Malaria Molecular Surveillance Study Design Workshop

Module 1: Sampling from a population

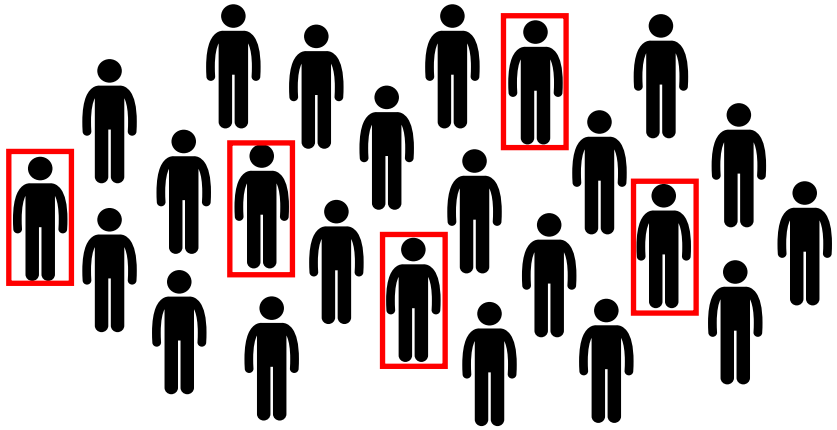
Prevalence estimation

We often want to estimate prevalence of:

- Drug resistance mutations
- Diagnostic resistance mutations
- etc…

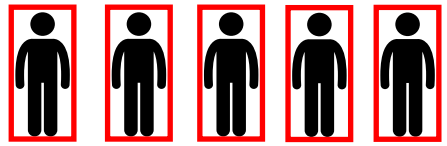
We can’t test everyone, we need to ***sample*** the population

What is a “population”?



Population

The complete pool of people we are interested in

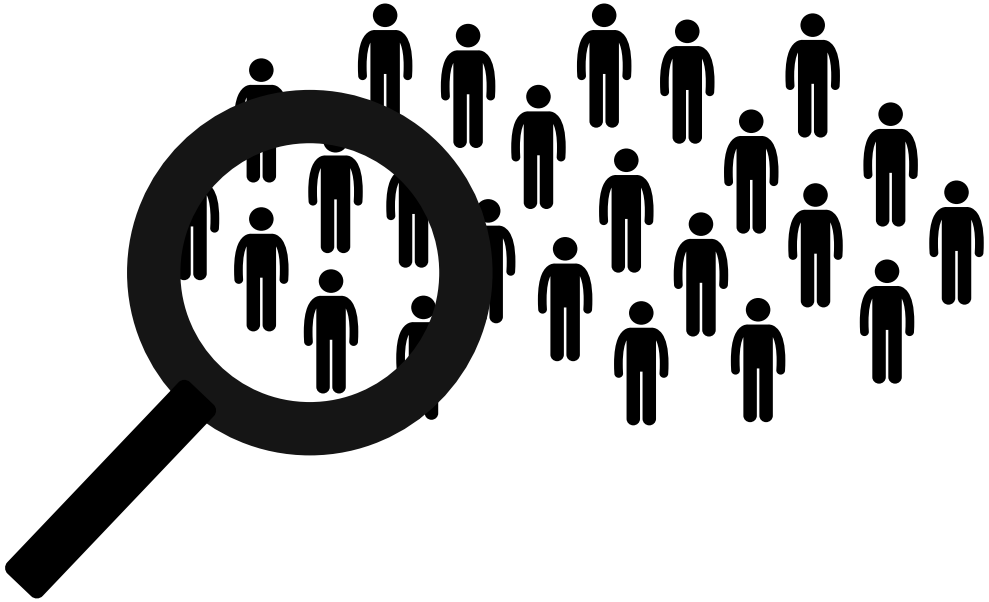


Sample

A subset of people that we use to draw conclusions about the population

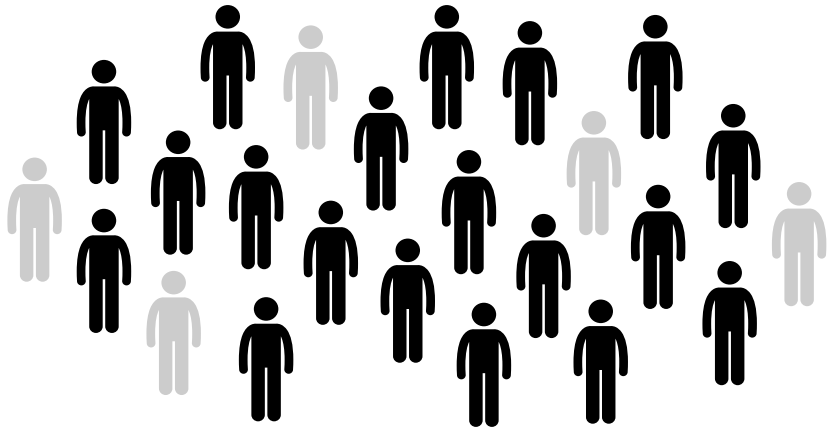
What is the target population?

Target population = sub-group of the population that is the focus of research interest



External validity = how generalizable are our results

What is the accessible population?



Accessible population

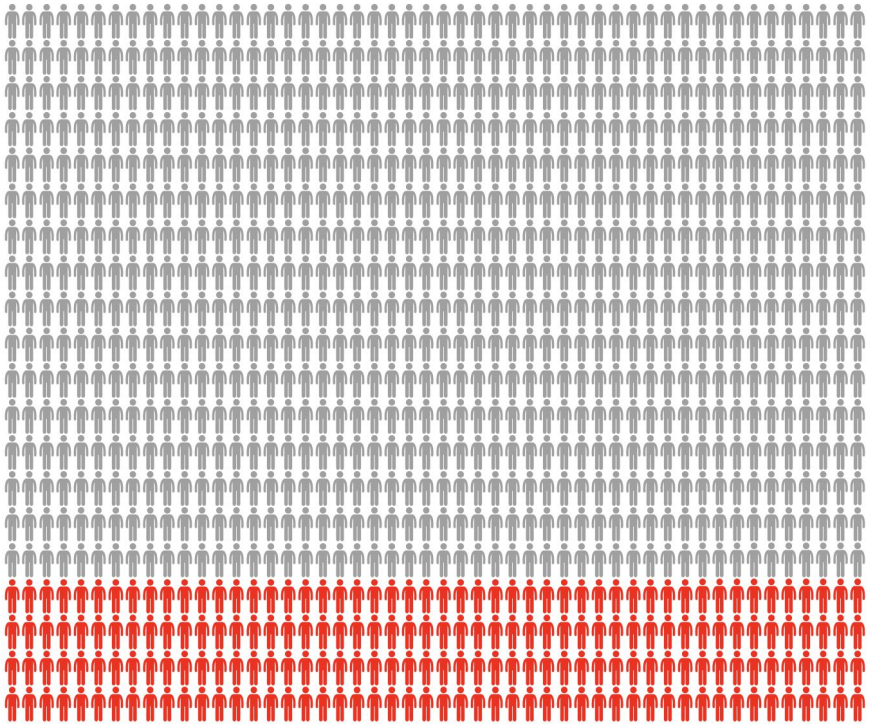
The portion of the target population to which you have reasonable access

Sampling variation and uncertainty

MRC Centre for Global Infectious Disease Analysis
IMPERIAL

Population size: 1000

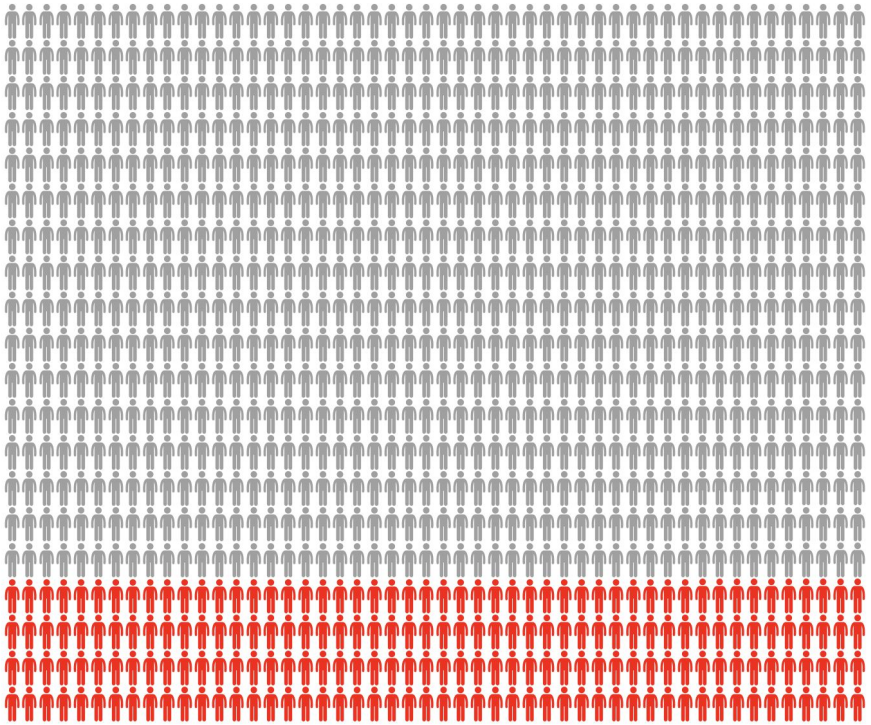
Population prevalence: 20%



Sampling variation and uncertainty

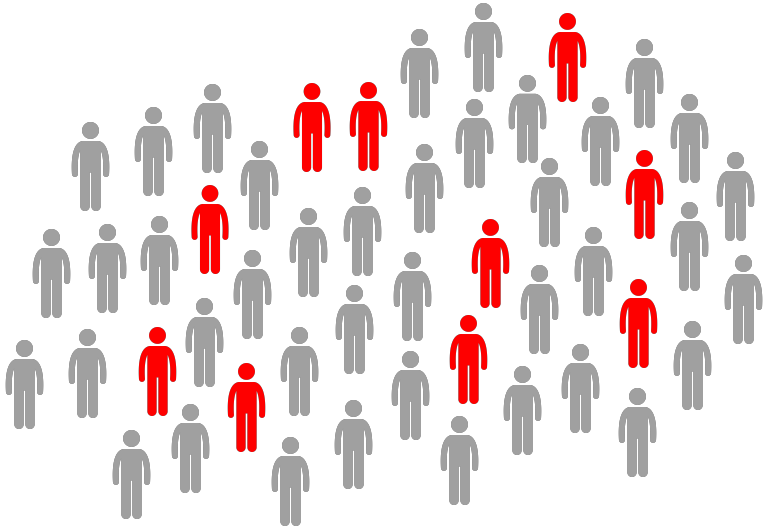
Population size: 1000

Population prevalence: 20%



Sample size: 50

Sample prevalence: 20%

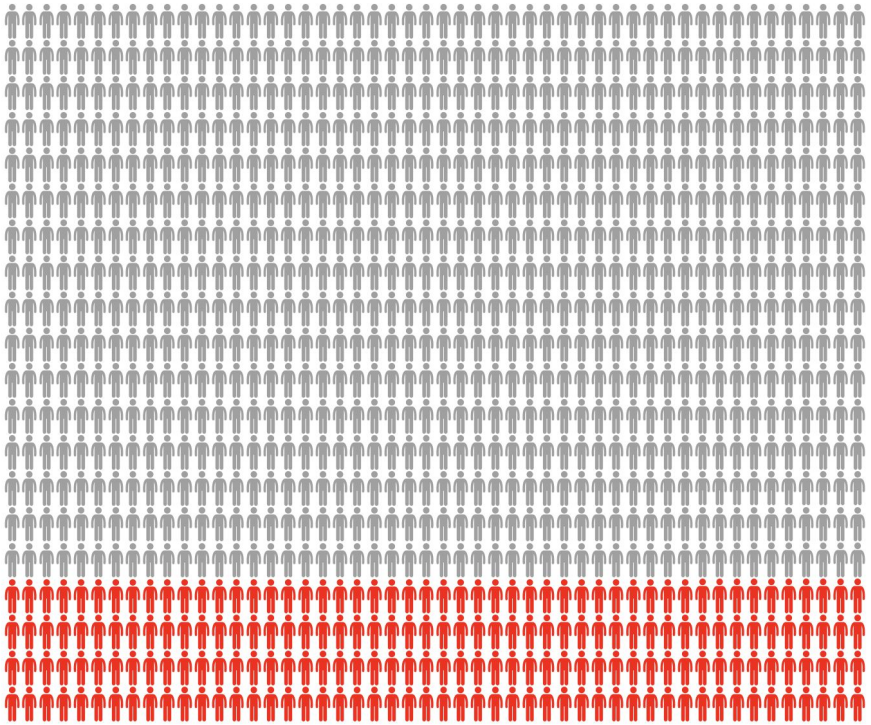


Sampling variation and uncertainty

MRC Centre for Global Infectious Disease Analysis
IMPERIAL

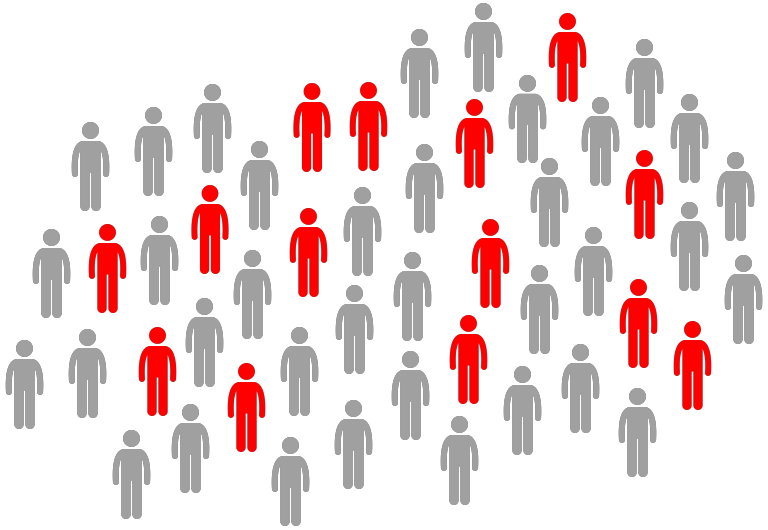
Population size: 1000

Population prevalence: 20%



Sample size: 50

Sample prevalence: 28%

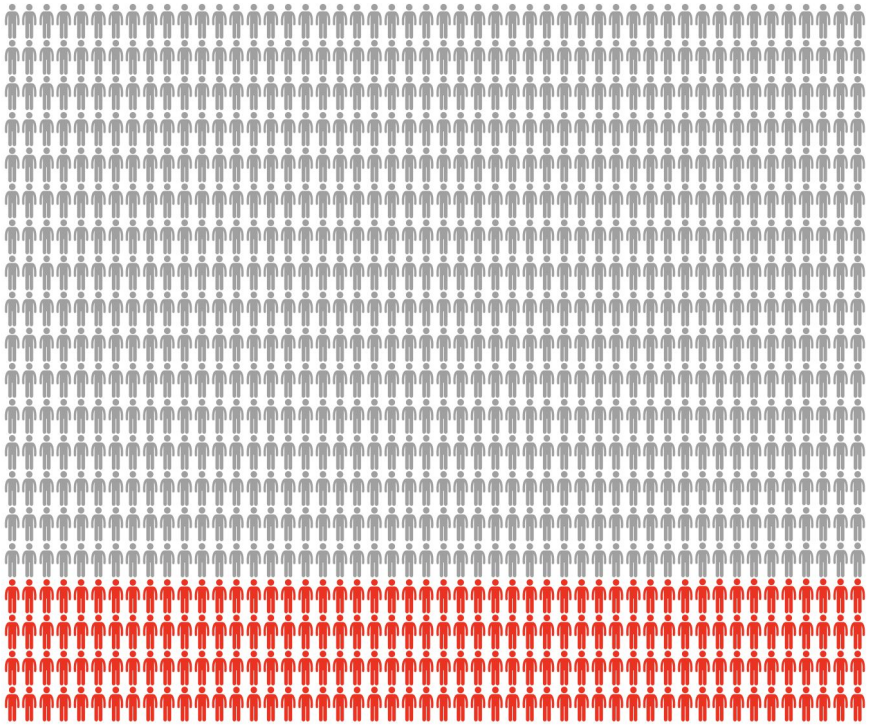


Sampling variation and uncertainty

MRC Centre for Global Infectious Disease Analysis IMPERIAL

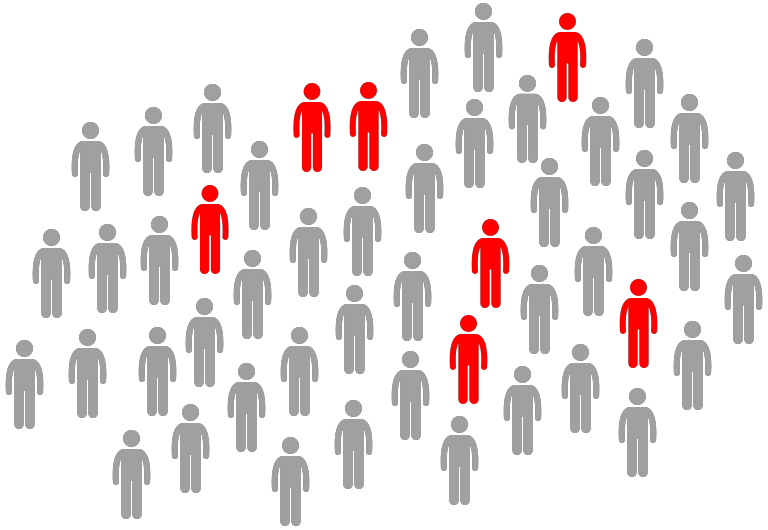
Population size: 1000

Population prevalence: 20%



Sample size: 50

Sample prevalence: 14%



Example.

Estimating the prevalence of SP drug resistance mutations

Population — All individuals in the region

Target population — Children under 6 years old in the region

Accessible population — Children visiting health facilities for routine vaccination

Hypothetical study results

We conducted our study and found **8 out of 50 children** with the SP mutation

What is the prevalence?

Hypothetical study results

We conducted our study and found **8 out of 50 children** with the SP mutation

What is the prevalence?

Number observed / sample size = **8 / 50**

Hypothetical study results

We conducted our study and found **8 out of 50 children** with the SP mutation

What is the prevalence?

Number observed / sample size = **8 / 50**

This is a point estimate. But, how *confident* are we in this estimate?

The Wald confidence interval

$$CI = \hat{p} \pm z_{1-\alpha/2} \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$$

Point estimate

$$CI = \hat{p} \pm z_{1-\alpha/2} \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$$

Point estimate = **8/50 = 0.16**

Critical *Z* value

$$CI = \hat{p} \pm z_{1-\alpha/2} \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$$

Alpha (α) = 0.05 (95% confidence)

1-(α/2) = **0.975** -> corresponds to ***Z = 1.96***

Critical *Z* value

$$CI = \hat{p} \pm \boxed{1.96} \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$$

Standard error

$$CI = \hat{p} \pm 1.96 \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$$

Putting it all together

$$CI = \overline{0.16} \pm 1.96 \sqrt{\frac{\overline{0.16}(1 - \overline{0.16})}{50}}$$

$$0.16 \pm 0.10$$

or

16% ± 10%

Summary

- We sample the population to **draw conclusions** about the population as a whole
  - *E.g. what is the prevalence of pfdhps K540E?*

- We can use the **Wald confidence interval** to calculate our 95% Confidence Interval (uncertainty around our point estimate)

Any questions?

Module 1 activity

Format: Interactive R code, accessed through the web

- Define target population
- Differentiate between population and sample
- Calculate the 95% CI
- Explore sampling variability
- Understand effect of sample size on CIs

Workshop materials

https://mrc-ide.github.io/MMS-SD_workshop/