

RESEARCH ARTICLE

One-step estimation of networked population size: Respondent-driven capture-recapture with anonymity

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Abstract

Size estimation is particularly important for populations whose members experience disproportionate health issues or pose elevated health risks to the ambient social structures in which they are embedded. Efforts to derive size estimates are often frustrated when the population is hidden or hard-to-reach in ways that preclude conventional survey strategies, as is the case when social stigma is associated with group membership or when group members are involved in illegal activities. This paper extends prior research on the problem of network population size estimation, building on established survey/sampling methodologies commonly used with hard-to-reach groups. Three novel one-step, network-based population size estimators are presented, for use in the context of uniform random sampling, respondent-driven sampling, and when networks exhibit significant clustering effects. We give provably sufficient conditions for the consistency of these estimators in large configuration networks. Simulation experiments across a wide range of synthetic network topologies validate the performance of the estimators, which also perform well on a real-world location-based social networking data set with significant clustering. Finally, the proposed schemes are extended to allow them to be used in settings where participant anonymity is required. Systematic experiments show favorable tradeoffs between anonymity guarantees and estimator performance. Taken together, we demonstrate that reasonable population size estimates are derived from anonymous respondent driven samples of 250-750 individuals, within ambient populations of 5,000-40,000. The method thus represents a novel and cost-effective means for health planners and those agencies concerned with health and disease surveillance to estimate the size of hidden populations. We discuss limitations and future work in the concluding section.

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Data Availability Statement: All Java software developed and used is available at <https://github.com/grouptheory/telefunken-support/tree/master/java>. All R software developed and used is available at <https://github.com/grouptheory/telefunkensupport/tree/master/R-v1>. All data inputs and outputs are available at https://github.com/grouptheory/telefunken-support/tree/master/figures_and_data.

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1 Introduction

Estimating the size of hidden and hard-to-reach populations is of critical importance to health officials seeking to mitigate the extent of health problems that may be concentrated within such populations [1], or when “reservoirs” of infection among a hidden population pose a

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