social transition Colorado driven bottleneck threshold design Markov correlation random Volz-Heckathorn **Galton-Watson** Variance 547(political blogs spectral tree graph nvectors respondent snowball eige Theorem friends

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A critical threshold for network driven sampling



Network driven sampling does not require a sampling frame.

- Standard sampling techniques like random digit dialing require a sampling frame "simple random sample"
- No sampling frame for:
 - homeless, twitter discussions, refugees, sex workers, jazz musicians.
- Even with a sampling frame, low response rates!

Respondent driven sampling (RDS) and snowball sampling are often used in social science research.

- To study the hard-to-reach and/or marginalized populations.
- Particularly prevalent in HIV research.
- Three risk populations: Men who have sex with men (MSM), people who inject drugs (PWID), and Female sex workers (FSW)

RDS for HIV is the motivating example, but network driven sampling appears elsewhere.

RDS relies on friends passing coupons.

- Find seeds from a convenience sample.
- Give each seed three coupons to refer friends.
- The coupons have a dual incentive structure
 - Pay the person for making a referral
 - Pay the person being referred
- Iterate through referral tree

Heckathorn, 1997.



RDS is increasingly popular

- The CDC manages the National HIV Behavioral Surveillance System
 - RDS every few years in 20 major metropolitan areas.
- The WHO and UNAIDS have published an extensive manual for how to properly implement RDS

We wish to estimate the proportion of the population that is HIV+.

A Major Assumption

- If people make random referrals then we can make statistical inferences using probabilistic tools and techniques
 - confidence intervals and p-values.
- Suppose you have X friends in the target population. The friend you refer is chosen uniformly at random from these X people.

Salganik and Heckathorn, 2004

A Major Assumption

- Under this model, the passing of the coupon is a random walk on the social network.
- For simplicity, temporarily suppose that there is only one coupon.

Salganik and Heckathorn, 2004

Friendships can be plotted as a graph. The circles are "nodes" or people. The lines are "edges" or friendships.





Unbiased estimation requires the inclusion probabilities.

People with large degrees are more likely to be sampled.

Using the random walk (and other) assumptions, we can approximate the inclusion probabilities.

The stationary distribution:

 $\pi_j = \lim_{t \to \infty} P(\text{referral } t \text{ is person } j | \text{seed is person } i)$

Salganik and Heckathorn, 2004

Using the random walk (and other) assumptions, we can approximate the inclusion probabilities.

$\pi_j \propto \text{number of friends of person } j$

- Assumptions:
 - uniform selection of friends, with replacement.
 - reversible Markov chain (i.e. "symmetric").
 - social network is connected and aperiodic
 - Asymptotic

Salganik and Heckathorn, 2004

Volz-Heckathorn (2008) estimator uses the stationary distribution to construct a Horvitz-Thompson estimator.

 $y_t = \begin{cases} 1 & \text{if person } t \text{ is HIV positive} \\ 0 & \text{if person } t \text{ is HIV negative} \end{cases}$ deg(t) = # of friends of person t

$$\hat{\mu}_{VH} = \sum_{t}^{n} w_t y_t \qquad w_t = \frac{1/deg(t)}{\sum_{j}^{n} 1/deg(j)}$$

Asymptotically unbiased!

What is the standard error of this estimator?

Computing the standard error is an essential step for creating confidence intervals and testing hypotheses.

What is the standard error of this estimator?

Classical standard error for simple random sample.



Usually, sigma is unknown.

What is the standard error of this estimator?

Classical standard error for simple random sample.



You can estimate it!



In this talk, we will find the analogue to the first formula for RDS.

Key difficulty with RDS data: samples are dependent.

- Friends are similar in many ways, including HIV status.
- If Fred refers Bill, they are likely to have similar HIV status.

Need to decide what to model as "random"

- Salganik and Heckathorn (and co-authors) typically model *referrals* as random.
- Giles and Handcock and others make an additional assumption that the network is random.
- There are currently three bootstrap techniques that build off of these assumptions.

Previous standard error estimators have modeled traits y as a first order Markov Chain

- Salganik (2006). "Variance estimation, design effects, and sample size calculations for respondentdriven sampling." *Journal of Urban Health*.
- This is an additional modeling assumption beyond what is needed for the unbiased-ness of VH.
- Underestimates variance. Neely [2009], Verdery et al. [2013]
- In Q/A, I can address when the "first order assumption" holds and when it does not.

Recap

- RDS is a network link tracing technique
- Three bits: social network, referral tree, HIV status
- Assumption of random referrals allow for statistical inference
- VH estimator is asymptotically unbiased
- We need to understand the variance.

Outline

- Model and notation.
 Markov transitions, sampling tree, node features.
- II. Key mathematical pieces.eigenvectors of PThe G function
- III. The true sampling variance



A. A scary story

IV. Designed RDS

The Markov transition matrix describes how coupons are passed along the social network.

- Markov transition matrix P is N x N.
 N = population size. (n will be sample size)
 - $P(\text{person } i \text{ refers person } j | \text{person } i \text{ has } 1 \text{ coupon}) = P_{ij}$
 - e.g. VH assumption: i chooses friend uniformly at random, so that

$$P_{ij} = \frac{\mathbf{1}(i, j \text{ friends})}{deg(i)}$$

Regularity conditions on P

- Assume P is reversible wrt the stationary distribution.
- $\pi_i P_{ij} = \pi_j P_{ji}$
- For random walk, equivalent to assuming an undirected network.
- Assume $|\lambda_2(P)| < 1$

(akin to connected and aperiodic)

 $\pi_j = \lim_{t \to \infty} P(\text{referral } t \text{ is person } j | \text{seed is person } i)$

Each person can refer up to three (sometimes five) future participants.

- To represent the referral process, we need a "tree"
- Call this object T. It is a graph, that contains elements 1, ..., n corresponding to the n samples.
- If i refers j into the study, then i —> j.



Standard Markov chain $\{X(i) \in \text{people} : i = 1, \dots, n\}$



Markov transitions on the referral tree.

$$\{X(i) \in \text{people} : i = 1, \dots, n\}$$
$$\{X_{\tau} \in \text{people} : \tau \in \mathbb{T}\}$$












Each node in the graph is either infected or not.

• For person i = 1, ..., N

$$y_i = \begin{cases} 1 & i \text{ sick} \\ 0 & i \text{ not sick} \end{cases}$$

We want to estimate y averaged across all nodes 1, ..., N in the social network.

Everything holds if y is continuous.

These terms constitute the core of the model and the notation.

I. Markov transition matrix P (underneath P, there is a social network)

II.Referral tree T, $\{1, \ldots, n\} \subset T$

III.Health status $y_j, j = 1, \ldots, N$

Outline

 Model and notation.
Network, Markov transitions, sampling tree, node features.

II. Key mathematical pieces. eigenvectors of P The G function $Var(\hat{\mu}) = \sum_{\ell=2}^{N} \langle y, f_{\ell} \rangle_{\pi}^{2} \mathbb{G}(\lambda_{\ell})$

III. The true sampling variance

A. A scary story

IV. Designed RDS

"Bottlenecks" can prevent representative samples.

- Suppose a town with two communities: EAST and WEST.
- All seeds belong to EAST.
- Few friendships cross the town.
- Will you collect enough data from WEST?
- What if EAST and WEST have same incidence of HIV?
- We need a mathematical way to express these "bottlenecks"...

Lemma 1.1. Let P be reversible with respect to the stationary distribution π . The eigenvectors of P, denoted as f_1, \ldots, f_N , are real valued functions of the nodes $i \in V$ and orthonormal with respect to the inner product

$$\langle f_a, f_b \rangle_{\pi} = \sum_{i \in V} f_a(i) f_b(i) \pi_i.$$
 (2)

When $|\lambda_2| < 1$, the leading eigenvector is constant vector of ones, $f_1 = 1$. Moreover, the probability of a transition from $i \in V$ to $j \in V$ in t steps can be written as

$$\mathbb{P}(X(t) = j | X(0) = i) = P_{ij}^t = \pi_j + \pi_j \sum_{\ell=2}^N \lambda_\ell^t f_\ell(i) f_\ell(j).$$

Chapter 12 of Levin et al. [2009]

Eigenvectors are a mathematical refinement for the concept of "bottlenecks"

Eigenvectors indicate the bottlenecks

$$f_{\ell}, \lambda_{\ell} \ \ell = 1, \dots, N$$

eigenvalues indicate the "strength" of the bottleneck.

These are well studied objects in linear algebra and spectral graph theory.

Eigenvectors are a mathematical refinement for the concept of "bottlenecks"

 $f_\ell(i)$

An eigenvector assigns a value to each node.

$|\mathsf{F}: \quad sign(f_{\ell}(i)) = sign(f_{\ell}(j))$

THEN: i and j are on the same side of this bottleneck.

For example, the EAST and WEST bottleneck would be represented by one eigenvector.

- The two communities are EAST and WEST.
- If this is the biggest bottleneck in the network, then the second eigenvector will have opposite signs on nodes from EAST and WEST.

Lemma 1.1. Let P be reversible with respect to the stationary distribution π . The eigenvectors of P, denoted as f_1, \ldots, f_N , are real valued functions of the nodes $i \in V$ and orthonormal with respect to the inner product

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Chapter 12 of Levin et al. [2009]

Political Blogs

1084 blogs edges are hyperlinks avg degree 30 Half support Kerry Half support Bush

Eigenvectors correspond to bottlenecks. $\langle y, f_\ell \rangle_\pi^2$ Each one has a value on each node. Bottlenecks are problematic when they correlate with y.



Eigenvalues indicate the strength of the bottleneck.

For all ℓ , $-1 \leq \lambda_{\ell} \leq 1$

 $\lambda_1 = 1$ Don't worry about the first eigenvalue.

If $\lambda_2 = 1$, then the graph is not connected!

If λ_2 is close to one, then the graph has a strong bottleneck.

N $Var(\hat{\mu}) = \sum \langle y, f_{\ell} \rangle_{\pi}^2 \mathbb{G}(\lambda_{\ell})$ $\ell = 2$

The G function measures the "stringiness" vs the "bushy-ness" of the tree T.

- Draw two observations I and J uniformly at random from T.
- D = d(I,J), graph distance in T.
- Then,

$$\mathbb{G}(z) = E(z^D) \text{ for } |z| < 1$$

Bushy trees have larger referral rates.

<u>"Bushy</u>"





m~2

m~1

average number of referrals = m

$\mathbb{G}(z) = E(z^D) \text{ for } |z| < 1$

G is an increasing function. G decreases when n increases. G is larger for bushy trees.



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 Suppose that (1) the Markov chain satisfies regularity conditions and that (2) the seed node is sampled from the stationary distribution.

$$\hat{\mu} = \frac{1}{n} \sum_{i \in T} y_i$$

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Squared correlation between y and bottleneck ℓ



G function evaluated at each eigenvalue. Recall: eigenvalue is large if bottleneck is strong.

Proof sketch

By reversibility:

For $\sigma, \tau \in \mathbb{T}, d(\sigma, \tau) = t \implies (X_{\sigma}, X_{\tau}) \stackrel{d}{=} (X(0), X(t))$

By spectral representation:

$$Cov_{\pi}(Y_{\sigma}, Y_{\tau}) = \sum_{\ell=2}^{N} \lambda_{\ell}^{d(\sigma, \tau)} \langle y, f_{\ell} \rangle_{\pi}^{2}$$

Summing over all (sigma, tau) and exchanging summations yields the result.

The theorem is stated for sample average. Variance of Horvitz-Thompson is a slight adjustment.

$$y^{\pi}(i) = \frac{y(i)}{\pi_i N}$$

$$\hat{\mu}_{HT} = \frac{1}{n} \sum_{i \in T} y_i^{\pi}$$



The theorem is stated for sample average. Variance of Horvitz-Thompson is a slight adjustment.



Two example networks to study this formula.

- Political Blog data from 2004 US presidential election
- Colorado Project 90 data. Census of heterosexuals at risk for HIV, living around Colorado Springs in ~1990.
- Both study the 2-core of the largest connected component.

Political Blogs

1084 blogs edges are hyperlinks avg degree 30 Half support Kerry Half support Bush



















The standard error is large because the bottleneck aligns with the outcome of interest.



number of samples (i.e. size of sampling tree)

Bushy tree creates much larger standard errors.



Project 90

- "Fully observed" network on at risk and marginalized population.
- CDC funded census of heterosexuals at risk for HIV transmission & living around Fort Collins, CO in ~1990.
- 2-core of largest connected component
 - N = 3615 people, mean degree = 9.7

Project 90 collected the network of heterosexuals at risk for HIV in Colorado Springs circa 1990



Data includes several covariates on the nodes.

gender sex.worker pimp sex.work.client drug.dealer drug.cook thief retired housewife

disabled unemployed homeless Native American Black Asian/Pacific Islander White Other



Breaches in data privacy have allowed the identification of some individuals!








Gov Engler?!





Different covariates can have drastically different standard errors.



Mean number of offspring = 2

female

drug.dealer







unemployed







random



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A. A scary story, the critical threshold

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For standard rates, we need the tree to grow in a way that G is order 1/n.

If y is correlated with f2, then under a certain technical condition,

 $c \mathbb{G}_n(\lambda_2) + o(\mathbb{G}_n(\lambda_2)) \le Var_{RDS}(\hat{\mu}) \le c \mathbb{G}_n(\lambda_2)$

Design effect

How much larger is an RDS confidence interval compared to an SRS confidence interval using the same number of samples?

If
$$y = f_2$$
, then

$$DE = \frac{\operatorname{Var}_{RDS}(\hat{\mu})}{\operatorname{Var}_{SRS}(\hat{\mu})} = \frac{\mathbb{G}(\lambda_2)}{1/n} = n\mathbb{G}(\lambda_2)$$

Because G characterizes the rates of convergence, we would like upper and lower bounds on G that depend on the sample size n (i.e. the number of nodes in the referral tree)

Under an m-tree, there is an easy lower bound.

The height of the m-tree is bounded:

$$h(\mathbb{T}) \leq \log_m n$$
$$\mathbb{F}(\lambda_2) = \mathbb{E}\lambda_2^D \geq \lambda_2^{2h(\mathbb{T})} \geq \lambda_2^{2\log_m n} = n^{-\log_m 1/\lambda_2^2}$$

Under an m-tree (i.e. everyone refers m people), there is an easy lower bound.

The height of the m-tree is bounded:

$$h(\mathbb{T}) \le \log_m n$$
$$\mathbb{F}(\lambda_2) = \mathbb{E}\lambda_2^D \ge \lambda_2^{2h(\mathbb{T})} \ge \lambda_2^{2\log_m n} = n^{-\log_m 1/\lambda_2^2}$$

 $m > 1/\lambda_2^2$

This fails to converge at the desired rate if

Threshold:	$m < 1/\lambda_2^2$	$m > 1/\lambda_2^2$
standard error:	$n^{-1/2}$	$n^{\log_m \lambda_2}$

- Lower bounds hold when tree is Galton Watson under the N log N assumption. m = expected # referrals.
- Upper bounds require more work and an additional assumption.
 - gives a matching threshold. rate matches (up to log terms).
 - Galton Watson trees satisfy this additional assumption under a bounded fourth moment assumption.



A recap of the scary story

 $\lambda_j: -1 < \lambda_j < 1$

- Close to 1 when bottleneck is strong
- Values larger than 0.9 not uncommon

• Say
$$\lambda_j = 0.7 \Rightarrow \frac{1}{\lambda_j^2} \approx 2$$

 $\lambda_j = 0.9 \Rightarrow \frac{1}{\lambda_j^2} \approx 1.23$

 If the average person refers more people than this, then the DE grows with n.



Design effects for 18 different empirical referral trees

Design effects under the 2-tree

There is a fundamental conflict between obtaining "enough data" and an unbiased sample.

- Volz-Heckathorn is *asymptotically unbiased*.
- Want *longer* chain
- Chains often die.
- Need several referrals to prevent chain death.
- This gives you a bushy tree.
 - As you gain more samples, standard errors decrease, but design effect can grow.

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- We derived variance of VH estimator under the assumptions needed for unbiasedness & initialization from stationary distribution.
- The variance depends on
 (1) the bottlenecks in the referral process,
 (2) how y correlates with the bottlenecks,
 (3) the tree structure.
- There is a fundamental conflict between obtaining "enough data" and an unbiased sample. If referral rate is too large, then design effect grows with n.

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Bottlenecks prevent accurate estimates

If the bottleneck is too strong, you get a growing design effect!

Designed RDS

 Joint research with Mohammad Khabbazian, Zoe Russek, and Bret Hanlon.

Designed RDS

- Seeks to minimize bottlenecks
- Classically, a sample design is defined as a way of assigning a probability to everyone in the population
- Designed RDS seeks referrals that cross bottlenecks

How do you do this?

- You could ask for it,
 - "Please refer someone from neighborhood x"
- Problems with this:
 - Need to know which bottlenecks are important
 - Hard to model as random

Anti-cluster sampling

"Please refer two people who don't know each other"

and/or

"Please refer someone who doesn't know the person who referred you"

Disclaimer: This is work in progress.



Anti-cluster sampling

- This can be modeled as a new Markov transition matrix P for the same graph G
- Random walk is "choose a friend uniformly at random"
- Anti-cluster can be modeled as "from your set of friends, find all pairs that don't know each other and select one pair uniformly at random."
- These sampling probabilities can be computed with matrix multiplication.

Under a "balanced" Stochastic Blockmodel with "within-block" probabilities larger than "out-of-block" probabilities, AC-RDS has smaller bottlenecks.

Lemma 5 (Spectral gap of the population graph). Let $\mathcal{A} := E[\mathcal{A}] = ZBZ^T$ under the stochastic block model with k blocks of equal sizes. Let $B_{ii} = p$ and $B_{ij} = q$ for $i \neq j$. If 0 < q < p < 1, then

$$0 < \lambda_2(\mathcal{P}^{AC}) < \lambda_2(\mathcal{P}^{RW}) < 1.$$

Work in progress

- Our current theory presumes that the underlying network is a stochastic block model
- Does it work in practice?
 - Need experiments!

- We derived variance of VH estimator under the assumptions needed for unbiasedness & initialization from stationary distribution.
- The variance depends on (1) the tree structure and (2) how y correlates with the bottlenecks.
- There is a fundamental conflict between obtaining "enough data" and an unbiased sample. If referral rate is too large, then design effect grows with n.

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