Using SQUEAC to assess the coverage of MAM and SAM treatment programs

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Background

The World Food Programme (WFP) and their implementing partners are showing considerable interest in assessing the coverage of therapeutic supplementary feeding programs (TSFP). These programs typically target children aged between 6 and 59 months with moderate acute malnutrition (MAM).

In response to requests from the WFP and their partners, the Coverage Monitoring Network (CNM) included TSFP coverage assessments in a handful of SQUEAC assessments. These SQUEAC assessments investigated coverage in both therapeutic feeding programs treating severe acute malnutrition (SAM) and TSFP programs treating MAM.

This report outlines the challenges faced, adaptations made, and experiences gained when using the SQUEAC coverage assessment methodology to assess program coverage for both SAM and MAM programming and is based upon work done in Kenya and South Sudan.

Methodological challenges and adaptations

The SQUEAC coverage assessment methodology was designed to assess coverage of programs treating SAM. A number of challenges were encountered at each stage of the SQUEAC investigations. These challenges and the adaptations made are shown in *Table 1*, *Table 2*, and *Table 3*.

Conclusions

SQUEAC can be used to simultaneously assess the coverage of both OTP and TSFP programs.

Table 1 : Challenges and adaptations to SQUEAC stage I

Activity	Methodological challenge	Adaptations
Collecting and analysing quantitative data	Routine program monitoring data proved difficult to get unless WFP was actively involved in program monitoring activities.	Sample from TSFP registers. The sample can be restricted to a small number of TSFP sites. Purposive selection (e.g. by area) of sites to be be sampled may be useful.

If beneficiary numbers are large then the collection or individual data could be restricted to recent admission and exits. A full year is the minimum period required to detect seasonality in admissions. Data on exits may be limited to (e.g.) the previous three months. Note that exits data may underestimate the number of defaults and deaths and overestimate the number cured. |
| | TSFP registers may not record important data such as home locations or distances from program site. | Location / distance data may be collected by questioning carers directly. An exhaustive or systematic sample (e.g. every fifth beneficiary) can be taken. Care needs to be taken to avoid introducing a sampling bias when (e.g.) beneficiaries from the same community or from sets of geographically close communities arrive together at sites at different times of day. |
| Collecting and analysing qualitative data | Separate programs may have different problems with regard to achieving and maintaining coverage. | Data should collected and analysed separately for each program.

If the SAM and MAM treatment programs are fully integrated (i.e. run by the same agency at the same sites) then data can be collected by the same staff on the same day but should still be recorded and analysed separately.

If the SAM and MAM treatment programs are **not** fully integrated then data will need to be collected separately for each program. This adds a data collection overhead that should be accounted for when planning the SQUEAC coverage assessment.

In the pilot studies reported here the barriers-boosters-questions (BBQ) analysis tended to be similar for the MAM and SAM programs operating in the same communities but this should **not** be assumed. Separate BBQ analyses should be maintained for each program and only merged for reporting purposed if they are similar to each other (differences should be reported). |
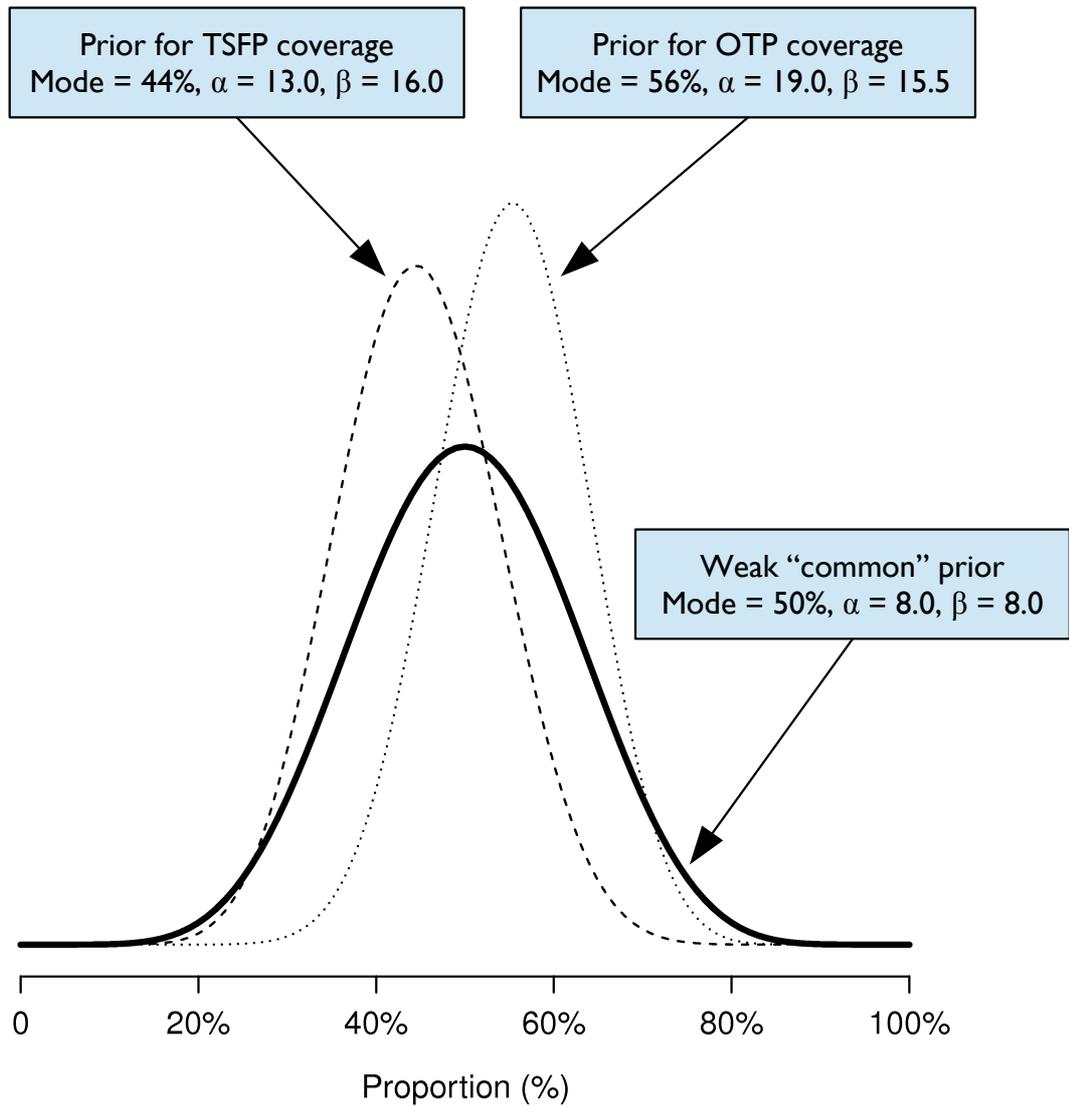
Table 2 : Challenges and adaptations to SQUEAC stage II

Activity	Methodological challenge	Adaptations
Hypothesis generation	Spatial (distance) hypotheses relating to coverage require spatial data which may not be available from TSFP reports and TSFP registers.	Data can be collected from a sample of program beneficiaries (see *Table 1*). An alternative approach it to undertake a series of small area surveys in villages with each study located at different distances from program sites.
	Data from TSFP reports and registers may be insufficient (or badly recorded) to support hypothesis generation.	Data on (e.g.) defaulting can be collected using qualitative techniques and / or small studies can be undertaken. It should be noted that data on barriers to access and coverage are collected in Stage I (qualitative data) and using the Stage III questionnaire that is applied to non-covered cases. This data is often sufficient to identify major barriers and inform sensible program reforms.
Case-finding	Some targeted supplementary feeding programs use complex case-definitions that include targeting criteria that are not easily observed or replicated (e.g. households in poverty identified by village leaders). This is unlikely to be the case with TSFP.	It is probably best not to try to assess the coverage of these types of programs using a routine SQUEAC assessment. A dedicated investigation is required.
	Active and adaptive case-finding procedures may not work well when used to find MAM cases.	Use house-to-house and door-to-door sampling. In small communities this should be an exhaustive sample of the whole community. In larger communities an exhaustive sample of a number of segments or blocks in the community (selected either randomly or systematically) may be used.

Table 3 : Challenges and adaptations to SQUEAC stage III

Activity	Methodological challenge	Adaptations
Setting priors	Coverage may differ between programs.	A single prior is unlikely to be appropriate for both programs. Separate priors should be developed for each program. MAM is a relatively common condition (i.e. compared to SAM). This means MAM cases should be easy to find and a "non-informative" prior (i.e. a prior with $\alpha_{Prior} = 1$ and $\beta_{Prior} = 1$) may be used for TSFP coverage. If the two coverages are unlikely to be **very** different from each other then a common weak prior (i.e. a prior with small values of α_{Prior} and β_{Prior}) may be used. The mode of the weak prior would be the average of the prior mode for the SAM program and the prior mode for the MAM program. An example of specifying a weak prior is shown in *Figure 1*. It will usually be more efficient to use separate priors for each program.
	Available data may not be sufficient to define a meaningful prior for TSFP coverage.	Use a non-informative prior (i.e. a prior with $\alpha_{Prior} = 1$ and $\beta_{Prior} = 1$).
Case-finding	Active and adaptive case-finding procedures may not work well when used to find MAM cases.	Use house-to-house and door-to-door sampling. In small communities this should be an exhaustive sample of the whole community. In larger communities an exhaustive sample of a number of segments or blocks in the community (selected either randomly or systematically) may be used.
	House-to-house and door-to-door sampling is expensive and time consuming.	MAM is a relatively common condition (i.e. compared to SAM). This means MAM cases may be easy to find and that you will need to sample fewer communities to collect the required sample of MAM cases. Care needs to be taken to maintain the spatial stratification of the MAM sample. *Figure 2* and *Figure 3* show examples of how this may be done. Both the SAM and MAM sample should be collected using house-to-house and door-to-door sampling in the villages where the MAM sample is taken. The number of villages to sample for MAM cases should be informed by the required sample size which can be calculated from the formulas given in the SQUEAC / SLEAC technical reference or with the `BayesSQUEAC` calculator (see *Box 1*)

Figure 1 : A weak common prior

Prior for TSFP coverage
Mode = 44%, α = 13.0, β = 16.0

Prior for OTP coverage
Mode = 56%, α = 19.0, β = 15.5

Weak "common" prior
Mode = 50%, α = 8.0, β = 8.0

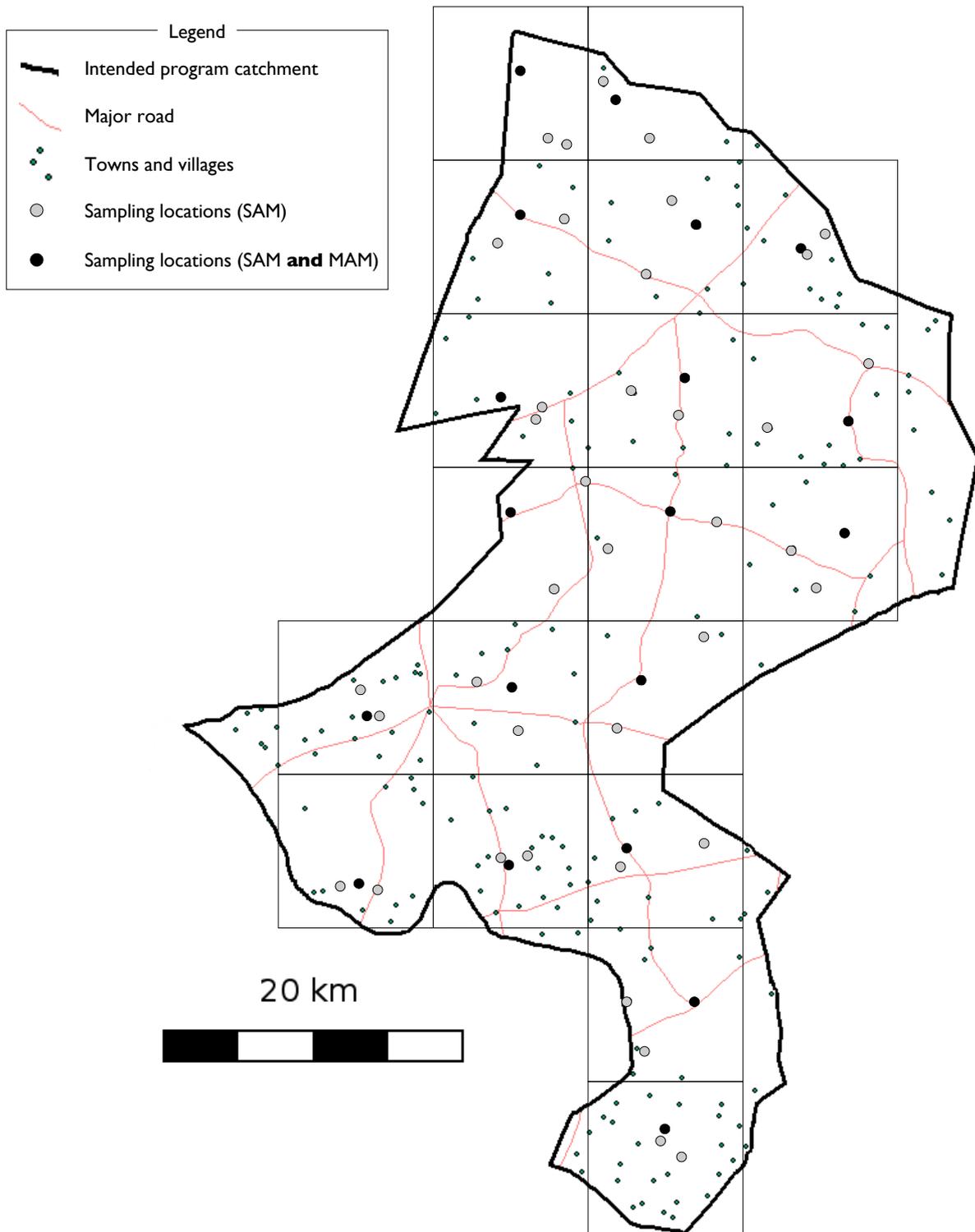Proportion (%)

0   20%   40%   60%   80%   100%

A *rule-of-thumb* for the weak common prior is that the sum of the α and β terms of the weak common prior should be about one quarter of the sum of the α and β terms of both individual priors:

$$\alpha_{Common} + \beta_{Common} \approx \frac{\alpha_{TSFP} + \beta_{TSFP} + \alpha_{OTP} + \beta_{OTP}}{4}$$

In this example:

$$8.0 + 8.0 \approx \frac{13.0 + 16.0 + 19.0 + 15.5}{4} \equiv 16 \approx \frac{63.5}{4}$$

**Figure 2 :** MAM and SAM samples using CSAS sampling

Sampling locations (villages) for the sample were selected using the CSAS methodology. The three villages located closest to the centre of each quadrat were selected.

The village closet to the centre of each quadrat was then selected for the combined SAM **and** MAM sample.

Note that both the SAM and the MAM sample are reasonably evenly spread over the entire survey area.

Figure 3 : MAM and SAM sample using spatially stratified systematic sampling
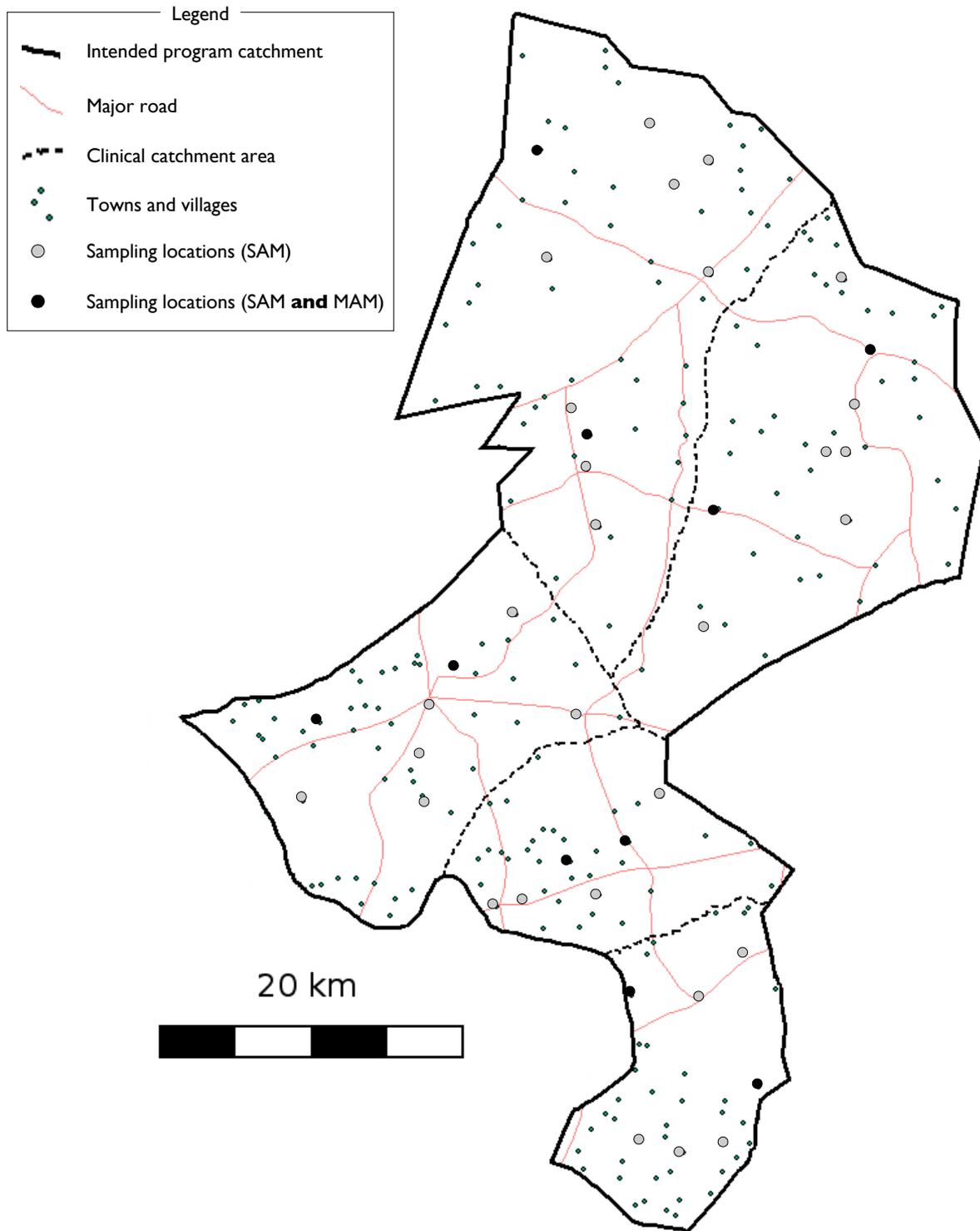
Sampling locations (villages) for the sample were selected systematically from a complete list of villages sorted by clinic catchment area. This method can be performed using village lists and does **not** require a map.

Two villages were then selected at random from each of the clinic catchment areas from amongst those already selected. These villages were used for the combined SAM **and** MAM sample.

Note that both the SAM and the MAM sample are reasonably evenly spread over the entire survey area.

Box 1 : Calculating sample sizes for SAM and MAM cases

The following data were used to calculate required sample sizes for SAM and MAM cases :

Parameter		SAM	MAM
Prior probability density for coverage proportion	mode	70%	55%
	α_{Prior}	20.5	19.1
	α_{Prior}	8.8	15.6
Prevalence		3.5%	12.6%
Average village population		278	
Proportion aged between 6 and 59 months		21%	
Desired precision of coverage estimate		± 10%	

The sample size required for estimating coverage of the SAM program was calculated as :

$$n_{Likelihood} = \left\lceil \frac{mode \times (1 - mode)}{(precision \div 1.96)^2} - (\alpha_{Prior} + \beta_{Prior} - 2) \right\rceil$$

$$n_{Likelihood} = \left\lceil \frac{0.7 \times (1 - 0.7)}{(0.1 \div 1.96)^2} - (20.5 + 8.8 - 2) \right\rceil = 54$$

to be collected from:

$$n_{villages} = \left\lceil \frac{n}{average\ block\ population_{all\ ages} \times \frac{percentage\ of\ population_{6-59\ months}}{100} \times \frac{SAM\ prevalence}{100}} \right\rceil$$

$$n_{villages} = \left\lceil \frac{54}{278 \times \frac{21}{100} \times \frac{3.5}{100}} \right\rceil = 27\ villages$$

The sample size required for estimating coverage of the MAM program was calculated as :

$$n_{Likelihood} = \left\lceil \frac{0.55 \times (1 - 0.55)}{(0.1 \div 1.96)^2} - (19.1 + 15.6 - 2) \right\rceil = 63$$

to be collected from:

$$n_{villages} = \left\lceil \frac{63}{278 \times \frac{21}{100} \times \frac{12.6}{100}} \right\rceil = 9\ villages$$

The SAM sample could (e.g.) be collected using a CSAS sample of three villages sampled from each of nine quadrats (i.e. $n_{villages} = 27$) and the MAM sample collected using the same CSAS sample but with only a single villages sampled from each of the nine quadrats (i.e. $N_{villages} = 9$).