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The chords R Package- A Principled Approach to Respondent Driven Sampling

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Abstract

The abstract of the article.

Keywords: RDS, estimation, counting-process, R.

1. Introduction

As the name suggests, Respondent Driven Sampling (RDS) is a framework for sampling by chain-referral. RDS is a bundle of a sampling mechanism and analysis methods, most common in the study of marginalized populations which do not lend themselves to simple sampling (Heckathorn 1997, 2002).

In RDS seeds are selected – usually by convenience – from the target population, and given coupons. They use these coupons to recruit others, who themselves become recruiters. Recruits are given an incentive, usually money, for taking part in the survey, and also for recruiting others. This process continues in recruitment waves until the survey is stopped, usually when a target sample size is reached.

With the above sampling mechanism, highly connected individuals will be overrepresented in the sample. If the attribute of interest is correlated with an individual's degree, as is often the case (e.g. HIV), naïveestimates will be biased towards the state of the highly connected subgroups. An unbiased Horowitz-Thompson-type estimator (Horvitz and Thompson 1952) would require the knowledge of frequency of each degree. Clearly, the frequency of each degree will also be biased towards higher degrees, and thus cannot be recovered from the knowledge of individuals' degrees alone. The common remedy to this matter is the inverse-degree weighting heuristic (Crawford, Wu, and Heimer 2015; Guntuboyina, Barbour, and Heimer 2012).

In Berchenko, Rosenblatt, and Frost (2013) we proposed a generative model for RDS. The model is based on the idea that RDS spreads like an epidemic, and we can thus borrow epidemiological generative models. In particular SIR [TODO: add citation], for likelihood based inference. Having assumed a generative process, we can now estimate degree frequencies, introduce covariates, check the goodness of fit, and discuss the model's assumptions.

The details of the assumed generative model can be found in Berchenko et al. (2013), but the essentials are now detailed for completeness.

Denote N_k the unknown population frequency of degree k, i.e., the number of individuals with k "friends". Denote $N := \sum_k N_k$, the total population size. Denote by x_t the degree of the respondent recruited at time t. Our task is to estimate $\hat{N}_1, \hat{N}_2, \ldots$, based on a sample of $x_{t_1}, \ldots, x_{t_\tau}$. Denote $\lambda_{k,t}$, the probability of recruiting an individual with degree k in the time interval $[t, t + \Delta]$. We assume the following generative multivariate counting model:

$$\lambda_{k,t} = \beta_k \frac{n_t}{N} (N_k - n_{k,t}) \Delta t + o(\Delta t), \tag{1}$$

where β_k is some base recruitment rate, n_t is the number of recruiting individuals at time t, and $n_{k,t} := \sum_{s \leq t} I_{\{x_s = k\}}$ the number of recruited individuals of degree k. It thus follows that $\frac{I_t}{N}$ is the recruiting population proportion, and $(N_k - n_{k,t})$ the recruitment "potential" of degree k. In these terms, our model implies that the recruitment probability, in short enough time periods, is proportional to the recruiting team (a.k.a. the "snowball") and the recruiting potential. For more on this model, and relations to other existing models, see Berchenko $et\ al.$ (2013).

Equipped with this generative model, we may state the estimation of N_1, N_2, \ldots as a likelihood maximization problem. Moreover, we show in Berchenko *et al.* (2013) that the maximum likelihood estimator (MLE) of N_1, N_2, \ldots is separable for the various k, and independent of β_k . This fact is used by Berchenko *et al.* (2013) for proof of the asymptotic properties of $\hat{N}_1, \hat{N}_2, \ldots$, and in the **chords** package to accelerate the estimation task.

2. Work Flow

3. Some Technicalities

4. Conclusion

5. Future Work

References

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