stacked samples)



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Estimates of μ

Estimators: Unweighted, CLW, ILR (stacked sample)

$$n_r = 100 \qquad \qquad n_r = 500$$





	$n_r = 100$		$n_r = 500$	
	Bias	MSE	Bias	MSE
Unweighted	-0.481	0.234	-0.481	0.234
CLW	-0.128	0.042	-0.047	0.023
ILR (stack)	0.012	0.011	0.001	0.007

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Summary

- The pseudo-likelihood CLW and stacked-samples based ILR approaches are asymptotically equivalent
- The stacked-samples ILR method is more efficient compared to CLW under practically important scenarios of:
 - a small reference sample and
 - a low overlap in covariates-defined domains (resulting in an insufficient representation of some population groups in either of the two samples)
- Future research: Linkage may lead to better estimates if a good matching quality could be achieved. However, thinking about the balance between cost/effort spent and the quality of record linkage, the question in context of estimation of participation probabilities is: Do we really have to link?

CONTACT INFORMATION

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Thank you!

