# Using Multiple Modes of Data Collection to Recruit Migrant Samples with Network Sampling with Memory: The Chinese Immigrants in the Raleigh-Durham Area Study (ChIRDU).<sup>1</sup>

Giovanna Merli, Ted Mouw, Allison Stolte, Claire Le Barbenchon and Francesca Florey Eischen

# Introduction

Obtaining representative samples of rare or hidden populations through conventional probability sampling designs can fail for two reasons: first, if the target population is well-identified but small, the sample size required to ensure the inclusion of a minimum number of members for analytical samples for inference can be extremely large. This can be overcome, to some degree, by carrying out stratified sampling or unequal probability sampling provided that the population is known, and a sampling frame exists. Notwithstanding, the large-scale screening required in these cases may be either prohibitively expensive or ineffective. Second, even when populations of interest are a large fraction of the population, obtaining probability samples can be challenging if behaviors defining membership in this group are difficult to identify because they are socially stigmatized and/or illegal. For this reason, when these groups are the target of surveys they can have very high non-response or non-interview rates. These concerns apply to the study of immigration because immigrant groups are often too small to be captured in standard probability sampling designs or they may be illegal, hence difficult to identify due to fear of repatriation. This can lead to incomplete coverage and partial inclusion of immigrants in data collection efforts that are used to describe these populations.

In addition to the difficulty and costs of collecting data on rare or hidden immigrant groups for representation, the study of immigration can benefit from the collection of data on immigrants' networks within and outside of their co-ethnic communities. Immigrant social networks are thought to be a substantially understudied but crucial feature of the immigration experience. There is a need to understand how co-ethnic and other types of social networks shape immigrants' labor market and health outcomes and assimilation.

Link-tracing designs, where referrals from previous respondents are the source of new respondents, may provide the solution to recruiting samples of hidden and rare population groups such as immigrants. These methods, often described as snowball sampling or chain-referral sampling, may offer better and more cost-effective coverage and reduce confidentiality concerns because they reach respondents through their social networks and because respondents are recruited into a study by peers, not by unknown interviewers. But samples recruited with these methods are regarded as convenience samples because of the absence of a sampling frame and the lack of a probability-based sampling strategy. Recently, two approaches have sought to turn chain referral sampling into probability sampling. The better-known Respondent Driven Sampling ("RDS", Heckathorn 1997; 2002) and the more recent Network Sampling with

<sup>&</sup>lt;sup>1</sup> Funding for the collection of the ChIRDU data come from NICHD grant R21 HD086738 (Merli and Mouw, PIs) and a pilot grant to Giovanna Merli from NICHD P2C HD065563 to Duke University.

Memory ("NSM", Mouw and Verdery) capitalize on the network structure of the target population to identify and interview multiple waves of respondents. Similar RDS, NSM is a linktracing sampling design, where referrals from a set of respondents are used to recruit other respondents. These methods capitalize on the network structure of the target population to identify and interview multiple waves of respondents.

RDS and NSM use, respectively, the assumed structure or actual knowledge of the network along with a process of recruitment running a the network to generate estimates of population proportions and use a post-recruitment weighting of cases to correct biases towards sampling popular individuals. Theoretical and empirically grounded evaluations of RDS have found that its estimates may be far from population parameters and that RDS estimators exhibit large sampling variance in mean estimates and large design effects (Gile and Handcock 2010; Merli et al. 2015; Tomas and Gile 2011; Verdery et al. 2015; Yamanis et al. 2013; Goel and Salganik 2010; Mouw and Verdery 2012). Reasons for the poor performance of RDS estimators include unrealistic assumptions about the underlying network structure over which the sampling process is running and about the sampling process itself.

NSM collects detailed network data and uses them to guide the sampling process into unexplored areas of the underlying social network and to improve the accuracy and precision of the resulting estimates. The statistical properties of the NSM sampling algorithm have been tested with simulated sampling showing the accuracy, precision and efficiency of NSM in comparison with RDS and other link-tracing designs to sample hidden and rare populations (Mouw and Verdery 2012).

Our team is currently completing a study to test the viability of NSM to collect useful samples of rare and hidden populations and evaluate the accuracy and representativeness of NSM samples of rare populations of immigrants. In the Chinese Immigrants in the Raleigh-Durham Area (ChIRDU) study, we are using NSM to recruit three samples, each with target of 200 members of the population of Chinese immigrants in the Raleigh-Durham metropolitan area of North Carolina for a total of 600 members. Each sample is recruited using a different survey mode: a mode which exclusively relies on telephone interviews; one that relies on in-person interviews; and a web version which uses online platforms including smart phones, to determine the implementation challenges of each mode and to identify an optimal single mode or a combination of modes that adequately cover the population under study.

In this paper, we will report the main findings of this study. In particular we plan to:

(a) Demonstrate that NSM is a practical means of accurately collecting large-scale samples in the field. We will compare the population estimates from the NSM samples recruited with different survey modes to a conventional probability sample drawn from the American Community Survey (ACS). Chinese immigrants are an ideal target population to test the accuracy of NSM because they are a rare population, yet sufficiently well sampled in the ACS data for the RDU metro area that we can compare the results from NSM to the ACS.

(b) Identify factors that enable NSM to generate large-scale samples with minimum cost and maximum response rates. We will evaluate the impact of administering each mode on multiple measures of data quality, including response rates and number of nominated contacts, and cost.

Our experience in the evaluation of NSM in the field contributes to research on network data collection and survey research with hidden and hard-to-reach populations. Additionally, this evaluation is also relevant to those interested in seeking alternatives to conventional data collection schemes (Brick 2011). Response rates to government and privately sponsored household surveys for social science research have been falling throughout the world's high-income countries (De Leeuw and De Heer, 2002), including the United States (NAS 2013) with reasons attributed to increased technological (call screening) and physical (gated entryway) barriers and potential respondents' decreased propensity to participate when contacted by researchers (Miller 2017). The costs involved with attempts to increase response rates, minimize the risk of bias in estimates and preserve research designs are high (Curtin, Presser and Singer 2005; NAS 2013). The identification of new approaches that change the interaction of interviewer and that could increase respondents' motivation to participate in surveys is a central part of an agenda to develop better approaches to increase survey response (NAS 2013). It is important to establish the feasibility and performance in the field of sampling approaches where the interaction between interviewer and respondent is filtered by peer recruitment.

#### **NSM Sampling Design**

NSM (Mouw and Verdery 2012) improves on RDS by collecting network information as part of the survey. To improve precision and efficiency, it then uses this information to map the underlying population network and direct the sampling process with an algorithm which identifies whom to sample next. NSM also provides explicit diagnostics to help researchers gauge when the sample size is sufficiently large to approximate the statistical features of a simple random sample of the target population, offering researchers crucial information on when to stop sampling (Mouw and Verdery 2012). In this sense, NSM increases the representativeness and precision of the sample compared to RDS, which typically requires samples orders of magnitude larger than traditional survey designs (Goel & Salganik 2010).

NSM sample recruitment starts with the identification of a limited number of initial respondents ("seeds") selected by convenience, who are asked to provide minimally identifying information (e.g. initials of last name and full first name, last four digits of cell number, gender, or any other sufficiently detailed information) on a given number of friends and acquaintances who are members of their social network. Seeds are then asked to nominate and refer a subset of their alters who are invited to participate in the study, and so on and so forth until the desire sample size is reached. Typically respondents are given space to nominate their alters with the following question wording: "a person whose name you know and he or she know your and you might stop and talk at least for a moment with if you ran into them on the street." This type of question is referred to in the literature as a "name generator," which is a common and well-studied method of eliciting socially relevant peers with reasonably high levels of validity despite some biases

toward nominating peers who respondents interact with more frequently (Campbell and Lee 1991; Marsden 1993; Straights 2000; Marin 2004). Minimally identifying information collected in this roster allows one to combine all nominated individuals in a single network and to enumerate people who were nominated by more than one respondent. As the sample progresses, this reconstructed network increasingly resembles the true social network linking members of the target population. To accelerate this process, NSM uses the revealed network at each step and a sampling algorithm to direct the recruitment process to spread through the underlying network by placing higher sampling probability on nodes in the network who have been nominated less frequently by previously sampled respondents. This sampling process is aided by two sampling modes: "search" and "list."

The "search" mode uses the global nomination data in the network to look for bridge nodes to areas of the network that are currently hidden or underexplored. A bridge node is a respondent who has a statistically anomalous number of nominated friends who have not been nominated by anyone else in the sample (Mouw and Verdery 2012). The search mode prioritizes sampling the unsampled friends of bridge nodes, which forces the sampling algorithm to the frontier of the currently revealed network and speeds the process of exploration. As a result, in contrast to the RDS sampling process which oversamples network clusters or may terminate easily when the network is sparse, NSM's search mode avoids sampling in clusters of the network where there have already been multiple interviews and is able to recruit samples over sparse networks, thereby making it an appropriate technique to sample various types of rare and hidden populations with different types of networks.

In contrast to the search mode, the "list" mode samples with replacement from the current list of everyone who has been nominated in the survey. The benefit of the list mode is its simplicity: as the survey progresses, the list of all individuals who have been nominated in the survey approaches the sampling frame of all members of the connected component of the target population, and the list mode gradually becomes equivalent to a simple random sample from a pre-defined sampling frame. NSM starts in search mode but switches to the list mode once the network has been explored, that is once a specified percentage of the nominated individuals have been nominated more than once, an indicator of the degree to which the initial phase of network exploration has been completed. The NSM sampling algorithm places higher sampling probabilities on people who have been nominated less frequently by previously sampled respondents, increasing the chance of discovering unknown sections of the network.

Mouw and Verdery (2012) used computer-assisted simulated sampling in a large sample of 162 known school and university social networks from Add Health and Facebook to show that NSM results in a 98.5% reduction in design effects relative to RDS, along with asymptotically unbiased population estimates. Smaller design effects imply that researchers can achieve the same or better statistical precision (and, consequently, narrower confidence intervals) using NSM on the basis of smaller samples than would be required for RDS, i.e., with NSM they need only collect samples in the hundreds rather than in the thousands to obtain precise and accurate estimates (Mouw and Verdery 2012). However, while simulated sampling is useful to test the

statistical properties of the NSM sampling algorithm relative to simple random sampling, less is known about how this approach performs in the field.

#### The Chinese Immigrants in the Raleigh Durham Area Study (ChIRDU)

The ChIRDU study was launched in early March 2018. Using NSM procedures we are recruiting three samples of respondents born in China, Taiwan and Hong Kong-born age 18+ who are resident in the Raleigh Durham (RDU) Area of North Carolina. Respondents are recruited via three different interview modes (in person, telephone and web). The in person and telephone modes were launched first, followed by the web component which was launched in June 2018. To date, the sample size of 200 for each of the interview modes is close to target for the inperson and telephone mode components. We are now at 381 completed interviews and we expect to reach 400 in the next 7-10 days. The web component is progressing more slowly with an expected closing date by year-end. The overall response rate for the in person and telephone components is quite high. Since its launch in early March, the ChIRDU response rate for inperson and telephone interviews is 70%, computed as I/(I+R+NR) where I is completed interview, R is known refusal and NR is Non-Respondent as per AAPOR (2016). Although finding a few good comparators for our population sample is difficult, and despite heightened concerns of confidentiality and data access related to migration affecting the current survey climate in the United States, a response rate of 70% for the in-person and telephone interviews is high. This rate compares well with the 69.2% response rate reached by the 2014 nationally representative General Social Survey (which only included those able to take the survey in English or Spanish) and a rate of 68.6% in the 2003 New Immigrant Survey cohort of 12,500 newly admitted to legal permanent residence. The response rate for the web-component of our ChIRDU study to date is lower than that measured in the in-person and telephone components, at 50%, but it is higher than an average of 39.6% (SD=19.6%) across 49 studies that relied on 68 web-surveys (Cook, Heath and Thompson 2000).

As we demonstrated in a paper presented at the Population Association of America in Denver in May (Merli and Mouw, 2018), we believe responsiveness to our ChIRDU survey is due, at least in part, to our efforts to implement recruitment strategies that combine well known models of survey participation derived from social exchange theory (Dillman, Smyth and Christian 2014) and leverage salience theory (Groves, Singer and Corning 2000; Groves et al. 1992; Groves, Presser and Dipko 2004) with the peer referral element.

The ChIRDU in person and telephone survey began with the selection of seven seed respondents known to the researchers, stratified by socioeconomic status and geographic location of residence. Respondents who agree to participate are administered two questionnaires: the main questionnaire and a network roster questionnaire. The individual questionnaire permits the characterization of the population and their migration experience: individual demographic characteristics including family background and detailed educational history, migration history, immigration and citizenship status, job histories in the place of origin and the U.S. and perception of discriminations and quality of life in the U.S. The network roster questionnaire is

administered to all respondents after the main interview. Respondents are asked to nominate up to 6 alters defined as other Chinese-born individuals they know who reside in the Raleigh Durham area using the name generator discussed in the prior section. After nominations are elicited, respondents are asked to provide the initial of the last name and full first name (Chinese and English first names) of the nominated alter, as well as the basic demographic information (gender, age, education attainment, and province origin in China) of each of their nominated alters. As explained above, this minimally identified information allows us to combine all nominated individuals into a single network and to identify individuals nominated by more than one respondent.

To illustrate the power of NSM to recruit a sample of respondents and their nominations, the graph below displays the current network generated by 381 respondents to in person and phone interviews and their 1,731 nominations. This suggests an average of 4.5 nominations per respondent, a number that is quite close to the 6 nominations sought per respondent. Most respondents and their nominations (the nodes in the graph) are member of a very large connected components with only a few small isolated clusters.

Although there are a number of benefits of our NSM-generated network data to analyze networkrelated social processes associated with labor market and network-based measures of immigrant social incorporation, the goal of the present paper is to evaluate the performance of NSM in the field and its ability to generate population-representative samples of rare and hard to survey populations.



#### **Planned Data Analyses**

We first plan to examine whether each of the samples recruited with different modes matches the demographic characteristics of the Chinese-born sample in the ACS pooled across multiple years to obtain robust results. The geographic coverage restriction of the survey to the three counties (Orange, Durham, Wake counties) that comprise the core of the Raleigh-Durham metropolitan area of North Carolina enables the comparison with a geographically comparable population from the 2013-2016 ACS which has an estimated population size for the three counties of 39,400. This comparison will focus on three demographic characteristics: the proportion female, the proportion with more than a high school education and the proportion age 60 and older.

These observed proportions in the ACS are 0.53, 0.75, and 0.17, respectively. The Research Triangle Area of North Carolina is the home of three major universities, two of which with large university health systems, high-tech companies and enterprises. Chinese immigrants provide an ideal population to evaluate the accuracy of NSM in the field because while they are a small proportion of the total population (0.77% of the total U.S. population and 0.65% of the population of the NC counties studied), it is believed that they represent a much smaller share of the unauthorized immigrant population compared to other immigrant groups (Hoefer et al. 2011) and that they are sufficiently well sampled in the ACS data for the RDU metro area that we can compare the NSM results to the ACS. Since our goal is to evaluate the performance of NSM against the ACS and since the ACS may undercount undocumented migrants, we have chosen a population for comparison where this is likely less of an issue.

For each mode of our survey, we will test whether the sampled proportion for each of these three characteristics is equal to the proportion in ACS data and the other two survey modes using a sample proportion z-test. Our analysis is powered to detect moderate differences in proportions with 80% power and an alpha of 0.05 for each of these three characteristics. For the comparison between the ACS and each individual sampling mode from our survey, we will need a minimum of 94 cases for each survey mode, and the corresponding analysis for each of these characteristics between pairs of survey modes requires at least 172 cases for each mode. The identification of areas of non-overlap between the NSM and the ACS samples for each survey mode will inform the selection of an optimal single mode or a mixed-mode approach that maximizes coverage of the population under study.

To identify factors that affect the ability of NSM to generate large-scale immigrant samples with minimum cost and maximum response rates, we will compare response rates to each survey mode, record the characteristics of those who responded to each mode (for the web mode we will record the characteristics of respondents who access the survey on a browser or on a smartphone platform), compare features unique to NSM (e.g. number of friends listed in the network roster, willingness to provide nominations and to refer new respondents with full contact information), costs per valid survey across the three survey modes, duration of implementation, as well as each mode's geographic reach based on respondents' zip codes. This, together with respondents' reported reasons for failing to provide contact information or to refer their friends will determine strengths, limitations and cost effectiveness of each survey mode. In particular, we will test whether the response rates differ between modes of the survey using two-sample proportion ztests (Test 1), and whether the mean number of network members nominated differs between modes using a comparison of means t-test (Test 2). In addition, we will take advantage of a unique feature of NSM data: survey respondents report on the characteristics of non-respondents they nominate to be in the survey. We will use this information to test a multivariate model of response likelihoods as a function of the survey mode and individual characteristics (age, gender, and education of the respondent or non-respondent) fitting Logit models to the pooled data for the entire survey (Test 3). This will allow us to compare which individual characteristics (gender, age, education) are most strongly associated with response vs. non-response in each of the survey modes which can inform a strategy to minimize non-sampling errors in our target population and in other populations with different distributions of observed characteristics. We report the minimum sample size required to achieve 80% power with an alpha of 0.05 for both Tests 1 and 2. For Test 1, in order to detect moderate differences in response rates between all pairs of

survey modes, we would need at least 170 cases for each survey mode. For Test 2, in order to detect a difference in the mean number of network members nominated between survey modes of more than 2, we would need at least 64 cases per survey mode. This calculation is based on conservative estimates of the mean and standard deviation of the number of network members nominated ( $\mu$ = 6, s.d.=4) from previous experience collecting network data from an immigrant population (Mouw, Chavez et al 2014).

### Weighting schemes

For the comparison of the population characteristics of the NSM sample with those estimated from ACS, we will use and compare the following schemes to construct sampling weights and adjust NSM sample proportions.

Mouw and Verdery (2012) showed that the average of the mean estimates from NSM samples across repeated simulated samples converge to the population mean (i.e. it is unbiased) when the revealed network size converges with the size of the population social network estimated with a capture-recapture approach, a method for estimating population size based on network data (e.g. Dombrowski et al. 2012). To reduce potential biases due to seed dependence and other biases arising from an incompletely revealed network and to correct biases towards sampling popular individuals, we will leverage the unique data collected in NSM to construct bootstrap sampling weights that we will use to re-weight cases. Weights for each respondent will be constructed based on the number of times he or she was sampled in simulated NSM sampling chains running over synthetic population social networks using a procedure similar to that proposed by Gile and Handcock (2015) which relies on an ERGM model run on the empirical network data to predict the ties between nominated but unsampled nodes. These sampling weights have been shown to reduce potential biases due to small sample sizes (Mouw, Merli and Verdery 2014) but to have little impact on the design effect (Mouw and Verdery 2012).

An alternative method for calculating sampling weights from link-tracing samples was proposed by Thompson (2018). This approach uses the sampling design to repeatedly draw samples from the network that was collected as a result of the link-tracing survey. It is simpler than the procedure proposed by Gile and Handcock (2015) because it relies on the observed structure of the network and doesn't use a statistical model to predict the ties between individuals in the network who were nominated in the survey but not sampled. To implement this approach, we will use the network composed of all sampled individuals as well as all unsampled individuals who were nominated by at least two respondents. To construct the sampling weights, we will draw 500 bootstrap samples starting with the initial seeds, and we will use the proportion of times an individual case was sampled (out of 500) as an inverse probability weight. Thus, seeds will have a weight of 1 (they are always sampled), and cases that are on the edge of the known network will have a higher weight (because they will not be sampled in all of the bootstrap samples).

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